

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: May 14, 2004, 00:22:53 ; Search time 10175.3 Seconds  
(without alignments)  
12622.391 Million cell updates/sec

Title: US-09-931-157-2  
Perfect score: 4301  
Sequence: 1 gagacattccggtgggggac.....ctgggaaaaaaaaaaaaaa 4301

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : EST:\*  
1: em\_estba:\*  
2: em\_esthum:\*  
3: em\_estin:\*  
4: em\_estmu:\*  
5: em\_estov:\*  
6: em\_estpl:\*  
7: em\_estro:\*  
8: em\_htc:\*  
9: gb\_est1:\*  
10: gb\_est2:\*  
11: gb\_htc:\*  
12: gb\_est3:\*  
13: gb\_est4:\*  
14: gb\_est5:\*  
15: em\_estfun:\*  
16: em\_estom:\*  
17: em\_gss\_hum:\*  
18: em\_gss\_inv:\*  
19: em\_gss\_pln:\*  
20: em\_gss\_vrt:\*  
21: em\_gss\_fun:\*  
22: em\_gss\_mam:\*  
23: em\_gss\_mus:\*  
24: em\_gss\_pro:\*  
25: em\_gss\_rod:\*  
26: em\_gss\_phg:\*  
27: em\_gss\_vrl:\*

28: gb\_gss1:\*

29: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

| Result | %      |       | Query  |    | DB       |  | ID       | Description |
|--------|--------|-------|--------|----|----------|--|----------|-------------|
|        |        |       |        |    |          |  |          |             |
| No.    | Score  | Match | Length | DB | ID       |  |          |             |
| 1      | 1372.2 | 31.9  | 3878   | 11 | AK083415 |  | AK083415 | Mus muscu   |
| 2      | 1371.2 | 31.9  | 3990   | 11 | AK085532 |  | AK085532 | Mus muscu   |
| 3      | 1329   | 30.9  | 1329   | 29 | AY415512 |  | AY415512 | Homo sapi   |
| 4      | 1137.6 | 26.4  | 2521   | 11 | AK082103 |  | AK082103 | Mus muscu   |
| 5      | 1126.4 | 26.2  | 3611   | 11 | AK085165 |  | AK085165 | Mus muscu   |
| 6      | 1020   | 23.7  | 2669   | 11 | AK076426 |  | AK076426 | Mus muscu   |
| 7      | 996    | 23.2  | 1329   | 29 | AY415514 |  | AY415514 | Mus muscu   |
| c 8    | 987    | 22.9  | 1201   | 9  | AL571798 |  | AL571798 | AL571798    |
| 9      | 936.6  | 21.8  | 1144   | 29 | AY415513 |  | AY415513 | Pan trogl   |
| c 10   | 866    | 20.1  | 957    | 12 | BI520706 |  | BI520706 | 603071813   |
| c 11   | 860.2  | 20.0  | 1201   | 9  | AL553041 |  | AL553041 | AL553041    |
| 12     | 851    | 19.8  | 942    | 9  | AL543805 |  | AL543805 | AL543805    |
| 13     | 848    | 19.7  | 891    | 13 | BQ229233 |  | BQ229233 | AGENCOURT   |
| 14     | 816.2  | 19.0  | 1201   | 9  | AL546465 |  | AL546465 | AL546465    |
| 15     | 808.6  | 18.8  | 972    | 12 | BI858627 |  | BI858627 | 603389094   |
| c 16   | 802.4  | 18.7  | 942    | 9  | AL570142 |  | AL570142 | AL570142    |
| 17     | 794.8  | 18.5  | 884    | 13 | BU557315 |  | BU557315 | AGENCOURT   |
| 18     | 792    | 18.4  | 911    | 13 | BQ719386 |  | BQ719386 | AGENCOURT   |
| c 19   | 788    | 18.3  | 1201   | 9  | AL571072 |  | AL571072 | AL571072    |
| 20     | 773.6  | 18.0  | 852    | 13 | BU172663 |  | BU172663 | AGENCOURT   |
| 21     | 772    | 17.9  | 1201   | 9  | AL553065 |  | AL553065 | AL553065    |
| c 22   | 766.6  | 17.8  | 775    | 14 | CA771707 |  | CA771707 | io81f04.x   |
| 23     | 741.8  | 17.2  | 770    | 12 | BM014035 |  | BM014035 | 603639686   |
| c 24   | 740.2  | 17.2  | 942    | 13 | BX345882 |  | BX345882 | BX345882    |
| 25     | 738    | 17.2  | 999    | 13 | BX417121 |  | BX417121 | BX417121    |
| 26     | 736    | 17.1  | 1201   | 9  | AL545283 |  | AL545283 | AL545283    |
| 27     | 734.2  | 17.1  | 978    | 13 | BQ683643 |  | BQ683643 | AGENCOURT   |
| 28     | 732.8  | 17.0  | 1121   | 12 | BM926545 |  | BM926545 | AGENCOURT   |
| 29     | 729.2  | 17.0  | 758    | 12 | BM014042 |  | BM014042 | 603639695   |
| 30     | 727.8  | 16.9  | 885    | 12 | BG769122 |  | BG769122 | 602743382   |
| 31     | 718    | 16.7  | 785    | 9  | AU117045 |  | AU117045 | AU117045    |
| 32     | 712.8  | 16.6  | 743    | 9  | AU138228 |  | AU138228 | AU138228    |
| 33     | 708.8  | 16.5  | 961    | 12 | BM804821 |  | BM804821 | AGENCOURT   |
| c 34   | 706.2  | 16.4  | 800    | 9  | AI760041 |  | AI760041 | wg57e06.x   |
| 35     | 705    | 16.4  | 716    | 9  | AL699988 |  | AL699988 | DKFZp686K   |
| c 36   | 703    | 16.3  | 722    | 12 | BM970305 |  | BM970305 | UI-CF-EC1   |
| c 37   | 698.8  | 16.2  | 726    | 9  | AI422064 |  | AI422064 | tf57c12.x   |
| c 38   | 697.4  | 16.2  | 866    | 9  | AI188458 |  | AI188458 | qdl4d01.x   |
| 39     | 696.8  | 16.2  | 771    | 9  | AU116904 |  | AU116904 | AU116904    |
| 40     | 691.4  | 16.1  | 934    | 13 | BQ718019 |  | BQ718019 | AGENCOURT   |
| 41     | 686.4  | 16.0  | 839    | 9  | AU136164 |  | AU136164 | AU136164    |
| c 42   | 679.4  | 15.8  | 771    | 9  | AI567763 |  | AI567763 | tr62c07.x   |
| c 43   | 673    | 15.6  | 699    | 12 | BM974913 |  | BM974913 | UI-CF-EC1   |
| c 44   | 662.6  | 15.4  | 751    | 9  | AA651686 |  | AA651686 | nn47b02.r   |
| 45     | 661.6  | 15.4  | 941    | 13 | BX345883 |  | BX345883 | BX345883    |

## ALIGNMENTS

## RESULT 1

AK083415

LOCUS AK083415 3878 bp mRNA linear HTC 20-SEP-2003

DEFINITION Mus musculus 9 days embryo whole body cDNA, RIKEN full-length enriched library, clone:D030003K13 product:ENDOTHELIN B RECEPTOR PRECURSOR, full insert sequence.

ACCESSION AK083415

VERSION AK083415.1 GI:26350536

KEYWORDS HTC; CAP trapper.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

## REFERENCE 1

AUTHORS Carninci,P. and Hayashizaki,Y.

TITLE High-efficiency full-length cDNA cloning

JOURNAL Meth. Enzymol. 303, 19-44 (1999)

MEDLINE 99279253

PUBMED 10349636

## REFERENCE 2

AUTHORS Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.

TITLE Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes

JOURNAL Genome Res. 10 (10), 1617-1630 (2000)

MEDLINE 20499374

PUBMED 11042159

## REFERENCE 3

AUTHORS Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.

TITLE RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer

JOURNAL Genome Res. 10 (11), 1757-1771 (2000)

MEDLINE 20530913

PUBMED 11076861

## REFERENCE 4

AUTHORS The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.

TITLE Functional annotation of a full-length mouse cDNA collection

JOURNAL Nature 409, 685-690 (2001)

## REFERENCE 5

AUTHORS The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I &amp; II Team.

TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

JOURNAL Nature 420, 563-573 (2002)

## REFERENCE 6

(bases 1 to 3878)

AUTHORS Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W., Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T., Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T., Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M., Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N., Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N., Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S., Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A., Muramatsu,M. and Hayashizaki,Y.

TITLE Direct Submission

JOURNAL Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)

COMMENT cdNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. Please visit our web site for further details. URL:http://genome.gsc.riken.go.jp/ URL:http://fantom.gsc.riken.go.jp/.

FEATURES

source Location/Qualifiers

1. .3878

/organism="Mus musculus"

/mol\_type="mRNA"

/strain="C57BL/6J"

/db\_xref="FANTOM\_DB:D030003K13"

/db\_xref="MGI:2418502"

/db\_xref="taxon:10090"

/clone="D030003K13"

/tissue\_type="whole body"

/clone\_lib="RIKEN full-length enriched mouse cdNA library"

/dev\_stage="9 days embryo"

CDS

109. .1437

/note="unnamed protein product; ENDOTHELIN B RECEPTOR PRECURSOR (SWISSPROT|P48302, evidence: FASTY, 100%ID, 100%length, match=1326) putative"

/codon\_start=1

/protein\_id="BAC38908.1"

/db\_xref="GI:26350537"

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polyA\_signal

3859. .3864



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polyA_site                    3878
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ORIGIN

Query Match          31.9%;  Score 1372.2;  DB 11;  Length 3878;
Best Local Similarity 66.0%;  Pred. No. 8.1e-254;
Matches 2665;  Conservative 0;  Mismatches 1043;  Indels 327;  Gaps 34;

Qy      193  AAAGTGGGAGCGGCCACCGGACGCCTTCTGGAGCAGGTAGCAGCATGCAGCCGCTCCA 252
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Db      64  AAACAGCAGAGCGGCTACCAGACTCTCACAGGAGCAAGCTGTAACATGCAATCGCCGCA 123

Qy      253  AGTCTGTGCGGACGCGCCCTGGTTGCGCTGGTTCTTGCCTGCGGCCCTGTCGCGGATCTGG 312
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Qy      313  GGAGAGGAGAGAGGCTTCCCGCCTGCAGGGCCACTC---CGCTTTTGCAAACCGCAGAG 369
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Db      184  GGAGAGAAAAGAGGATTCCACCTGCCCAAGCCACGCTGTCACTTCTCGGGACTAAAGAG 243

Qy      370  ATAATGACGCCACCCACTAAGACCTTATGGCCCAAGGGTTCCAACGCCAGTCTGGCGCGG 429
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Qy      430  TCGTTGGCACCTGCGGAGGTGCCTAAAGGAGACAGGACGGCAGGATCTCCGCCACGCACC 489
          || | ||||| ||||| ||||| ||||| ||| ||| ||| ||||| | |
Db      304  TCCTCCGCACCTGCGGAGGTGACCAAAGGAGGGAGGGGGGCTGGAGTCCCGCCAAGATC- 362

Qy      490  ATCTCCCCCTCCCCCGTGCCAAGGACCCATCGAGATCAAGGAGACTTTCAAATACATCAAC 549
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Qy      550  ACGGTTGTGTCTCTGCCTTGTGTTTCGTGCTGGGGATCATCGGGAACCTCCACACTTCTGAGA 609
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Db      421  ACGATTGTGTCTCTGCCTCGTGTTCGTGCTAGGCATCATCGGGAACCTCCACGCTGCTAAGA 480

Qy      610  ATTATCTACAAGAACAAGTGCATGCGAAACGGTCCCAATATCTTGATCGCCAGCTTGGCT 669
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Qy      670  CTGGGAGACCTGCTGCACATCGTCATTGACATCCCTATCAATGTCTACAAGCTGCTGGCA 729
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Db      541  CTGGGAGACCTACTGCACATCATCATAGACATACCCATTAACACCTACAAGTTGCTCGCA 600

Qy      730  GAGGACTGGCCATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTCATACAGAAAGCCTCC 789
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Qy      790  GTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATATCGAGCTGTTGCT 849
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Db      661  GTGGGAATCACAGTGTGCTGAGTCTTTGTGCTCTAAGTATTGACAGATATCGAGCTGTTGCT 720

Qy      850  TCTTGGAGTAGAATTAAAGGAATTGGGGTTCCAAATGGACAGCAGTAGAAATTGTTTTG 909
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Db      721  TCTTGGAGTCGAATTAAAGGAATTGGGGTTCCAAATGGACAGCAGTAGAAATTGTTTTA 780

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|    |      |  |      |
|----|------|--|------|
| Qy | 910  | ATTTGGGTGGTCTCTGTGGTTCTGGCTGTCCCTGAAGCCATAGGTTTTGATATAATTACG   | 969  |
| Db | 781  | ATTTGGGTGGTCTCTGTGGTTCTGGCTGTCCCGAAGCCATAGGTTTTGATATGATTACG    | 840  |
| Qy | 970  | ATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTTCAGAAGACAGCT   | 1029 |
| Db | 841  | TCGGACTACAAAGGAAAGCCCCTAAGGGTCTGCATGCTTAATCCCTTTCAGAAAACAGCC   | 900  |
| Qy | 1030 | TTCATGCAGTTTTTACAAGACAGCAAAAGATTGGTGGCTGTTTCAGTTTCTATTTCTGCTTG | 1089 |
| Db | 901  | TTCATGCAGTTTTTACAAGACAGCCAAAGATTGGTGGCTGTTTCAGTTTCTACTTCTGCTTG | 960  |
| Qy | 1090 | CCATTGGCCATCACTGCATTTTTTTATACACTAATGACCTGTGAAATGTTGAGAAAGAAA   | 1149 |
| Db | 961  | CCGCTAGCCATCACTGCAGTCTTTTATACCTGATGACCTGCGAAATGCTCAGGAAGAAG    | 1020 |
| Qy | 1150 | AGTGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAAGTGCCAAAACC    | 1209 |
| Db | 1021 | AGCGGTATGCAGATTGCTTTGAATGATCACTTAAAGCAGAGACGAGAAGTGCCAAAGACA   | 1080 |
| Qy | 1210 | GTCTTTTGCCTGGTCTTGTCTTTGCCCTCTGCTGGCTTCCCCTTCACCTCAGCAGGATT    | 1269 |
| Db | 1081 | GTCTTCTGCCTGGTCTCTGTCTTGTCTGCTTGGCTTCCCCTTCACCTCAGCCGGATC      | 1140 |
| Qy | 1270 | CTGAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGAACTTTTGAGCTTTCTG   | 1329 |
| Db | 1141 | CTGAAGCTCACCTGTATGACCAGAGCAATCCACACAGGTGTGAGCTTCTGAGCTTTTTG    | 1200 |
| Qy | 1330 | TTGGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCTGCATTAACCCAATT    | 1389 |
| Db | 1201 | TTGGTTTTGGACTACATTGGTATCAACATGGCTTCTTTGAACTCCTGCATCAATCCAATC   | 1260 |
| Qy | 1390 | GCTCTGTATTTGGTGAGCAAAAGATTCAAAACTGCTTTAAGTCATGCTTATGCTGCTGG    | 1449 |
| Db | 1261 | GCTCTGTATTTGGTGAGCAAAAGATTCAAAACTGCTTTAAGTCATGTTTGTGCTGCTGG    | 1320 |
| Qy | 1450 | TGCCAGTCATTTGAAGAAAAACAGTCCTTGGAGGAAAAGCAGTCGTGCTTAAAGTTCAA    | 1509 |
| Db | 1321 | TGCCAAACGTTTGAGGAAAAGCAGTCCTTGGAGGAGAAGCAGTCCTGCCTGAAGTTCAA    | 1380 |
| Qy | 1510 | GCTAATGATCACGGATATGACAACCTCCGTTCCAGTAATAAATACAGCTCATCTTGAAAG   | 1569 |
| Db | 1381 | GCCAACGATCACGGATATGACAACCTCCGGTCCAGCAATAAATACAGCTCGTCTTGAAAG   | 1440 |
| Qy | 1570 | AAGAACTATTCACTGTATTTCAATTTCTTTATATTGGACCGAAGTCATTAAAACAAAATG   | 1629 |
| Db | 1441 | CAAGAACACTCGCCGAATCTCACTGTCCTCATTGTGGACAGATAACATTAAAACAAAATG   | 1500 |
| Qy | 1630 | AAACATTTGCCAAAACAAAACAAAAAATATGTATTTGCACAGCACACTATTAAAATATT    | 1689 |
| Db | 1501 | AAACCGTTGCCAAATCAAATGGAAAAAACCATGCTAGCAGAAAGGTGTGCGCGCGTGTG    | 1560 |
| Qy | 1690 | AAGTGTAATTATTTTAACACTCACAGCTACATATGAC-----ATTTTATGAGCTGTTTAC   | 1744 |
| Db | 1561 | AGAGGGATTATTTTTAACTGTTCTGACGCTCAACACCGGATATATTCACGGGCTGTTTAC   | 1620 |
| Qy | 1745 | GGCATGGAAAGAAAATCAGTGGGAATTAAGAAAGCCTCGTTCGTGAAAGCACTTAATTTTT  | 1800 |

|    |      |  |      |
|----|------|--|------|
| Db | 1621 | AACCTAAGAAAGCTGTGGGAAGGAATGAAGCCCTCCTCCGTGGGGAAGCACTTAGATTCT   | 1680 |
| Qy | 1805 | TACAGTTAGCACTTCAACATAGCTCTTAACAACCTCCAGGATATTCACACAACACTTAGG   | 1864 |
| Db | 1681 | T--AGTCAGCACTTCAGCAGAGCTCTTAAAGCCCCTAGTGC GTTCACATGCCACTTACG   | 1738 |
| Qy | 1865 | CTTAAAAATGAGCTCACTCAGAATTTCTATTCTTTCTAAAAAGAGATTTATTTTTAAATC   | 1924 |
| Db | 1739 | TTTAAAAA-----AACGAGAACTTCACTGAAGTTCTGTTCAGGAGTTTATTATCCAGT     | 1791 |
| Qy | 1925 | AATGGGACTCTGATATAAAGGAAGAATAAGTCACTGTAAACAGAACTTTTAAATGAAGC    | 1984 |
| Db | 1792 | CCTATGAATCTGGATTCAAGAAAGCAT--GACATTGCAAAACAATTCTTAAACGAAGTT    | 1849 |
| Qy | 1985 | TTAAATTACTCAATTTAAAAATTTTAAAAATCCTTTAAACAACCTTTTCAATTAATATTATC | 2044 |
| Db | 1850 | TCAATTGCTTAATTTGAAACTTAAAAAAAAAAAACTAATAAATTTTATGCATACTATC     | 1909 |
| Qy | 2045 | --ACACTATTATCAGATTGTAATTAGATGCAAAAGAGAGAGCAGTTTAGTTGTTGCA--TT  | 2101 |
| Db | 1910 | ATACCCACTAATCTGATTGTAACATATATGCAAAAGAAAAGGCAATATGGTTGGTAAACTT  | 1969 |
| Qy | 2102 | TTTCGGACACTGGAAACATTTAAATGATCAGGAGGGAGTAACAGAAAGACGAAGGCTGTT   | 2161 |
| Db | 1970 | TTTTGGTCATTACCAACATGAAATGATCAGAATTCTGGGGGAAGAAA-----           | 2016 |
| Qy | 2162 | TTTGAAAATCATTACACTTTCACTAGAAAGCCCAAACCTCAGCATTTCTGCAATATGTAACC | 2221 |
| Db | 2017 | -----AGACAGCC  | 2024 |
| Qy | 2222 | AACATGTCAAAACAAGCAGCATGTAAACAGACTGGCACATGTGCCAGCTGAATTTAAAT    | 2281 |
| Db | 2025 | TGCGAATGCCACAGAGAAAACATGGGAAAGCGTG-----                        | 2058 |
| Qy | 2282 | ATAATACTTTTAAAAAGAAAATTATTACATCCTTTACATTCAGTTAAGATCAAACCTCAC   | 2341 |
| Db | 2059 | -----AGCTGCTATGCCTGAGACTTCTGAAATTCCTTCACACATACTCTGCAG          | 2106 |
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| Db | 2107 | AAAGACACAAA-----ACAGAACACTACCTATGATTTCTTTAAAGTTCTTTCAAAT       | 2157 |
| Qy | 2402 | ATACCCTGTGAAGACAATACTATCTACAATTTTTTTCAGGATTATTAAAAATCTTCTTTTTT | 2461 |
| Db | 2158 | ATCCTTTCATGATTGAAGTTTAAATCCATGTGTTCAACTTCATCA-----             | 2203 |
| Qy | 2462 | CACTATCGTAGCTTAAACTCTGTTTGGTTTTGTCATCTGTAAATACTTACCTACATACAC   | 2521 |
| Db | 2204 | -----TCTGTAAATACTTAGCTATTAGCTATAAGCAC                          | 2235 |
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| Db | 2236 | TACACGTAGAGGACTTAACAAAGGGCAGGTCCAGCGTTCGTAGCTTTCTGACAAAGAGA    | 2295 |
| Qy | 2580 | TGCCAGTGACCTCATAAT--AAAGACTGTGAAGTGCCTGGTGCAGTGTCCACATGACAAA   | 2637 |

|    |      |  |      |
|----|------|--|------|
| Db | 2296 | TGCCAGTAACCCGGTTATAGACAGAAATGTGAATTGCCCGGTGCAGTGTCCACATGGCAAA  | 2355 |
| Qy | 2638 | GGGGCAGGTAGCACCCCTCTCTCACCCATGCTGTGGTTAAAAATGGTTTCTAGCATATGTAT | 2697 |
| Db | 2356 | GAAGCAGGGAGCATC--CTTTCAGCCATGCTGTAGAGAAAATGGTCCACAGC-----AC    | 2407 |
| Qy | 2698 | AATGCTATAGTTAAAAATACTATTTTTTCAAAATCATACAGATTAGT-ACATTTAACAGCTA | 2756 |
| Db | 2408 | AATATGATAGCGAAAATACCGTGGTTTAAACGCCATAGAAAATAGTCACTGTAACCAGCTC  | 2467 |
| Qy | 2757 | CCTGTAAAGCTTATTACTAA-TTTTTGTATTATTTTTGTAAATAGCCAATAGAAAAGTTT   | 2815 |
| Db | 2468 | TCTCGGAGGCATACTACCAACTTTTTATGTTATTCCTGAAAATAGCCAATAGAAAGGCGT   | 2527 |
| Qy | 2816 | GCTTGACATGGTGCTTTTTCTTTCATCTAGAGGCAAACTGCTTTTTGAGACCGTAAGAAC   | 2875 |
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| Qy | 2876 | CTCTTAGCTTTGTGCGTTCCTGCCTAATTTTTTATATCTTCTAAGCAAA-----         | 2923 |
| Db | 2588 | CTCCT--CTTTGCGCATTCCTGTCTAGGTTTTTTTTTTTTTTTTTTTAAATCTCCTTCCAG  | 2645 |
| Qy | 2924 | --GTGCCTTAGGATAGCTTGGGATGAGATGTGTGTGAAAGTATGTACAAGAGAAAACGGA   | 2981 |
| Db | 2646 | ACGTGCCTTAGGTTCACTCCGGATGAGCGGTGTGTGAAAGAATGCCCAAGAGAAAACCTGA  | 2705 |
| Qy | 2982 | AGAGAGAGGAAATGAGGTGGGGTTGGAGGAAACCCATGGGGACAGATTCCCATTCTTAGC   | 3041 |
| Db | 2706 | AGAGAGAGGAAATGAGGTGGGGCCAGAGGAAGCCCGTGGGGAAATATTCCCATTCTTAGC   | 2765 |
| Qy | 3042 | CTAACGTTTCGTCATTGCCTCGTCACATCAATGCAAAGGTCCTGATTTTGTTCAGCAAA    | 3101 |
| Db | 2766 | CCTGTGTTTCGTCACTGCCACGTCATGTCGGTGTGAAAGGTCCTGGTTCGGCTCCAGCAAA  | 2825 |
| Qy | 3102 | ACACAGTGCAATGTTCTCAGAGTGACTTTCGAAATAAATTGGGCCCAAGAGCTTTAACTC   | 3161 |
| Db | 2826 | ACAAAGCGCAGCGTTCTCAGCGTGAC-TCGGGAACAAACCAAGCCCGAGAGCTTTAACCT   | 2884 |
| Qy | 3162 | GGTCTTAAAATATGCCCAAATTTT-----                                  | 3185 |
| Db | 2885 | TGTCTTAAAATATAACAGATTTTCCTTCCTTCCTTTTTCTCTTCTTCTCTTCTCTC       | 2944 |
| Qy | 3186 | -----TACTTTGTTTTTCTTTTAATAGGCTGGGCCACATG                       | 3220 |
| Db | 2945 | TTCTCTTCTCTTCTCTTCTCTTCTCTTCTCTTCTTTTCATAACCCAGGCCACATG        | 3004 |
| Qy | 3221 | TTGGAATAAGCTAGTAATGTTGTTTTCTGTCAATATTGAATGTGATGGTACAGTAAACC    | 3280 |
| Db | 3005 | TTGAAAATGAGCTTAACAATGCAGTTTTCTACCAAATCATTGTGACAATACAATAAACC    | 3064 |
| Qy | 3281 | AAAACCCAACAATGTGGCCAGAAAGAAAGAGCAATAATAATTAATTCACACACCATATGG   | 3340 |
| Db | 3065 | CAAACGGGACAATGAGGTAAAAAACCAAGAACAATACTGAATCCACGTGACAC----ATG   | 3120 |
| Qy | 3341 | ATTCTATTTATAAATCACCCACAAACTGTTCTTTAATTTTCATCCCAATCACTTTTTTCAG  | 3400 |
| Db | 3121 | ACTCTCTTTAGGAGTCACCCACAGTTCTTGTGTGTA-----CAGAT                 | 3161 |



DEFINITION Mus musculus 0 day neonate kidney cDNA, RIKEN full-length enriched library, clone:D630038G12 product:ENDOTHELIN B RECEPTOR PRECURSOR, full insert sequence.

ACCESSION AK085532

VERSION AK085532.1 GI:26351656

KEYWORDS HTC; CAP trapper.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1

AUTHORS Carninci,P. and Hayashizaki,Y.

TITLE High-efficiency full-length cDNA cloning

JOURNAL Meth. Enzymol. 303, 19-44 (1999)

MEDLINE 99279253

PUBMED 10349636

REFERENCE 2

AUTHORS Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.

TITLE Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes

JOURNAL Genome Res. 10 (10), 1617-1630 (2000)

MEDLINE 20499374

PUBMED 11042159

REFERENCE 3

AUTHORS Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.

TITLE RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer

JOURNAL Genome Res. 10 (11), 1757-1771 (2000)

MEDLINE 20530913

PUBMED 11076861

REFERENCE 4

AUTHORS The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.

TITLE Functional annotation of a full-length mouse cDNA collection

JOURNAL Nature 409, 685-690 (2001)

REFERENCE 5

AUTHORS The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.

TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

JOURNAL Nature 420, 563-573 (2002)

REFERENCE 6 (bases 1 to 3990)

AUTHORS Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W., Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T., Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T., Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M., Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N., Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N.,

Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T.,  
 Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S.,  
 Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A.,  
 Muramatsu,M. and Hayashizaki,Y.

TITLE Direct Submission  
 JOURNAL Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of  
 Physical and Chemical Research (RIKEN), Laboratory for Genome  
 Exploration Research Group, RIKEN Genomic Sciences Center (GSC),  
 RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,  
 Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp,  
 URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222,  
 Fax:81-45-503-9216)  
 COMMENT cDNA library was prepared and sequenced in Mouse Genome  
 Encyclopedia Project of Genome Exploration Research Group in Riken  
 Genomic Sciences Center and Genome Science Laboratory in RIKEN.  
 Division of Experimental Animal Research in Riken contributed to  
 prepare mouse tissues.  
 Please visit our web site for further details.  
 URL:http://genome.gsc.riken.go.jp/  
 URL:http://fantom.gsc.riken.go.jp/.  
 FEATURES Location/Qualifiers  
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# ORIGIN

Query Match 31.9%; Score 1371.2; DB 11; Length 3990;  
 Best Local Similarity 66.0%; Pred. No. 1.3e-253;  
 Matches 2664; Conservative 0; Mismatches 1043; Indels 327; Gaps 34;

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| Qy | 193 | AAACTGCGGAGCGGCCACCGGACGCCTTCTGGAGCAGGTAGCAGCATGCAGCCGCCTCCA   | 252  |
|    |     |  |      |
| Db | 177 | AAACAGCAGAGCGGCTACCACTCTCACAGGAGCAAGCTGTAACATGCAATCGCCCGCA     | 236  |
| Qy | 253 | AGTCTGTGCGGACGCGCCCTGGTTGCGCTGGTTCTTGCCTGCGGCCTGTGCGGATCTGG    | 312  |
|    |     |  |      |
| Db | 237 | AGCCGGTGCGGACGCGCCTTGGTGGCGCTGCTGCTGGCCTGTGGCTTCTTGGGGGTATGG   | 296  |
| Qy | 313 | GGAGAGGAGAGAGGCTTCCCGCTGACAGGGCCACTC---CGCTTTTGCAAACCGCAGAG    | 369  |
|    |     |  |      |
| Db | 297 | GGAGAGAAAAGAGGATTCCACCTGCCCAAGCCACGCTGTCACTTCTCGGGACTAAAGAG    | 356  |
| Qy | 370 | ATAATGACGCCACCCACTAAGACCTTATGGCCCAAGGGTTCCAACGCCAGTCTGGCGCGG   | 429  |
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| Db | 357 | GTAATGACGCCACCCACTAAGACCTCCTGGACCAGAGGTTCCAACCTCCAGTCTGATGCGT  | 416  |
| Qy | 430 | TCGTTGGCACCTGCGGAGGTGCCTAAAGGAGACAGGACGGCAGGATCTCCGCCACGCACC   | 489  |
|    |     |  |      |
| Db | 417 | TCCTCCGCACCTGCGGAGGTGACCAAAGGAGGGAGGGGGGCTGGAGTCCCGCCAAGATC-   | 475  |
| Qy | 490 | ATCTCCCCTCCCCCGTGCCAAGGACCCATCGAGATCAAGGAGACTTTCAAATACATCAAC   | 549  |
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| Db | 476 | --CTTCCCTCCTCCGTGCCAACGAAATATTGAGATCAGCAAGACTTTTAAATACATCAAC   | 533  |
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| Db | 534 | ACGATTGTGTCTGTCCTCGTGTTCGTGCTAGGCATCATCGGGAACCTCCACGCTGCTAAGA  | 593  |
| Qy | 610 | ATTATCTACAAGAACAAGTGCATGCGAAACGGTCCCAATATCTTGATCGCCAGCTTGGCT   | 669  |
|    |     |  |      |
| Db | 594 | ATCATCTACAAGAACAAGTGCATGCGCAATGGTCCCAATATCTTGATCGCCAGTCTGGCT   | 653  |
| Qy | 670 | CTGGGAGACCTGCTGCACATCGTCATTGACATCCCTATCAATGTCTACAAGCTGCTGGCA   | 729  |
|    |     |  |      |
| Db | 654 | CTGGGAGACCTACTGCACATCATCATAGACATACCCATTAAACACCTACAAGTTGCTCGCA  | 713  |
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|    |     |  |      |
| Db | 714 | GAGGACTGGCCATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTCATACAGAAGGCTTCT   | 773  |
| Qy | 790 | GTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATATCGAGCTGTTGCT   | 849  |
|    |     |  |      |
| Db | 774 | GTGGGAATCACAGTGCTGAGTCTTTGTGCTCTAAGTATTGACAGATATCGAGCTGTTGCT   | 833  |
| Qy | 850 | TCTTGGAGTAGAATTAAAGGAATTGGGGTTCCAAAATGGACAGCAGTAGAAATTGTTTTG   | 909  |
|    |     |  |      |
| Db | 834 | TCTTGGAGTCGAATTAAAGGAATTGGGGTTCCAAAATGGACAGCAGTAGAAATTGTTTTA   | 893  |
| Qy | 910 | ATTTGGGTGGTCTCTGTGGTTCTGGCTGTCCCTGAAGCCATAGGTTTTGATATAATTACG   | 969  |
|    |     |  |      |
| Db | 894 | ATTTGGGTGGTCTCTGTGGTTCTGGCTGTCCCGAAGCCATAGGTTTTGATATGATTACG    | 953  |
| Qy | 970 | ATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTTTCAGAAGACAGCT  | 1029 |
|    |     |  |      |
| Db | 954 | TCGGACTACAAAGGAAAGCCCTAAGGGTCTGCATGCTTAATCCCTTTCAGAAAACAGCC    | 1013 |



|    |      |  |      |
|----|------|--|------|
| Qy | 1030 | TTCATGCAGTTTTTACAAGACAGCAAAAGATTGGTGGCTGTTTCAGTTTCTATTTCTGCTTG | 1089 |
| Db | 1014 | TTCATGCAGTTTTTACAAGACAGCCAAAGATTGGTGGCTGTTTCAGTTTCTACTTCTGCTTG | 1073 |
| Qy | 1090 | CCATTGGCCATCACTGCATTTTTTTATACACTAATGACCTGTGAAATGTTGAGAAAGAAA   | 1149 |
| Db | 1074 | CCGCTAGCCATCACTGCAGTCTTTTATACCCTGATGACCTGCGAAATGCTCAGGAAGAAG   | 1133 |
| Qy | 1150 | AGTGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAAGTGCCCAAAACC   | 1209 |
| Db | 1134 | AGCGGTATGCAGATTGCTTTGAATGATCACTTAAAGCAGAGACGAGAAGTGCCCAAGACA   | 1193 |
| Qy | 1210 | GTCTTTTGCCTGGTCTTGTCTTTGCCCTCTGCTGGCTTCCCCTTACCTCAGCAGGATT     | 1269 |
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| Qy | 1270 | CTGAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGAACCTTTTGTGCTTTCTG  | 1329 |
| Db | 1254 | CTGAAGCTCACCTGTATGACCAGAGCAATCCACACAGGTGTGAGCTTCTGAGCTTTTTTG   | 1313 |
| Qy | 1330 | TTGGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCCTGCATTAACCCAATT   | 1389 |
| Db | 1314 | TTGGTTTTGGACTACATTGGTATCAACATGGCTTCTTTGAACCTCCTGCATCAATCCAATC  | 1373 |
| Qy | 1390 | GCTCTGTATTTGGTGAGCAAAAGATTCAAAAAGTCTTTAAGTCATGCTTATGCTGCTGG    | 1449 |
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| Qy | 1450 | TGCCAGTCATTTGAAGAAAAACAGTCCTTGGAGGAAAAGCAGTCGTGCTTAAAGTTCAA    | 1509 |
| Db | 1434 | TGCCAAACGTTTGAGGAAAAGCAGTCCTTGGAGGAGAAGCAGTCCTGCCTGAAGTTCAA    | 1493 |
| Qy | 1510 | GCTAATGATCACGGATATGACAACTTCCGTTCCAGTAATAAATACAGCTCATCTTGAAAG   | 1569 |
| Db | 1494 | GCCAACGATCACGGATATGACAACTTCCGGTCCAGCAATAAATACAGCTCGTCTTGAAGG   | 1553 |
| Qy | 1570 | AAGAACTATTCACTGTATTTTCATTTTCTTTATATTGGACCGAAGTCATTAACAAAATG    | 1629 |
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|    |      |   |      |
|----|------|---|------|
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| Db | 2581 | TCTCGGAGGCATACTACCAACTTTTTATGTTATTCTCTGAAAATAGCCAATAGAAAGGCGT | 2640 |
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|    |      |   |      |
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| Db | 3058 | TTCTCTTCTCTTCTCTTCTCTTCTCTTCTCTTCTCTTCTTTTCATAACCCAGGCCACATG  | 3117 |
| Qy | 3221 | TTGGAAATAAGCTAGTAATGTTGTTTTCTGTCAATATTGAATGTGATGGTACAGTAAAC   | 3280 |
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| Db | 3118 | TTGAAATGAGCTTAACAATGCAGTTTTCTACCAAATCATTGTGACAATACAATAAACC    | 3177 |
| Qy | 3281 | AAAACCCAACAATGTGGCCAGAAAGAAAGAGCAATAATAATTAATTCACACACCATATGG  | 3340 |
|    |      |   |      |
| Db | 3178 | CAAACGGGACAATGAGGTAAAAAACCAAGAACAATACTGAATCCACGTGACAC----ATG  | 3233 |
| Qy | 3341 | ATTCTATTTATAAATCACCCACAACTTGTTCTTTAATTTTCATCCCAATCACTTTTTTCAG | 3400 |
|    |      |   |      |
| Db | 3234 | ACTCTCTTTAGGAGTCACCCACAGTTCTTGTGTGTA-----CAGAT                | 3274 |
| Qy | 3401 | AGGCCTGTTATCATAGAAGTCATTTTAGACTCTCAATTTTAAATTAATT-TTGAATCACT  | 3459 |
|    |      |   |      |
| Db | 3275 | TGCTTTTTAATCATAAAGGACGCCCCAGATCTTCAATTTTAAGTTAGTTATTGGCTCCCC  | 3334 |
| Qy | 3460 | AATATTTTTCACAGTTTATTAATATATTTAATTTCTATTTAAATTTTAGATTATTTTTATT | 3519 |
|    |      |   |      |
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Qy 3520 ACCATGTACTGAATTTTTACATCCTGATACCCTTTCCTTCTCCATGT-----CAGTA 3571  
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 Db 3394 GTTGTGTTCTAAATTCTTAAGTCCTAACATCTTTGTTAACCCAGATGTTCCCTCCCTCT 3453  
 Qy 3572 TCATGTTCTCTAATTATCTTGCCAAATTTGAAACTACACACAAAAAGCATACTTGCATT 3631  
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 Db 3454 TCATGGGCAATAATCGTCCTGCCAAATTATGAAATGGCATAAGAATACTATTACATAAT 3513  
 Qy 3632 ATTTATAATAAAATTGCATTTCAGTGGCTTTTTAAAAAAATGTTTGATTCAAACTTTAA 3691  
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 Db 3514 ATATACAATAAACTATATTAAGTGGCTTTTTATTAAAAATTTAGCACA-----CAG 3567  
 Qy 3692 CATACTGATAAGTAAGAAACAATTATAATTTCTTTACATACTCAAAACCAAGATAGAAAA 3751  
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 Db 3568 ACCAAGGGTGATAAGAAAAAAACATGATTCCTTGCATAATTAACCAAGATAAGAGA 3627  
 Qy 3752 AGGTGCTATCGTTCAACTTCAAACATGTTTCCTAGTATTAAGGACTTTAATATAGCAAC 3811  
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 Db 3628 AGGTACCATCT---AATTTAAAGCATATTTTCTAACATTTAAGTAGCCTAATATAGCAAT 3684  
 Qy 3812 AGACAAAATTATTGTTAACATGGATGTTACAGCTCAAAGATTATATAAAGATTTTAACC 3871  
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 Db 3685 GCATAAAAATAGTGTTAACAAGGATGTTAGAGGTCAAACGATTTGTAAGTGACTTCAGCC 3744  
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 Db 3745 TATTTTCTCCCAAATTATTTACTGCTATTTTGGTCTGTGTTCAAACA-TTTTCAGTATT 3803  
 Qy 3932 GATAGCTTACATATGGCCAAAGGAATACAGTTTATAGCAAACATGGGTATGCTGTAGCT 3991  
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 Db 3804 GATAATGTGCA-ACAGCCAAAGGAACACTGTTTTTCATCCAAATGCGGGTGTGTTGTACCT 3862  
 Qy 3992 AACTTTATAAAAGTGTAATATAACAATGTAAAAAATTATATATCTGGGAGGATTTTTTGG 4051  
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 Db 3863 AAC---ATGCACTTGTAATAAAGCCGTGTAAAA---TAACTGTGTTTGTGTTTGCTCTGG 3916  
 Qy 4052 TTGCCTAAAGTGGC-----TATAGTTACTGATTTTTTTATTATGTAAGCAAACCAATAA 4105  
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 Db 3917 TCACCTAAAGTGGCAGCTTGTGTCGTTGCTAACTTCTTGTTGAGTAAGCAAACCAATAA 3976  
 Qy 4106 AAATTTAAGTTTTT 4119  
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 Db 3977 ACGTTCAAATGGTT 3990

# RESULT 3

AY415512

LOCUS AY415512 1329 bp DNA linear GSS 17-DEC-2003

DEFINITION Homo sapiens EDNRB gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.

ACCESSION AY415512

VERSION AY415512.1 GI:39771471

KEYWORDS GSS.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE 1 (bases 1 to 1329)  
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,  
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,  
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,  
Adams,M.D. and Cargill,M.  
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous  
gene trios  
JOURNAL Science 302 (5652), 1960-1963 (2003)  
PUBMED 14671302  
REFERENCE 2 (bases 1 to 1329)  
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,  
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,  
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,  
Adams,M.D. and Cargill,M.  
TITLE Direct Submission  
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,  
Rockville, MD 20850, USA  
COMMENT This sequence was made by sequencing genomic exons and ordering  
them based on alignment.  
FEATURES Location/Qualifiers  
source 1. .1329  
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gene <1..>1329  
/gene="EDNRB"  
/locus\_tag="HCM5582"

# ORIGIN

Query Match 30.9%; Score 1329; DB 29; Length 1329;  
Best Local Similarity 100.0%; Pred. No. 2.2e-245;  
Matches 1329; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      238 ATGCAGCCGCCTCCAAGTCTGTGCGGACGCGCCCTGGTTGCGCTGGTTCTTGCCTGCGGC 297
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Qy      298 CTGTCGCGGATCTGGGGAGAGGAGAGAGGCTTCCCGCCTGACAGGGCCACTCCGCTTTTG 357
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Db      61 CTGTCGCGGATCTGGGGAGAGGAGAGAGGCTTCCCGCCTGACAGGGCCACTCCGCTTTTG 120

Qy      358 CAAACCGCAGAGATAATGACGCCACCCACTAAGACCTTATGGCCCAAGGGTTCCAACGCC 417
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Db      121 CAAACCGCAGAGATAATGACGCCACCCACTAAGACCTTATGGCCCAAGGGTTCCAACGCC 180

Qy      418 AGTCTGGCGGGTCGTTGGCACCTGCGGAGGTGCCTAAAGGAGACAGGACGGCAGGATCT 477
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Db      181 AGTCTGGCGGGTCGTTGGCACCTGCGGAGGTGCCTAAAGGAGACAGGACGGCAGGATCT 240

Qy      478 CCGCCACGCACCATCTCCCTCCCCCGTGCCAAGGACCCATCGAGATCAAGGAGACTTTC 537
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Db      241 CCGCCACGCACCATCTCCCTCCCCCGTGCCAAGGACCCATCGAGATCAAGGAGACTTTC 300

Qy      538 AAATACATCAACACGGTTGTGTCTGCCTTGTGTTTCGTGCTGGGGATCATCGGGAATCC 597
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Db      301 AAATACATCAACACGGTTGTGTCTGCCTTGTGTTTCGTGCTGGGGATCATCGGGAATCC 360

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| Qy | 598  | ACACTTCTGAGAATTATCTACAAGAACAAGTGCATGCGAAACGGTCCCAATATCTTGATC | 657  |
|    |      |  |      |
| Db | 361  | ACACTTCTGAGAATTATCTACAAGAACAAGTGCATGCGAAACGGTCCCAATATCTTGATC | 420  |
| Qy | 658  | GCCAGCTTGGCTCTGGGAGACCTGCTGCACATCGTCATTGACATCCCTATCAATGTCTAC | 717  |
|    |      |  |      |
| Db | 421  | GCCAGCTTGGCTCTGGGAGACCTGCTGCACATCGTCATTGACATCCCTATCAATGTCTAC | 480  |
| Qy | 718  | AAGCTGCTGGCAGAGGACTGGCCATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTCATA | 777  |
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| Db | 481  | AAGCTGCTGGCAGAGGACTGGCCATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTCATA | 540  |
| Qy | 778  | CAGAAAGCCTCCGTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATAT | 837  |
|    |      |  |      |
| Db | 541  | CAGAAAGCCTCCGTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATAT | 600  |
| Qy | 838  | CGAGCTGTTGCTTCTTGGAGTAGAATTAAAGGAATTGGGGTTCCAAAATGGACAGCAGTA | 897  |
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| Db | 601  | CGAGCTGTTGCTTCTTGGAGTAGAATTAAAGGAATTGGGGTTCCAAAATGGACAGCAGTA | 660  |
| Qy | 898  | GAAATTGTTTTGATTTGGGTGGTCTCTGTGGTCTGGCTGTCCCTGAAGCCATAGGTTTT  | 957  |
|    |      |  |      |
| Db | 661  | GAAATTGTTTTGATTTGGGTGGTCTCTGTGGTCTGGCTGTCCCTGAAGCCATAGGTTTT  | 720  |
| Qy | 958  | GATATAATTACGATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTT | 1017 |
|    |      |  |      |
| Db | 721  | GATATAATTACGATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTT | 780  |
| Qy | 1018 | CAGAAGACAGCTTTCATGCAGTTTTACAAGACAGCAAAAGATTGGTGGCTGTTCAGTTTC | 1077 |
|    |      |  |      |
| Db | 781  | CAGAAGACAGCTTTCATGCAGTTTTACAAGACAGCAAAAGATTGGTGGCTGTTCAGTTTC | 840  |
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|    |      |  |      |
| Db | 841  | TATTTCTGCTTGCCATTGGCCATCACTGCATTTTTTTATACACTAATGACCTGTGAAATG | 900  |
| Qy | 1138 | TTGAGAAAGAAAAGTGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAA | 1197 |
|    |      |  |      |
| Db | 901  | TTGAGAAAGAAAAGTGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAA | 960  |
| Qy | 1198 | GTGGCCAAAACCGTCTTTTGCCTGGTCCTTGTCTTTGCCCTCTGCTGGCTTCCCCTTCAC | 1257 |
|    |      |  |      |
| Db | 961  | GTGGCCAAAACCGTCTTTTGCCTGGTCCTTGTCTTTGCCCTCTGCTGGCTTCCCCTTCAC | 1020 |
| Qy | 1258 | CTCAGCAGGATTCTGAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGAACTT | 1317 |
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| Db | 1021 | CTCAGCAGGATTCTGAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGAACTT | 1080 |
| Qy | 1318 | TTGAGCTTTCTGTTGGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCCTGC | 1377 |
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| Db | 1081 | TTGAGCTTTCTGTTGGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCCTGC | 1140 |
| Qy | 1378 | ATTAACCCAATTGCTCTGTATTTGGTGAGCAAAAGATTCAAAAAGTCTTTAAGTCATGC  | 1437 |
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| Db | 1141 | ATTAACCCAATTGCTCTGTATTTGGTGAGCAAAAGATTCAAAAAGTCTTTAAGTCATGC  | 1200 |

Qy 1438 TTATGCTGCTGGTGCCAGTCATTTGAAGAAAAACAGTCCTTGGAGGAAAAGCAGTCGTGC 1497  
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 Db 1261 TTAAAGTTCAAAGCTAATGATCACGGATATGACAACTTCCGTTCCAGTAATAAATACAGC 1320  
 Qy 1558 TCATCTTGA 1566  
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 Db 1321 TCATCTTGA 1329

#### RESULT 4

AK082103

LOCUS AK082103 2521 bp mRNA linear HTC 20-SEP-2003

DEFINITION Mus musculus 0 day neonate cerebellum cDNA, RIKEN full-length enriched library, clone:C230007M01 product:ENDOTHELIN B RECEPTOR PRECURSOR, full insert sequence.

ACCESSION AK082103

VERSION AK082103.1 GI:26349538

KEYWORDS HTC; CAP trapper.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

#### REFERENCE

1

AUTHORS Carninci,P. and Hayashizaki,Y.

TITLE High-efficiency full-length cDNA cloning

JOURNAL Meth. Enzymol. 303, 19-44 (1999)

MEDLINE 99279253

PUBMED 10349636

#### REFERENCE

2

AUTHORS Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.

TITLE Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes

JOURNAL Genome Res. 10 (10), 1617-1630 (2000)

MEDLINE 20499374

PUBMED 11042159

#### REFERENCE

3

AUTHORS Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.

TITLE RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer

JOURNAL Genome Res. 10 (11), 1757-1771 (2000)

MEDLINE 20530913

PUBMED 11076861

#### REFERENCE

4

AUTHORS The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.

TITLE Functional annotation of a full-length mouse cDNA collection

JOURNAL Nature 409, 685-690 (2001)

REFERENCE 5

AUTHORS The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.

TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

JOURNAL Nature 420, 563-573 (2002)

REFERENCE 6 (bases 1 to 2521)

AUTHORS Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W., Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T., Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T., Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M., Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N., Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N., Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S., Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A., Muramatsu,M. and Hayashizaki,Y.

TITLE Direct Submission

JOURNAL Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)

COMMENT cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.  
Please visit our web site for further details.  
URL:http://genome.gsc.riken.go.jp/  
URL:http://fantom.gsc.riken.go.jp/.

FEATURES Location/Qualifiers

source 1..2521  
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ORIGIN

Query Match 26.4%; Score 1137.6; DB 11; Length 2521;  
 Best Local Similarity 76.4%; Pred. No. 1.2e-208;  
 Matches 1507; Conservative 0; Mismatches 439; Indels 26; Gaps 8;

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| Qy | 253 | AGTCTGTGCGGACGCGCCCTGGTTGCGCTGGTTCTTGCCTGCGGCCTGTGCGGGATCTGG | 312 |
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| Qy | 670 | CTGGGAGACCTGCTGCACATCGTCATTGACATCCCTATCAATGTCTACAAGCTGCTGGCA | 729 |
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| Db | 705 | GAGGACTGGCCATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTCATACAGAAGGCTTCT | 764 |
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 Qy 1925 AATGGGACTCTGATATAAAGGAAGAATAAGTCACTGTAAACAGAACTTTTAAATGAAGC 1984  
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 Qy 1985 TTAAATTACTCAATTTAAAAATTTTAAAAATCCTTTAAAAACAACCTTTTCAATTAATATTATC 2044  
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 Db 2013 ATACCCACTAATCTGATTGTAACATATGCAAAAGAAAAGGCAATATGGTTGGTAAACTT 2072  
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 Db 2073 TTTTGGTCATTACCAACATTGAAATGATCAGAATTCGGGGGAAGAAAAGACA 2124

# RESULT 5

AK085165

LOCUS AK085165 3611 bp mRNA linear HTC 20-SEP-2003

DEFINITION Mus musculus 13 days embryo lung cDNA, RIKEN full-length enriched library, clone:D430047G06 product:ENDOTHELIN B RECEPTOR PRECURSOR, full insert sequence.

ACCESSION AK085165

VERSION AK085165.1 GI:26351484

KEYWORDS HTC; CAP trapper.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

## REFERENCE 1

AUTHORS Carninci, P. and Hayashizaki, Y.

TITLE High-efficiency full-length cDNA cloning

JOURNAL Meth. Enzymol. 303, 19-44 (1999)

MEDLINE 99279253

PUBMED 10349636

## REFERENCE 2

AUTHORS Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.

TITLE Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes

JOURNAL Genome Res. 10 (10), 1617-1630 (2000)

MEDLINE 20499374  
 PUBMED 11042159  
 REFERENCE 3  
 AUTHORS Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,  
 Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M.,  
 Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A.,  
 Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K.,  
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 Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J.,  
 Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.  
 TITLE RIKEN integrated sequence analysis (RISA) system--384-format  
 sequencing pipeline with 384 multicapillary sequencer  
 JOURNAL Genome Res. 10 (11), 1757-1771 (2000)  
 MEDLINE 20530913  
 PUBMED 11076861  
 REFERENCE 4  
 AUTHORS The RIKEN Genome Exploration Research Group Phase II Team and the  
 FANTOM Consortium.  
 TITLE Functional annotation of a full-length mouse cDNA collection  
 JOURNAL Nature 409, 685-690 (2001)  
 REFERENCE 5  
 AUTHORS The FANTOM Consortium and the RIKEN Genome Exploration Research  
 Group Phase I & II Team.  
 TITLE Analysis of the mouse transcriptome based on functional annotation  
 of 60,770 full-length cDNAs  
 JOURNAL Nature 420, 563-573 (2002)  
 REFERENCE 6 (bases 1 to 3611)  
 AUTHORS Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P.,  
 Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W.,  
 Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T.,  
 Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T.,  
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 Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S.,  
 Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A.,  
 Muramatsu,M. and Hayashizaki,Y.  
 TITLE Direct Submission  
 JOURNAL Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of  
 Physical and Chemical Research (RIKEN), Laboratory for Genome  
 Exploration Research Group, RIKEN Genomic Sciences Center (GSC),  
 RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,  
 Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp,  
 URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222,  
 Fax:81-45-503-9216)  
 COMMENT cDNA library was prepared and sequenced in Mouse Genome  
 Encyclopedia Project of Genome Exploration Research Group in Riken  
 Genomic Sciences Center and Genome Science Laboratory in RIKEN.  
 Division of Experimental Animal Research in Riken contributed to  
 prepare mouse tissues.  
 Please visit our web site for further details.  
 URL:http://genome.gsc.riken.go.jp/  
 URL:http://fantom.gsc.riken.go.jp/.  
 FEATURES Location/Qualifiers  
 source 1. .3611

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# ORIGIN

```

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Matches 2333; Conservative 0; Mismatches 952; Indels 336; Gaps 30;

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Db      292 GGAGAGAAAAGAGGATTCCACCTGCCCAAGCCACGCTGTCACTTCTCGGGACTAAAGAG 351

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Qy      550 ACGGTTGTGTCCTGCCTTGTGTTTCGTGCTGGGGATCATCGGGAACCTCCACACTTCTGAGA 609
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Db 649 CTGGGAGACCTACTGCACATCATCATAGACATAACCATTAACACCTACAAGTTGCTCGCA 708

Qy 730 GAGGACTGGCCATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTCATACAGAAAGCCTCC 789  
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Db 709 GAGGACTGGCCATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTCATACAGAAGGCTTCT 768

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Db 829 TCTTGGAGTCGAATTAAAGGAATTGGGGTTCCAAAATGGACAGCAGTAGAAATTGTTTTA 888

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Db 889 ATTTGGGTGGTCTCTGTGGTTCTGGCTGTCCCGAAGCCATAGGTTTTGATATGATTACG 948

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Qy 1089 GCCATTGGCCATCACTGCATTTTTTTTATACACTAATGACCTGTGAAATGTTGAGAAAGAA 1148  
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Db 1069 GCCGCTAGCCATCACTGCAGTCTTTTATACCCTGATGACCTGCGAAATGCTCAGGAAGAA 1128

Qy 1149 AAGTGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAAGTGGCCAAAAC 1208  
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Db 1129 GAGCGGTATGCAGATTGCTTTGAATGATCACTTAAAGCAGAGACGAGAAGTGGCCAAGAC 1188

Qy 1209 CGTCTTTTGCCTGGTCCTTGTCTTTGCCCTCTGCTGGCTTCCCCTTCACCTCAGCAGGAT 1268  
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Db 1189 AGTCTTCTGCCTGGTCCTCGTGTGCTCTGTTGGCTTCCCCTTCACCTCAGCCGGAT 1248

Qy 1269 TCTGAAGCTCA-CTCTTTATAATCAGAATGATCCCAATAGATGTGAACTTTTGAGCTTTC 1327  
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Db 1249 CCTGAAGCTCAGCCCTGTATGACCAGAGCAATCCACACAGGTGTGAGCTTCTGAGCTTTT 1308

Qy 1328 TGTTGGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCCTGCATTAACCCAA 1387  
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Db 1309 TGTTGGTTTTGGACTACATTGGTATCAACATGGCTTCTTTGAACTCCTGCATCAATCCAA 1368

Qy 1388 TTGCTCTGTATTTGGTGAGCAAAAGATTCAAAAAGTCTTTAAGTCATGCTTATGCTGCT 1447  
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| Qy | 1508 | AAGCTAATGATCACGGATATGACAACTTCCGTTCCAGTAATAAATACAGCTCATCTTGAA  | 1567 |
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| Qy | 1568 | AGAAGAACTATTCACTGTATTTCATTTTCTTTATATTGGACCGAAGTCATTAAAAACAAA  | 1627 |
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| Qy | 1688 | TTAAGTGTAATTATTTTAACACTCACAGCTACATATGAC-----ATTTTATGAGCTGTTT  | 1742 |
| Db | 1669 | TGAGAGGGATTATTTTTAACTGTTCTGACGCTCAACACCGGATATATTCACGGGCTGTTT  | 1728 |
| Qy | 1743 | ACGGCATGGAAAGAAAATCAGTGGAATTAAGAAAGCCTCGTCGTGAAAGCACTTAATTT   | 1802 |
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| Qy | 1803 | TTTACAGTTAGCACTTCAACATAGCTCTTAACAACTCCAGGATATTCACACAACACTTA   | 1862 |
| Db | 1789 | CTT--AGTCAGCACTTCAGCAGAGCTCTTAAAGCCCCCTAGTGCCTTCACATGCCACTTA  | 1846 |
| Qy | 1863 | GGCTTAAAAATGAGCTCACTCAGAATTTCTATTCTTTCTAAAAAGAGATTTATTTTTAAA  | 1922 |
| Db | 1847 | CGTTTTAAAAA-----AACGAGAACTTCACTGAAGTTCTGTTTCAGGAGTTTATTATCCA  | 1899 |
| Qy | 1923 | TCAATGGGACTCTGATATAAAGGAAGAATAAGTCACTGTAAAACAGAACTTTTAAATGAA  | 1982 |
| Db | 1900 | GTCCTATGAATCTGGATTCAAGAAAGCAT--GACATTGCAAACAATTCTTAAACGAAG    | 1957 |
| Qy | 1983 | GCTTAAATTACTCAATTTAAAATTTTAAAATCCTTTAAAACAACCTTTTCAATTAATATTA | 2042 |
| Db | 1958 | TTTCAATTGCTTAATTTGAAACTTAAAAAAAAAAAACTAATAAATTTTATGCATACTA    | 2017 |
| Qy | 2043 | TC--ACACTATTATCAGATTGTAATTAGATGCAATGAGAGAGCAGTTTAGTTGTTGCA-   | 2099 |
| Db | 2018 | TCATACCCACTAATCTGATTGTAAGTATATGAAAAGAAAAGGCAATATGGTTGGTAAAC   | 2077 |
| Qy | 2100 | TTTTTCGGACACTGGAAACATTTAAATGATCAGGAGGGAGTAACAGAAAGAGCAAGGCTG  | 2159 |
| Db | 2078 | TTTTTTGGTCATTACCAACATTGAAATGATCAGAATTCGGGGGAAGAAAAGACAG-----  | 2132 |
| Qy | 2160 | TTTTTGAAAATCATTACACTTTCACTAGAAGCCCAAACCTCAGCATTCTGCAATATGTAA  | 2219 |
| Db | 2133 | -----   | 2132 |
| Qy | 2220 | CCAACATGTCACAAACAAGCAGCATGTAACAGACTGGCACATGTGCCAGCTGAATTTAAA  | 2279 |
| Db | 2133 | CCTGCGAATGCCACAGAGAAAACATGGGAAAGCGTG-----                     | 2168 |
| Qy | 2280 | ATATAATACTTTTAAAAAGAAAATTATTACATCCTTTACATTCAAGTAAAGATCAAACCTC | 2339 |

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| Db | 2169 | -----AGCTGCTATGCCTGAGACTTCTGAAATTCCTCACACATACTCTGC            | 2214 |
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| Qy | 2400 | ACATACCCTGTGAAGACAATACTATCTACAATTTTTTCAGGATTATTAAAACTTCTTTT   | 2459 |
| Db | 2266 | ATATCCTTTTCATGATTGAAGTTTAAATTCATGTGTTCAACTTCATCA-----         | 2313 |
| Qy | 2460 | TTCACTATCGTAGCTTAAACTCTGTTTGGTTTGTTCATCTGTAAATACTTACCTACATAC  | 2519 |
| Db | 2314 | -----TCTGTAAATACTTAGCTATTAGCTATAAGC                           | 2343 |
| Qy | 2520 | ACTGCATGTAGATGATTAAATGA--GGGCAGGCCCTGTGCTCATAGCTTTACGATGGAGA  | 2577 |
| Db | 2344 | ACTACACGTAGAGGACTTAACAAAGGGCAGGTCCCAGCGTTCGTAGCTTTCTGACAAAGA  | 2403 |
| Qy | 2578 | GATGCCAGTGACCTCATAAT--AAAGACTGTGAAGTGCCTGGTGCAGTGTCCACATGACA  | 2635 |
| Db | 2404 | GATGCCAGTAACCCGGTTATAGACAGAATGTGAATTGCCCGGTGCAGTGTCCACATGGCA  | 2463 |
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| Db | 2516 | ACAATATGATAGCGAAAATACCGTGGTTTAAACGCCATAGAAAATAGTCACTGTAACCAGC | 2575 |
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| Db | 2636 | GTTCTGGACATGGTGCTTTTCTAAAACGTAGAAGCCAAACTGCTTCGGGGTCTGCAAGA   | 2695 |
| Qy | 2874 | ACCTCTTAGCTTTGTGCGTTCCTGCCTAATTTTTATATCTTCTAAGCAAAGTGCCTTAGG  | 2933 |
| Db | 2696 | TCCTCCTCTTTGCGCATTCTTGTCTAGGTTTTTTTTTTTTTTTTTAAATCTCCTTTCCA   | 2755 |
| Qy | 2934 | ATAGCTTGGGATGAGATGTGTGTGAAAGTATGTA-----                       | 2967 |
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| Qy | 2968 | --CAAGAGAAAACGGAAGAGAGAGGAAATGAGGTGGGGTTGGAGG-----AAA         | 3013 |
| Db | 2816 | CCCAAGAGAAAACCTTAAAGAGAGAAGGAAATTTGAGGTTGGGGGCCAGAAAGAAAAGC   | 2875 |
| Qy | 3014 | CCCATGGGG-----ACAGATTCCCATCTTAGCCTAACGTTTCGTACTGCTCGTCACA     | 3067 |
| Db | 2876 | CCCTTGGGGGAAAATAAATATTCCCATCTTAGCCCTGTGTTTCGTCACTGCCACGTCATG  | 2935 |
| Qy | 3068 | TCAATGCAAAAGGTCCTGATTTTGTTCAGCAAAACACAGTGCAATGTTCTCAGAGTGAC   | 3127 |



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Qy 3128 TTTTCGAAATAAATTGGGCCCCAAGAGCTTTAACTCGGTCTTAAAATATGCCCAAATT---- 3183  
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Db 2996 -TCGGGAACAAACCAAGCCCGAGAGCTTTAACCTTGTCTTAAAATATAACAGATTTTCTCT 3054

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Qy 3187 ACTTTGTTTTTCTTTTAATAGGCTGGGCCACATGTTGGAAATAAGCTAGTAATGTTGTTT 3246  
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Db 3332 AGATCTTCAATTTTAAGTTAGTTATTGGCTCCCCAGTAGTTTCACAGCGTGGATATATTT 3391

Qy 3486 TTAATTTCTATTTAAATTTTAGATTATTTTATTACCATGTACTGAATTTTACATCCTG 3545  
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Db 3392 TTAATTTTACT-AAGTTTGTAGATTGGTTTTATTGTTGTGTTCTAAATCTTAAGTCCTA 3450

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Db 3511 TTATGAAATGGCATAAGAATACTATTACATAATATATACAATAAAACTATATTAAGTGG 3570

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Db 3571 CTTTTTTTATTAAAAATTTTA 3591

# RESULT 6

AK076426

LOCUS AK076426 2669 bp mRNA linear HTC 18-SEP-2003

DEFINITION Mus musculus 0 day neonate head cDNA, RIKEN full-length enriched library, clone:4832401B07 product:ENDOTHELIN B RECEPTOR PRECURSOR, full insert sequence.

ACCESSION AK076426

VERSION AK076426.1 GI:26345371

KEYWORDS HTC; CAP trapper.

SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1  
AUTHORS Carninci, P. and Hayashizaki, Y.  
TITLE High-efficiency full-length cDNA cloning  
JOURNAL Meth. Enzymol. 303, 19-44 (1999)  
MEDLINE 99279253  
PUBMED 10349636

REFERENCE 2  
AUTHORS Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,  
Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.  
TITLE Normalization and subtraction of cap-trapper-selected cDNAs to  
prepare full-length cDNA libraries for rapid discovery of new genes  
JOURNAL Genome Res. 10 (10), 1617-1630 (2000)  
MEDLINE 20499374  
PUBMED 11042159

REFERENCE 3  
AUTHORS Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,  
Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M.,  
Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A.,  
Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,  
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Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J.,  
Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.  
TITLE RIKEN integrated sequence analysis (RISA) system--384-format  
sequencing pipeline with 384 multicapillary sequencer  
JOURNAL Genome Res. 10 (11), 1757-1771 (2000)  
MEDLINE 20530913  
PUBMED 11076861

REFERENCE 4  
AUTHORS The RIKEN Genome Exploration Research Group Phase II Team and the  
FANTOM Consortium.  
TITLE Functional annotation of a full-length mouse cDNA collection  
JOURNAL Nature 409, 685-690 (2001)

REFERENCE 5  
AUTHORS The FANTOM Consortium and the RIKEN Genome Exploration Research  
Group Phase I & II Team.  
TITLE Analysis of the mouse transcriptome based on functional annotation  
of 60,770 full-length cDNAs  
JOURNAL Nature 420, 563-573 (2002)

REFERENCE 6 (bases 1 to 2669)  
AUTHORS Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P.,  
Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W.,  
Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T.,  
Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T.,  
Kato, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M.,  
Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M.,  
Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N.,  
Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N.,  
Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T.,  
Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S.,  
Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A.,  
Muramatsu, M. and Hayashizaki, Y.  
TITLE Direct Submission  
JOURNAL Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of  
Physical and Chemical Research (RIKEN), Laboratory for Genome

Exploration Research Group, RIKEN Genomic Sciences Center (GSC),  
RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,  
Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp,  
URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222,  
Fax:81-45-503-9216)

COMMENT cDNA library was prepared and sequenced in Mouse Genome  
Encyclopedia Project of Genome Exploration Research Group in Riken  
Genomic Sciences Center and Genome Science Laboratory in RIKEN.  
Division of Experimental Animal Research in Riken contributed to  
prepare mouse tissues.  
Please visit our web site for further details.  
URL:http://genome.gsc.riken.go.jp/  
URL:http://fantom.gsc.riken.go.jp/.

FEATURES Location/Qualifiers  
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#### ORIGIN

Query Match 23.7%; Score 1020; DB 11; Length 2669;  
Best Local Similarity 84.7%; Pred. No. 5.1e-186;  
Matches 1169; Conservative 0; Mismatches 205; Indels 6; Gaps 2;

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Best Local Similarity 85.3%;  Pred. No. 2.5e-181;
Matches 1136;  Conservative 0;  Mismatches 190;  Indels 6;  Gaps 2;

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# RESULT 8

AL571798/c

LOCUS AL571798 1201 bp mRNA linear EST 31-MAY-2003

DEFINITION AL571798 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA clone CS0DI030YM19 3-PRIME, mRNA sequence.

ACCESSION AL571798

VERSION AL571798.2 GI:31293189

KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 1201)  
 AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.  
 TITLE Full-length cDNA libraries and normalization  
 JOURNAL Unpublished (2001)  
 COMMENT On Feb 16, 2001 this sequence version replaced gi:12929453.  
 Contact: Genoscope  
 Genoscope - Centre National de Sequencage  
 BP 191 91006 EVRY cedex - France  
 Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr  
 Library was constructed by Life Technologies, a division of  
 Invitrogen. This sequence belongs to sequence cluster 7006.r For  
 more information about this cluster, see  
[http://www.genoscope.cns.fr/](http://www.genoscope.cns.fr/cgi-bin/cluster.cgi?seq=CS0DI030AG10NP1&cluster=7006.r)  
<http://www.genoscope.cns.fr/cgi-bin/cluster.cgi?seq=CS0DI030AG10NP1&cluster=7006.r>. Contact :  
 Feng Liang Email : fliang@lifetech.com URL :  
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#### ORIGIN

Query Match 22.9%; Score 987; DB 9; Length 1201;  
 Best Local Similarity 96.0%; Pred. No. 1.4e-179;  
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| Db | 893  | TCTGGGAGACCTGCTGCACATCGTCATTGACATCCCTATCAATGTCTACAAGCTGCTGGC   | 834  |
| Qy | 729  | AGAGGACTGGCCATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTCATACAGAAAGCCTC   | 788  |



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|----|------|--|------|
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 genomic survey sequence.  
 ACCESSION AY415513  
 VERSION AY415513.1 GI:39771472  
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 SOURCE Pan troglodytes (chimpanzee)  
 ORGANISM Pan troglodytes  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.  
 REFERENCE 1 (bases 1 to 1144)  
 AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,  
 Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,  
 Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,  
 Adams,M.D. and Cargill,M.  
 TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous  
 gene trios  
 JOURNAL Science 302 (5652), 1960-1963 (2003)  
 PUBMED 14671302  
 REFERENCE 2 (bases 1 to 1144)  
 AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,  
 Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,  
 Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,  
 Adams,M.D. and Cargill,M.  
 TITLE Direct Submission  
 JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,  
 Rockville, MD 20850, USA  
 COMMENT This sequence was made by sequencing genomic exons and ordering  
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# ORIGIN

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Qy      483 ACGCACCATCTCCCCTCCCCCGTGCCAAGGACCCATCGAGATCAAGGAGACTTTCAAATA 542
          |||
Db      61 ACGCACCATCTCCCCTCCCCCGTGCCAAGGACCCATCGAGATCAAGGAGACTTTCAAATA 120

Qy      543 CATCAACACGGTTGTGTCCTGCCTTGTGTTTCGTGCTGGGGATCATCGGGAACCTCCACACT 602
          |||
Db      121 CATNNACACGGTTGTGTCCTGCCTTGTGTTTCGTGCTGGGGATCATCGGGAACCTCCACACT 180

Qy      603 TCTGAGAATTATCTACAAGAACAAGTGCATGCGAAACGGTCCCAATATCTTGATCGCCAG 662

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|    |      |   |      |
|----|------|---|------|
| Db | 181  | TCTGAGNNTTATCTACAAGAACAAGTGCATGCGAAACGGTCCCAATATCTTGATCGCCAG      | 240  |
| Qy | 663  | CTTGGCTCTGGGAGACCTGCTGCACATCGTCATTGACATCCCTATCAATGTCTACAAGCT      | 722  |
| Db | 241  | CTTGGCTCTGGNNCT | 300  |
| Qy | 723  | GCTGGCAGAGGACTGGCCATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTCATACAGAA      | 782  |
| Db | 301  | GCTGGCAGAGGACTGGCCATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTCATACAGAA      | 360  |
| Qy | 783  | AGCCTCCGTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATATCGAGC      | 842  |
| Db | 361  | AGCCTCCGTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATATCGAGC      | 420  |
| Qy | 843  | TGTTGCTTCTTGGAGTAGAATTAAAGGAATTGGGGTTCCAAAATGGACAGCAGTAGAAAT      | 902  |
| Db | 421  | TGTTGCATCTTGGAGTAGAATTAAAGGAATTGGGGTTCCAAAATGGACAGCAGTAGAAAT      | 480  |
| Qy | 903  | TGTTTTGATTTGGGTGGTCTCTGTGGTTCTGGCTGTCCCTGAAGCCATAGGTTTTGATAT      | 962  |
| Db | 481  | TGTTTTGATTTGGGTGGTCTCTGTGGTTCTAGCTGTCCCTGAAGCCATAGGTTTTGATAT      | 540  |
| Qy | 963  | AATTACGATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTTCAGAA      | 1022 |
| Db | 541  | AATTACGATGGACTACAAAGGAAGTTATCTACGAATCTGCTTGCTTCATCCCGTTCAGAA      | 600  |
| Qy | 1023 | GACAGCTTTCATGCAGTTTTTACAAGACAGCAAAAGATTGGTGGCTGTTGAGTTTCTATTT     | 1082 |
| Db | 601  | GACAGCTTTCATGCAGNN  | 660  |
| Qy | 1083 | CTGCTTGCCATTGGCCATCACTGCATTTTTTTTATACACTAATGACCTGTGAAATGTTGAG     | 1142 |
| Db | 661  | NN    | 720  |
| Qy | 1143 | AAAGAAAAGTGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAAGTGGC      | 1202 |
| Db | 721  | NN    | 780  |
| Qy | 1203 | CAAAACCGTCTTTTGCCTGGTCCTTGTCTTTGCCCTCTGCTGGCTTCCCCTTCACCTCAG      | 1262 |
| Db | 781  | CAAAACTGTCTTTTGCCTGGTCCTTGTCTTTGCCCTCTGCTGGCTTCCCCTTCACCTCAG      | 840  |
| Qy | 1263 | CAGGATTCTGAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGAACCTTTGAG      | 1322 |
| Db | 841  | CAGGATTCTGAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGAACCTTTGAG      | 900  |
| Qy | 1323 | CTTTCTGTTGGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCCTGCATTAA      | 1382 |
| Db | 901  | CTTTCTGTTGGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCCTGCATTAA      | 960  |
| Qy | 1383 | CCCAATTGCTCTGTATTTGGTGAGCAAAAGATTCAAAAAGCTTTAAGTCATGCTTATG        | 1442 |
| Db | 961  | CCCAATTGCTCTGTATTTGGTGAGCAAAAGATTCAAAAAGCTTTAAGTCATGCTTATG        | 1020 |
| Qy | 1443 | CTGCTGGTGCCAGTCATTTGAAGAAAAACAGTCCTTGGAGGAAAAGCAGTCGTGCTTAAA      | 1502 |

Db 1021 CTGCTGGTGCCAGTCATTTGAAGAAAAACAGTCCTTGGAGGAAAAGCAGTCGTGCTTAAA 1080

Qy 1503 GTTCAAAGCTAATGATCACGGATATGACAACCTCCGTTCCAGTAATAAATACAGCTCATC 1562  
 |||

Db 1081 GTTCAAAGCTAATGATCACGGATATGACAACCTCCGTTCCAGTAATAAATACAGCTCATC 1140

Qy 1563 TTGA 1566  
 |||

Db 1141 TTGA 1144

RESULT 10

BI520706/c

LOCUS BI520706 957 bp mRNA linear EST 29-AUG-2001

DEFINITION 603071813T1 NIH\_MGC\_119 Homo sapiens cDNA clone IMAGE:5163746 3',  
 mRNA sequence.

ACCESSION BI520706

VERSION BI520706.1 GI:15345498

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 957)

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)

Tissue Procurement: Life Technologies, Inc.

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: LLAM11406 row: j column: 03

High quality sequence start: 4

High quality sequence stop: 954.

FEATURES

source

Location/Qualifiers

1. .957

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:5163746"

/tissue\_type="medulla"

/lab\_host="DH10B"

/clone\_lib="NIH\_MGC\_119"

/note="Organ: brain; Vector: pCMV-SPORT6; Site\_1: NotI;  
 Site\_2: EcoRV (destroyed); RNA source normal medulla from  
 anonymous male age 27. Library is oligo-dT primed and  
 directionally cloned (EcoRV site is destroyed upon  
 cloning). Average insert size 1.3 kb, insert size range  
 0.9-3 kb. Library is normalized and enriched for  
 full-length clones and was constructed by C. Gruber  
 (Invitrogen). Research Genetics tracking code 013. Note:  
 this is a NIH\_MGC Library."

ORIGIN

Query Match 20.1%; Score 866; DB 12; Length 957;  
 Best Local Similarity 96.5%; Pred. No. 2.8e-156;  
 Matches 917; Conservative 0; Mismatches 30; Indels 3; Gaps 3;

|    |      |  |      |
|----|------|--|------|
| Qy | 569  | TGTTTCGTGCTGGGGATCATCGGGAACCTCCACACTTCTGAGAATTATCTACAAGAACAAGT | 628  |
|    |      |  |      |
| Db | 956  | TGTTTCGTGCTGGGGATCATCCGGAACCTCCACACTTCTGAGAATACTCTACAGAACCAAGG | 897  |
| Qy | 629  | GCATGCGAAACGGTCCCAATATCTTGATCGCCAGCTTGGCTCTGGGAGACCTGCTGCACA   | 688  |
|    |      |  |      |
| Db | 896  | CAATGCGAAACGGTCCCAATATCTGATCGCCAGCTTGGCTTCTGGGAGACCTGCTGCACA   | 837  |
| Qy | 689  | TCGTCATTGACATCCCTATCAATGTCTACAAGCTGCTGGCAGAGGACTGGCCATTTGGAG   | 748  |
|    |      |  |      |
| Db | 836  | TCGTCATTGACATCCCTATCAAGGTCTACAAGCTG-TTGCAGAGGACTGGCCATTTGGAG   | 778  |
| Qy | 749  | CTGAGATGTGTAAGCTGGTGCCTTTCATACAGAAAGCCTCCGTGGGAATCACTGTGCTGA   | 808  |
|    |      |  |      |
| Db | 777  | CTGAGATGTGTAAGCTGGTGCCTTTCATACAGAAAGCCTCCGTGGGAATCACTGTGCTGA   | 718  |
| Qy | 809  | GTCTATGTGCTCTGAGTATTGACAGATATCGAGCTGTTGCTTCTTGAGTAGAATTAAAG    | 868  |
|    |      |  |      |
| Db | 717  | GTCTATGTGCTCTGAGTATTGACAGATATCGAGCTGTTGCTTCTTGAGTAGAATTAAAG    | 658  |
| Qy | 869  | GAATTGGGGTTCCAAAATGGACAGCAGTAGAAATTGTTTTGATTTGGGTGGTCTCTGTGG   | 928  |
|    |      |  |      |
| Db | 657  | GAATTGGGGTTCCAAAATGGACAGCAGTAGAAATTGTTTTGATTTGGGTGGTCTCTGTGG   | 598  |
| Qy | 929  | TTCTGGCTGTCCCTGAAGCCATAGTTTTGATATAATTACGATGGACTACAAAGGAAGTT    | 988  |
|    |      |  |      |
| Db | 597  | TTCTGGCTGTCCCTGAAGCCATAGTTTTGATATAATTACGATGGACTACAAAGGAAGTT    | 538  |
| Qy | 989  | ATCTGCGAATCTGCTTGCTTCATCCCCTCAGAAGACAGCTTTCATGCAGTTTACAAGA     | 1048 |
|    |      |  |      |
| Db | 537  | ATCTGCGAATCTGCTTGCTTCATCCCCTCAGAAGACAGCTTTCATGCAGTTTACAAGA     | 478  |
| Qy | 1049 | CAGCAAAAGATTGGTGGCTGTTCAAGTTTCTATTTCTGCTTGCCATTGGCCATCACTGCAT  | 1108 |
|    |      |  |      |
| Db | 477  | CAGCAAAAGATTGGTGGCTGTTCAAGTTTCTATTTCTGCTTGCCATTGGCCATCACTGCAT  | 418  |
| Qy | 1109 | TT-TTTTATACACTAATGACCTGTGAAATGTTGAGAAAGAAAAGTGGCATGCAGATTGCT   | 1167 |
|    |      |  |      |
| Db | 417  | TTGTTTTATACACTAATGACCTGTGAAATGTTGAGAAAGAAAAGTGGCATGCAGATTGCT   | 358  |
| Qy | 1168 | TTAAATGATCACCTAAAGCAGAGACGGGAAGTGGCCAAAACCGTCTTTTGCCTGGTCCTT   | 1227 |
|    |      |  |      |
| Db | 357  | TTAAATGATCACCTAAAGCAGAGACGGGAAGTGGCCAAAACCGTCTTTTGCCTGGTCCTT   | 298  |
| Qy | 1228 | GTCTTTGCCCTCTGCTGGCTTCCCCTTCACCTCAGCAGGATTCTGAAGCTCACTCTTTAT   | 1287 |
|    |      |  |      |
| Db | 297  | GTCTTTGCCCTCTGCTGGCTTCCCCTTCACCTCAGCAGGATTCTGAAGCTCACTCTTTAT   | 238  |
| Qy | 1288 | AATCAGAATGATCCCAATAGATGTGAACCTTTTGAAGCTTCTGTTGGTATTGGACTATATT  | 1347 |
|    |      |  |      |
| Db | 237  | AATCAGAATGATCCCAATAGATGTGAACCTTTTGAAGCTTCTGTTGGTATTGGACTATATT  | 178  |

Qy 1348 GGTATCAACATGGCTTCACTGAATTCCTGCATTAACCCAATTGCTCTGTATTTGGTGAGC 1407  
 |||  
 Db 177 GGTATCAACATGGCTTCACTGAATTCCTGCATTAACCCAATTGCTCTGTATTTGGTGAGC 118  
 Qy 1408 AAAAGATTCAAAAAGCTGCTTTAAGTCATGCTTATGCT-GCTGGTGCCAGTCATTTGAAGA 1466  
 |||  
 Db 117 AAAAGATTCAACAAGCTGCTTTAAGTCATGCTTATGCTGGCTGGTGCCAGTCATTTGAAGA 58  
 Qy 1467 AAAACAGTCCTTGGAGGAAAAGCAGTCGTGCTTAAAGTTCAAAGCTAATG 1516  
 |||  
 Db 57 AAAACAGTCCTTGGAGGAAAAGCAGTCGTGCTTAAAGTTACAGCTAAGG 8

RESULT 11

AL553041/c

LOCUS AL553041 1201 bp mRNA linear EST 31-MAY-2003

DEFINITION AL553041 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA  
 clone CSODI072YK22 3-PRIME, mRNA sequence.

ACCESSION AL553041

VERSION AL553041.2 GI:31274855

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 1201)

AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.

TITLE Full-length cDNA libraries and normalization

JOURNAL Unpublished (2001)

COMMENT On Feb 15, 2001 this sequence version replaced gi:12892503.

Contact: Genoscope

Genoscope - Centre National de Sequencage

BP 191 91006 EVRY cedex - France

Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr

Library was constructed by Life Technologies, a division of  
 Invitrogen. This sequence belongs to sequence cluster 7006.r For  
 more information about this cluster, see

<http://www.genoscope.cns.fr/>

[cgi-bin/cluster.cgi?seq=CSODI072BF11NP1&cluster=7006.r](http://www.genoscope.cns.fr/cgi-bin/cluster.cgi?seq=CSODI072BF11NP1&cluster=7006.r). Contact :

Feng Liang Email : [fliang@lifetech.com](mailto:fliang@lifetech.com) URL :

<http://fulllength.invitrogen.com/> InVitroGen Corporation 1600

Faraday Avenue Genoscope sequence ID : CSODI072BF11NP1.

FEATURES

Location/Qualifiers

source

1. .1201

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="CSODI072YK22"

/tissue\_type="PLACENTA COT 25-NORMALIZED"

/clone\_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"

/note="1st strand cDNA was primed with a NotI-oligo(dT)  
 primer. Five prime end enriched, double-strand cDNA was  
 digested with Not I and cloned into the Not I and EcoR V  
 sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

Query Match 20.0%; Score 860.2; DB 9; Length 1201;  
 Best Local Similarity 89.9%; Pred. No. 3.5e-155;  
 Matches 966; Conservative 32; Mismatches 54; Indels 22; Gaps 7;

|    |      |   |      |
|----|------|---|------|
| Qy | 3179 | AAATTTTACTTTGTTTTCTTTTAATAGGCTGGGCCACATGTTGGAAATAAGCTAGTAA    | 3238 |
|    |      | ::  :     : :    : : :     : :                                |      |
| Db | 1061 | AAATCCMAAATTAMCTTTTTYYTTWAAWGKCKGKCCACWKTKKRAAAAK-----CTWKA   | 1007 |
| Qy | 3239 | TGTTGTTTTCTGTCAATATTGAATGTGATGGTACAGTAAACCAAAACCAACAATGTGGC   | 3298 |
|    |      | :   :             |      |
| Db | 1006 | AATTTKTTTCTTCCAATATTAATTTT-----TTTACATAAAACCAAAACCAACAATTTKCC | 952  |
| Qy | 3299 | CAGAAAGAAAGAGCAATAATAATTAATTCACACACCATATGGATTCTATTTATAAATCAC  | 3358 |
|    |      | :   :   :       : :     :   :                                 |      |
| Db | 951  | ATAAAKTAA--KKTCAWTATWATTAATTCACMCMCCATATKTATYCTATTTATAAATCAC  | 894  |
| Qy | 3359 | CCACAAACTTGTCTTTAATTTTCATCCCAATCACTTTTTTCAGAGGCCTGTTATCATAGAA | 3418 |
|    |      | :    :      :                  :                              |      |
| Db | 893  | CCACAWACTTKTTCTTTAATTCMWTCCCAATCACTTTTTTCAGAGKCTGTTATCATAGAA  | 834  |
| Qy | 3419 | GTCATTTTAGACTCTCAATTTTAAATT-AATTTTGAATCACTAATATTTTCACAGTTTAT  | 3477 |
|    |      |   |      |
| Db | 833  | GTCATTTTAGACTCTCAATTTTAAATTAAATTTTGAATCACTAATATTTTCACAGTTTAT  | 774  |
| Qy | 3478 | TAATATATTTAATTTCTATTTAAATTTTAGATTATTTTATTACCATGTACTGAATTTT    | 3537 |
|    |      |   |      |
| Db | 773  | TAATATATTTAATTTCTATTTAAATTTTAGATTATTTTATTACCATGTACTGAATTTT    | 714  |
| Qy | 3538 | ACATCCTGATACCCTTTCCTTCTCCATGTCAGTATCATGTTCTCTAATTATCTTGCCAAA  | 3597 |
|    |      |   |      |
| Db | 713  | ACATCCTGATACCCTTTCCTTCTCCATGTCAGTATCATGTTCTCTAATTATCTTGCCAAA  | 654  |
| Qy | 3598 | TTTTGAAACTACACACAAAAAGCATACTTGCATTATTTATAATAAAATGTCATTTCAGTGG | 3657 |
|    |      |   |      |
| Db | 653  | TTTTGAAACTACACACAAAAAGCATACTTGCATTATTTATAATAAAATCGCATTTCAGTGG | 594  |
| Qy | 3658 | CTTTTTAAAAAAATGTTTGATTCAAAACTTTAACATACTGATAAGTAAGAAACAATTAT   | 3717 |
|    |      | :   |      |
| Db | 593  | CTTTTT-AAAAAATGTTTGATTCAAAACTTTVACATACTGATAAGTAAGAAACAATTAT   | 535  |
| Qy | 3718 | AATTTCTTTACATACTCAAAACCAAGATAGAAAAGGTGCTATCGTTCAACTTCAAAACA   | 3777 |
|    |      |   |      |
| Db | 534  | AATTTCTTNACATACTCAAAACCAAGATAGAAAAGGTGCTATCGTTCAACTTCAAAACA   | 475  |
| Qy | 3778 | TGTTTCCTAGTATTAAGGACTTTAATATAGCAACAGACAAAATTATTGTTAACATGGATG  | 3837 |
|    |      | : :   |      |
| Db | 474  | TGTTTCCTAGTATTAAGGACTTTAATATVGCACAGACAAAATTATTGTTAACATGGATG   | 415  |
| Qy | 3838 | TTACAGCTCAAAAGATTTATAAAAGATTTTAACCTATTTTCTCCCTTATTATCCACTGCT  | 3897 |
|    |      |   |      |
| Db | 414  | TTACAGCTCAAAAGATTTATAAAAGATTTTAACCTATTTTCTCCCTTATTATCCACTGCT  | 355  |
| Qy | 3898 | AATGTGGATGTATGTTCAAACACCTTTTAGTATTGATAGCTTACATATGGCCAAAGGAAT  | 3957 |
|    |      |   |      |
| Db | 354  | AATGTGGATGTATGTTCAAACACCTTTTAGTATTGATAGCTTACATATGGCCAAAGGAAT  | 295  |
| Qy | 3958 | ACAGTTTATAGCAAAACATGGGTATGCTGTAGCTAACTTTATAAAAGTGTAATATAACAA  | 4017 |

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Db      294  |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
          ACAGTTTATAGCAAAACATGGGTATGCTGTAGCTAACTTTATAAAAGTGTAATATAACAA 235

Qy      4018 TGTAAAAAATTATATATCTGGGAGGATTTTTTGGTTGCCTAAAGTGGCTATAGTTACTGA 4077
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      234  TGTAAAAAATTATATATCTGGGAGGATTTTTTGGTTGCCTAAAGTGGCTATAGTTACTGA 175

Qy      4078 TTTTTTTATTATGTAAGCAAAACCAATAAAAAATTTAAGTTTTTTTTT-AACAACTACCTTATT 4136
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      174  TTTTTTTATTATGTAAGCAAAACCAATAAAAAATTTAAGTTTTTTTTTCAACAACTACCTTATT 115

Qy      4137 TTTCACTGTACAGACACTAATTCATTAAATACTAA-----TTGATTGTTTAAAAGAAA 4189
          ||||||||||||||||||||||||||||||||||| |||||||||||||||
Db      114  TTTCACTGTACAGACACTAATTCATTAAATACTCACACTCTCGCACTTGTTTAAAAGAAA 55

Qy      4190 TATAAATGTGACAAGTGGACATTATTTATGTTAAATATACAATTATCAAGCAAG 4243
          |||||:|:|:|||||||||||||||||||||
Db      54   TATAAAKGBGMCAAGTGGACATTATTTATGTTAAATATACAATTATCAAGCAAG 1

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# RESULT 12

AL543805

LOCUS AL543805 942 bp mRNA linear EST 31-MAY-2003

DEFINITION AL543805 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA clone CS0DI005YG20 5-PRIME, mRNA sequence.

ACCESSION AL543805

VERSION AL543805.2 GI:31265651

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 942)

AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.

TITLE Full-length cDNA libraries and normalization

JOURNAL Unpublished (2001)

COMMENT On Feb 15, 2001 this sequence version replaced gi:12876284.

Contact: Genoscope

Genoscope - Centre National de Sequencage

BP 191 91006 EVRY cedex - France

Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr

Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 7006.r For more information about this cluster, see

<http://www.genoscope.cns.fr/>

[cgi-bin/cluster.cgi?seq=CS0DI005BD10QP1&cluster=7006.r](http://cgi-bin/cluster.cgi?seq=CS0DI005BD10QP1&cluster=7006.r). Contact :

Feng Liang Email : [fliang@lifetech.com](mailto:fliang@lifetech.com) URL :

<http://fulllength.invitrogen.com/> InVitroGen Corporation 1600

Faraday Avenue Genoscope sequence ID : CS0DI005BD10QP1.

## FEATURES

source

Location/Qualifiers

1. .942

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="CS0DI005YG20"

/tissue\_type="PLACENTA COT 25-NORMALIZED"

/clone\_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"



```
/note="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
```

Query Match 19.8%; Score 851; DB 9; Length 942;  
Best Local Similarity 98.1%; Pred. No. 2.2e-153;  
Matches 876; Conservative 4; Mismatches 11; Indels 2; Gaps 2;

|    |      |   |      |
|----|------|---|------|
| Qy | 1803 | TTTACAGTTAGCACTTCAACATAGCTCTTAACAACCTCCAGGATATTCACACAACACTTA  | 1862 |
| Db | 51   | TTCCCGGGATGCACTTCAACATAGCTCTTAACAACCTCCAGGATATTCACACAACACTTA  | 110  |
| Qy | 1863 | GGCTTAAAAATGAGCTCACTCAGAATTTCTATTCTTTCTAAAAAGAGATTATTTTAAAA   | 1922 |
| Db | 111  | GGCTTAAAAATGAGCTCACTCAGAATTTCTATTCTTTCTAAAAAGAGATTATTTTAAAA   | 170  |
| Qy | 1923 | TCAATGGGACTCTGATATAAAGGAAGAATAAGTCACTGTAAAACAGAACTTTTAAATGAA  | 1982 |
| Db | 171  | TCAATGGGACTCTGATATAAAGGAAGAATAAGTCACTGTAAAACAGAACTTTTAAATGAA  | 230  |
| Qy | 1983 | GCTTAAATTACTCAATTTAAAATTTTAAAATCCTTTAAAAC-ACTTTTCAATTAATATT   | 2041 |
| Db | 231  | GCTTAAATTACTCAATTTAAAATTTTAAAATCCTTTAAAAC-TAACTTTTCAATTAATATT | 290  |
| Qy | 2042 | ATCACACTATTATCAGATTGTAATTAGATGCAAATGAGAGAGCAGTTTAGTTGTTGCATT  | 2101 |
| Db | 291  | ATCACACTATTATCAGATTGTAATTAGATGCAAATGAGAGAGCAGTTTAGTTGTTGCATT  | 350  |
| Qy | 2102 | TTTCGGACACTGGAAACATTTAAATGATCAGGAGGGAGTAACAGAAAGAGCAAGGCTGTT  | 2161 |
| Db | 351  | TTTCGGACACTGGAAACATTTAAATGATCAGGAGGGAGTAACAGAAAGAGCAAGGCTGTT  | 410  |
| Qy | 2162 | TTTGAAAATCATTACACTTTCACTAGAAGCCCAAACCTCAGCATTCTGCAATATGTAACC  | 2221 |
| Db | 411  | TTTGAAAATCATTACACTTTCACTAGAAGCCCAAACCTCAGCATTCTGCAATATGTAACC  | 470  |
| Qy | 2222 | AACATGTCACAAACAAGCAGCATGTAACAGACTGGCACATGTGCCAGCTGAATTTAAAAT  | 2281 |
| Db | 471  | AACATGTCACAAACAAGCAGCATGTAACAGACTGGCACATGTGCCAGCTGAATTTWAAAT  | 530  |
| Qy | 2282 | ATAATACTTTTTAAAAGAAAATTATTACATCCTTTACATTAGTTAAGATCAAACCTCAC   | 2341 |
| Db | 531  | ATAATACTTTTTAAAAGARAATTATTACATCCTTTACATTAGTTAAGATCAAACCTCAC   | 590  |
| Qy | 2342 | AAAGAGAAATAGAATGTTTGAAAGGCTATCCCAAAGACTTTTTTGAATCTGTCATTCAC   | 2401 |
| Db | 591  | AAAGAGAAATAGAATGTTTGANAGGCTATCCCAAAGACTTTTTTGAATCTGTCNTTCTC   | 650  |
| Qy | 2402 | ATACCCTGTGAAGACAATACTATCTACAATTTTTTCAGGATTATTAATAATCTTCTTTTT  | 2461 |
| Db | 651  | ATACCCTGTGAAGACAATACTATCTACAATTTTTTCAGGATTATTAAMATCTTCTTCTTT  | 710  |
| Qy | 2462 | CACTATCGTAGCTTAAACTCTGTTTGGTTTTGTCATCTGTAAATACTTACCTACATACAC  | 2521 |
| Db | 711  | CACTATCGTAGCTTAAACTCTGTTTGGTTTTGTCATCTGTAAATACTTACCTACATACAC  | 770  |

Qy 2522 TGCATGTAGATGATTAAATGAGGGCAGGCCCTGTGCTCATAGCTTTACGATGGAGAGATG 2581  
 |||:|||||  
 Db 771 TGCATGTAGATGATTAAATGAGGGCAGGCCCTGTGCTCATAGCTTTACGATGGAGAGATG 830

Qy 2582 CCAGTGACCTCATAATAAAGACTGTGAACTGCCCTGGTGCAGTGTCCACATGACAAAGGGG 2641  
 |||:|||||  
 Db 831 CCAGTGACCTCATAATAAAGACTGTGAACTGCCCTGGTGCAGTGTCCACATGACAAAGGGG 890

Qy 2642 CAGGTAGCACCTCTCTCACCCATGCTGTGGTTAAAATGGTTTCTAGCATATG 2694  
 |||:|||||  
 Db 891 CAGGTAGCACCTCTCTCACCCATGCTGTGGTT-AAATGGTTTCTAGCATATG 942

# RESULT 13

BQ229233

LOCUS BQ229233 891 bp mRNA linear EST 02-MAY-2002

DEFINITION AGENCOURT\_7511051 NIH\_MGC\_72 Homo sapiens cDNA clone IMAGE:6055288  
 5', mRNA sequence.

ACCESSION BQ229233

VERSION BQ229233.1 GI:20410633

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 891)

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)

Tissue Procurement: ATCC/DCTD/DTP

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: LLAM13315 row: e column: 17

High quality sequence stop: 696.

FEATURES Location/Qualifiers

source 1..891

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:6055288"

/tissue\_type="melanotic melanoma"

/lab\_host="DH10B (phage-resistant)"

/clone\_lib="NIH\_MGC\_72"

/note="Organ: skin; Vector: pCMV-SPORT6; Site\_1: NotI;

Site\_2: SalI; Cloned unidirectionally. Primer: Oligo dT.

Average insert size 2 kb. Library constructed by Life  
 Technologies."

## ORIGIN

Query Match

19.7%; Score 848; DB 13; Length 891;

Best Local Similarity 99.1%; Pred. No. 8.3e-153;  
Matches 884; Conservative 0; Mismatches 5; Indels 3; Gaps 3;

|    |      |   |      |
|----|------|---|------|
| Qy | 2086 | GTTTAGTTGTTGCATTTTTCGGACACTGGAAACATTTAAATGATCAGGAGGGAGTAACAG  | 2145 |
|    |      |   |      |
| Db | 1    | GTTTAGTTGTTGCATTTTTCGGACACTGGAAACATTTAAATGATCAGGAGGGAGTAACAG  | 60   |
| Qy | 2146 | AAAGAGCAAGGCTGTTTTGAAAATCATTACACTTTCAC TAGAAGCCCAAACCTCAGCAT  | 2205 |
|    |      |   |      |
| Db | 61   | AAAGAGCAAGGCTGTTTTGAAAATCATTACACTTTCAC TAGAAGCCCAAACCTCAGCAT  | 120  |
| Qy | 2206 | TCTGCAATATGTAACCAACATGTCACAAACAAGCAGCATGTAACAGACTGGCACATGTGC  | 2265 |
|    |      |   |      |
| Db | 121  | TCTGCAATATGTAACCAACATGTCACAAACAAGCAGCATGTAACAGACTGGCACATGTGC  | 180  |
| Qy | 2266 | CAGCTGAATTTAAAATATAATACTTTTAAAAAGAAAATTATTACATCCTTTACATTTCAGT | 2325 |
|    |      |   |      |
| Db | 181  | CAGCTGAATTTAAAATATAATACTTTTAAAAAGAAAATTATTACATCCTTTACATTTCAGT | 240  |
| Qy | 2326 | TAAGATCAAACCTCACAAAGAGAAATAGAATGTTTGAAAGGCTATCCCAAAGACTTTTTT  | 2385 |
|    |      |   |      |
| Db | 241  | TAAGATCAAACCTCACAAAGAGAAATAGAATGTTTGAAAGGCTATCCCAAAGACTTTTTT  | 300  |
| Qy | 2386 | TGAATCTGTCATTACATACCCTGTGAAGACAATACTATCTACAATTTTTTTCAGGATTAT  | 2445 |
|    |      |   |      |
| Db | 301  | TGAATCTGTCATTACATACCCTGTGAAGACAATACTATCTACAATTTTTTTCAGGATTAT  | 360  |
| Qy | 2446 | TAAAATCTTCTTTTTTCACTATCGTAGCTTAAACTCTGTTTGGTTTTGTCATCTGTAAAT  | 2505 |
|    |      |   |      |
| Db | 361  | TAAAATCTTCTTCTTTCACTATCGTAGCTTAAACTCTGTTTGGTTTTGTCATCTGTAAAT  | 420  |
| Qy | 2506 | ACTTACCTACATACACTGCATGTAGATGATTAAATGAGGGCAGGCCCTGTGCTCATAGCT  | 2565 |
|    |      |   |      |
| Db | 421  | ACTTACCTACATACACTGCATGTAGATGATTAAATGAGGGCAGGCCCTGTGCTCATAGCT  | 480  |
| Qy | 2566 | TTACGATGGAGAGATGCCAGTGACCTCATAATAAAGACTGTGAAGTGCCTGGTGCAGTGT  | 2625 |
|    |      |   |      |
| Db | 481  | TTACGATGGAGAGATGCCAGTGACCTCATAATAAAGACTGTGAAGTGCCTGGTGCAGTGT  | 540  |
| Qy | 2626 | CCACATGACAAAGGGGCAGGTAGCACCCCTCTCTCACCCATGCTGTGGTTAAAATGGTTTC | 2685 |
|    |      |   |      |
| Db | 541  | CCACATGACAAAGGGGCAGGTAGCACCCCTCTCTCACCCATGCTGTGGTTAAAATGGTTTC | 600  |
| Qy | 2686 | TAGCATATGTATAATGCTATAGTTAAATACTATTTTTCAAATCATACAGATTAGTACA    | 2745 |
|    |      |   |      |
| Db | 601  | TAGCATATGTATAATGCTATAGTTAAATACTATTTTTCAAATCATACAGATTAGTACA    | 660  |
| Qy | 2746 | TTTAACAGCTACCTGTAAAGCTTATTACTAATTTTTGTATTATTTTTGTAAATAGCCAAT  | 2805 |
|    |      |   |      |
| Db | 661  | TTTAACAGCTACCTGTAAAGCTTATTACTAATTTTTGTATTATTTTTGTAAATAGCCAAT  | 720  |
| Qy | 2806 | AGAAAAGTTTGCTTGACATGGTGCTTTTCTTTCATCTAGAGGC-AAAAGTCTTTTTGAG   | 2864 |
|    |      |   |      |
| Db | 721  | AGAAAAGTTTGCTTGACATGGTGCTTTTCTTTCATCTAGAGGC-AAAAGTCTTTTTGAG   | 780  |
| Qy | 2865 | ACCGTAAGAACCTCTTAGCTTTGTGCGTTCCTGCCTAATTTTTATATCTTCTAAGCAAAG  | 2924 |
|    |      |   |      |

Db 781 ACCGTAAGAACCTCTTACCTTTGTGCGTTCCTGCCTAA-TTTTAAATCTTCTAAGCAAAG 839

Qy 2925 TGCCTTAGGATAGCTTGGG-ATGAGATGTGTGTGAAAGTATGTACAAGAGAA 2975  
 |||||

Db 840 TGCCTTAGGATAGCTTGGGAATGAGATGTGTGTGAAAATATGTACAAGAAAA 891

# RESULT 14

AL546465

LOCUS AL546465 1201 bp mRNA linear EST 31-MAY-2003

DEFINITION AL546465 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA  
 clone CS0DI030YM19 5-PRIME, mRNA sequence.

ACCESSION AL546465

VERSION AL546465.2 GI:31268299

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 1201)

AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.

TITLE Full-length cDNA libraries and normalization

JOURNAL Unpublished (2001)

COMMENT On Feb 15, 2001 this sequence version replaced gi:12879606.

Contact: Genoscope

Genoscope - Centre National de Sequencage

BP 191 91006 EVRY cedex - France

Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr

Library was constructed by Life Technologies, a division of  
 Invitrogen. This sequence belongs to sequence cluster 7006.r For  
 more information about this cluster, see

http://www.genoscope.cns.fr/

cgi-bin/cluster.cgi?seq=CS0DI030AG10QP1&cluster=7006.r. Contact :

Feng Liang Email : fliang@lifetech.com URL :

http://fulllength.invitrogen.com/ InVitroGen Corporation 1600

Faraday Avenue Genoscope sequence ID : CS0DI030AG10QP1.

## FEATURES

source

Location/Qualifiers

1. .1201

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="CS0DI030YM19"

/tissue\_type="PLACENTA COT 25-NORMALIZED"

/clone\_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"

/note="1st strand cDNA was primed with a NotI-oligo(dT)  
 primer. Five prime end enriched, double-strand cDNA was

digested with Not I and cloned into the Not I and EcoR V  
 sites of the pCMVSPORT 6 vector. Library was normalized."

## ORIGIN

Query Match 19.0%; Score 816.2; DB 9; Length 1201;

Best Local Similarity 97.2%; Pred. No. 1e-146;

Matches 854; Conservative 7; Mismatches 15; Indels 3; Gaps 3;

Qy 178 TGAAACTTGGCTCTGAAACTGCGGAGCGGCCACCGGACGCCTTCTGGAGCAGGTAGCAGC 237  
 || ||

Db 219 TGTCTCTAGGCTCTGAAACTGCGGAGCGGCCACCGGACGCCTTCTGGAGCAGGTAGCAGC 278

Qy 238 ATGCAGCCGCCTCCAAGTCTGTGCGGACGCGCCCTGGTTGCGCTGGTTCTTGCCTGCGGC 297  
 |||  
 Db 279 ATGCAGCCGCCTCCAAGTCTGTGCGGACGCGCCCTGGTTGCGCTGGTTCTTGCCTGCGGC 338  
 Qy 298 CTGTCGCGGATCTGGGGAGAGGAGAGAGAGGCTTCCCGCCTGACAGGGCCACTCCGCTTTTG 357  
 |||  
 Db 339 CTGTCGCGGATCTGGGGAGAGGAGAGAGAGGCTTCCCGCCTGACAGGGCCACTCCGCTTTTG 398  
 Qy 358 CAAACCGCAGAGATAATGACGCCACCCACTAAGACCTTATGGCCCAAGGGTTCCAACGCC 417  
 |||  
 Db 399 CAAACCGCAGAGATAATGACGCCACCCACTAAGACCTTATGGCCCAAGGGTTCCAACGCC 458  
 Qy 418 AGTCTGGCGCGGTCGTTGGCACCTGCGGAGGTGCCTAAAGGAGACAGGACGGCAGGATCT 477  
 |||  
 Db 459 AGTCTGGCGCGGTCGTTGGCACCTGCGGAGGTGCCTAAAGGAGACAGGACGGCAGGATCT 518  
 Qy 478 CCGCCACGCACCATCTCCCTCCCCCGTGCCAAGGACCCATCGAGATCAAGGAGACTTTC 537  
 |||  
 Db 519 CCGCCACGCACCATCTCCCTCCCCCGTGCCAAGGACCCATCGAGATCAAGGAGACTTTC 578  
 Qy 538 AAATACATCAACACGGTTGTGTCCTGCCTTGTGTTCTGCTGCTGGGGATCATCGGGAATCC 597  
 |||  
 Db 579 AAATACATCAACACGGTTGTGTCCTGCCTTGTGTTCTGCTGCTGGGGATCATCGGGAATCC 638  
 Qy 598 ACACTTCTGAGAATTATCTACAAGAACAAGTGCATGCGAAACGGTCCCAATATCTTGATC 657  
 |||  
 Db 639 ACACTTCTGAGAATTATCTACAAGAACAAGTGCATGCGAAACGGTCCCAATATCTTGATC 698  
 Qy 658 GCCAGCTTGGCTCTGGGAGACCTGCTGCACATCGTCATTGACATCCCTATCAATGTCTAC 717  
 |||  
 Db 699 GCCAGCTTGGCTCTGGGAGACCTGCTGCACATCGTCATTGACATCCCTATCAATGTCTAC 758  
 Qy 718 AAGCTGCTGGCAGAGGACTGGCCATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTTCATA 777  
 |||  
 Db 759 AAGCTGCTGGCAGAGGACTGGCCATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTTCATA 818  
 Qy 778 CAGAAAGCCTCCGTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATAT 837  
 |||  
 Db 819 CAGAAAGCCTCCGTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATAT 878  
 Qy 838 CGAGCTGTTGCTTCTTGGAGTAGAATTAAAGGAATTGGGGTTCCAAAATGGACAGCAGTA 897  
 |||  
 Db 879 CGAGCTGTTGCTTCTTGGAGTAGAATTAAAGGAATTGGGGTT-CAAAATGGACAGCAGTA 937  
 Qy 898 GAAATTGTTTTGATTTGGGTGGTCTCTGTGGTTCTGGCTGTCCCTGAAGCCATAGGTTTT 957  
 |||:||||  
 Db 938 GAAATTGTTTTKATTTGGGTGGTCTCTGTGGTTCTGGCTGTCCCTGAAGCCATAGGTVTT 997  
 Qy 958 GATATAATTACGATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTT 1017  
 |||:||||  
 Db 998 GATATAATTACGATGGACTACAAAGG-AGTTATCTGCGAATCTGCTTGCTT-MWCCSGT 1055  
 Qy 1018 CAGAAGACAGCTTTTCATGCAGTTTTACAAGACAGCAAAA 1056  
 :||| ||| : |||  
 Db 1056 YARAAGAAAGCTTTTCATGCAGTTTTACAAAAMAGCAAAA 1094

## RESULT 15

BI858627

LOCUS BI858627 972 bp mRNA linear EST 10-OCT-2001

DEFINITION 603389094F1 NIH\_MGC\_87 Homo sapiens cDNA clone IMAGE:5398054 5',  
mRNA sequence.

ACCESSION BI858627

VERSION BI858627.1 GI:15999374

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 972)

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)

Tissue Procurement: DCTD/DTP

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:<http://image.llnl.gov>

Plate: LLAM12014 row: 1 column: 23

High quality sequence stop: 899.

## FEATURES

source

Location/Qualifiers

1. .972

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:5398054"

/tissue\_type="mammary adenocarcinoma, cell line"

/lab\_host="DH10B (phage-resistant)"

/clone\_lib="NIH\_MGC\_87"

/note="Organ: breast; Vector: pCMV-SPORT6; Site\_1: NotI;

Site\_2: SalI; Cloned unidirectionally; oligo-dT primed.

Average insert size 1.383 kb. Library enriched for

full-length clones and constructed by Life Technologies.

Note: this is a NIH\_MGC Library."

## ORIGIN

Query Match 18.8%; Score 808.6; DB 12; Length 972;

Best Local Similarity 96.3%; Pred. No. 3.1e-145;

Matches 903; Conservative 0; Mismatches 25; Indels 10; Gaps 7;

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Qy      321 GAGAGGCTTCCCGCCTGACAGGGCCACTCCGCTTTTGCAAACCGCAGAGATAATGACGCC 380
          |||
Db       1 GAGAGGCTTCCCGCCTGACAGGGCCACTCCGCTTTTGCAAACCGCAGAGATAATGACGCC 60

Qy      381 ACCCACTAAGACCTTATGGCCCAAGGGTTCCAACGCCAGTCTGGCGCGGTTCGTTGGCACC 440
          |||
Db       61 ACCCACTAAGACCTTATGGCCCAAGGGTTCCAACGCCAGTCTGGCGCGGTTCGTTGGCACC 120

Qy      441 TGCGGAGGTGCCTAAAGGAGACAGGACGGCAGGATCTCCGCCACGCACCATCTCCCTCC 500
```

```

Db      121  TCGCGGAGGTGCCTAAAGGAGACAGGACGGCAGGATCTCCGCCACGCACCATCTCCCCTCC 180
Qy      501  CCCGTGCCAAGGACCCATCGAGATCAAGGAGACTTTCAAATACATCAACACGGTTGTGTC 560
Db      181  CCCGTGCCAAGGACCCATCGAGATCAAGGAGACTTTCAAATACATCAACACGGTTGTGTC 240
Qy      561  CTGCCTTGTGTTTCGTGCTGGGGATCATCGGGAACCTCCACACTTCTGAGAATTATCTACAA 620
Db      241  CTGCCTTGTGTTTCGTGCTGGGGATCATCGGGAACCTCCACACTTCTGAGAATTATCTACAA 300
Qy      621  GAACAAGTGCATGCGAAACGGTCCCAATATCTTGATCGCCAGCTTGGCTCTGGGAGACCT 680
Db      301  GAACAAGTGCATGCGAAACGGTCCCAATATCTTGATCGCCAGCTTGGCTCTGGGAGACCT 360
Qy      681  GCTGCACATCGTCATTGACATCCCTATCAATGTCTACAAGCTGCTGGCAGAGGACTGGCC 740
Db      361  GCTGCACATCGTCATTGACATCCCTATCAATGTCTACAAGCTGCTGGCAGAGGACTGGCC 420
Qy      741  ATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTTCATACAGAAAGCCTCCGTGGGAATCAC 800
Db      421  ATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTTCATACAGAAAGCCTCCGTGGGAATCAC 480
Qy      801  TGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATATCGAGCTGTTGCTTCTTGGAGTAG 860
Db      481  TGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATATCGAGCTGTTGCTTCTTGGAGTAG 540
Qy      861  AATTAAAGGAA-TTGGGGTTCCAAAATGGACAGCAGTAGAAATTGTTTTGATTGGGTGG 919
Db      541  AATTAAAGGAAC-TTGGGGTTCCAAAATGGACAGCAGTAGAAATCG-TTTGATTGGGTGG 599
Qy      920  TCTCTGTGGTTCTGGCTGTCCCTGAAGCCATAGGTTTTGATATAATTACGATGGACTACA 979
Db      600  TCTCTGTGGTTCTGGCTGTCCCTGAAGCCATAGG-TTTGATATAATTACGATGGACTACA 658
Qy      980  AAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTTCAGAAGACAGCTTTCATGCAGT 1039
Db      659  AAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTTCAGAAGACAGCTTTCATGCAGT 718
Qy      1040 TTTACAAGACAGCAAAAGATTGGT-GGCTGTTTCAGTTTCTATTTCTGCTTGCCATT-GGC 1097
Db      719  TTTACAAGACAGCAAAAGATTGGTGGGCTATTTCAGTTTCTATTTCTGCTTGCCATNGGGG 778
Qy      1098 CATCACTGCATTTTTTTTATACACTAATGACCTGTGAAATGTTGAGAAAGAAAAGTGGCAT 1157
Db      779  CATCACTGCATTTTTTTTATACACTAATGACCTGTGACATGTTGAGAACGAACAGTGGCTT 838
Qy      1158 GCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAAGTGGCCAAAACCGTCTTTTG 1217
Db      839  GCAGAT--GCTTTAATGATCACCTAAAGCAGAGACGGAA---GTGGCAAACCGTCTTTTG 893
Qy      1218 CCTGGTCCCTTGTCTTTTGCCCTCTGCTGGCTTCCCCTTC 1255
Db      894  CCTGGTCCCTTGTCTTTTGCCCTCTGCTGGGTTCCTTAC 931

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Search completed: May 14, 2004, 15:46:36

Job time : 10214.3 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 13, 2004, 23:17:23 ; Search time 16247.7 Seconds  
(without alignments)  
11473.517 Million cell updates/sec

Title: US-09-931-157-2  
Perfect score: 4301  
Sequence: 1 gagacattccggtgggggac.....ctgggaaaaaaaaaaaaaa 4301

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : GenEmbl:\*  
1: gb\_ba:\*  
2: gb\_htg:\*  
3: gb\_in:\*  
4: gb\_om:\*  
5: gb\_ov:\*  
6: gb\_pat:\*  
7: gb\_ph:\*  
8: gb\_pl:\*  
9: gb\_pr:\*  
10: gb\_ro:\*  
11: gb\_sts:\*  
12: gb\_sy:\*  
13: gb\_un:\*  
14: gb\_vi:\*  
15: em\_ba:\*  
16: em\_fun:\*  
17: em\_hum:\*  
18: em\_in:\*  
19: em\_mu:\*  
20: em\_om:\*  
21: em\_or:\*  
22: em\_ov:\*  
23: em\_pat:\*  
24: em\_ph:\*  
25: em\_pl:\*  
26: em\_ro:\*  
27: em\_sts:\*

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28: em_un:*
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31: em_htg_inv:*
32: em_htg_other:*
33: em_htg_mus:*
34: em_htg_pln:*
35: em_htg_rod:*
36: em_htg_mam:*
37: em_htg_vrt:*
38: em_sy:*
39: em_htgo_hum:*
40: em_htgo_mus:*
41: em_htgo_other:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

| Result | %      |       | Query  |    | DB       | ID | Description        |
|--------|--------|-------|--------|----|----------|----|--------------------|
|        |        |       |        |    |          |    |                    |
| No.    | Score  | Match | Length |    |          |    |                    |
| 1      | 4301   | 100.0 | 4301   | 6  | AR177880 |    | AR177880 Sequence  |
| 2      | 4301   | 100.0 | 4301   | 6  | E07650   |    | E07650 cDNA encodi |
| 3      | 4286   | 99.7  | 4286   | 9  | HUMETR   |    | D90402 Homo sapien |
| 4      | 4284.4 | 99.6  | 4286   | 6  | AX548828 |    | AX548828 Sequence  |
| 5      | 4284.4 | 99.6  | 4286   | 6  | AX587707 |    | AX587707 Sequence  |
| 6      | 4284.4 | 99.6  | 4286   | 9  | S57283   |    | S57283 Homo sapien |
| 7      | 2857   | 66.4  | 2972   | 9  | D13162S7 |    | D13168 Homo sapien |
| c 8    | 2841.8 | 66.1  | 183337 | 9  | AL139002 |    | AL139002 Human DNA |
| c 9    | 2792.4 | 64.9  | 201093 | 2  | AC144750 |    | AC144750 Pan trogl |
| 10     | 2610   | 60.7  | 2720   | 11 | G06417   |    | G06417 human STS W |
| c 11   | 2550   | 59.3  | 169751 | 2  | AC130785 |    | AC130785 Papio anu |
| c 12   | 2550   | 59.3  | 185870 | 2  | AC129069 |    | AC129069 Papio anu |
| 13     | 1691.8 | 39.3  | 1873   | 6  | AR165435 |    | AR165435 Sequence  |
| 14     | 1691.8 | 39.3  | 1873   | 6  | E15242   |    | E15242 Human mRNA  |
| 15     | 1690.8 | 39.3  | 1872   | 9  | S44866   |    | S44866 ETB endothe |
| 16     | 1495.4 | 34.8  | 1719   | 9  | HUMEDNRB |    | L06623 Homo sapien |
| 17     | 1466.8 | 34.1  | 1470   | 6  | AR270640 |    | AR270640 Sequence  |
| 18     | 1466.8 | 34.1  | 1470   | 9  | HUMETSR  |    | M74921 Human endot |
| 19     | 1389   | 32.3  | 1603   | 9  | BC014472 |    | BC014472 Homo sapi |
| 20     | 1389   | 32.3  | 1632   | 6  | AX342673 |    | AX342673 Sequence  |
| 21     | 1361.4 | 31.7  | 1765   | 9  | AF114165 |    | AF114165 Homo sapi |
| 22     | 1327.4 | 30.9  | 1329   | 9  | AY275463 |    | AY275463 Homo sapi |
| 23     | 1322.6 | 30.8  | 1329   | 6  | AX280873 |    | AX280873 Sequence  |
| 24     | 1222.8 | 28.4  | 1669   | 4  | AF019072 |    | AF019072 Equus cab |
| 25     | 1220.4 | 28.4  | 1578   | 9  | HSX99250 |    | X99250 H.sapiens m |
| 26     | 1197.8 | 27.8  | 2026   | 4  | BOVEETBR |    | D90456 Bos taurus  |
| 27     | 1186   | 27.6  | 1452   | 4  | AF034530 |    | AF034530 Canis fam |
| 28     | 1113   | 25.9  | 2018   | 10 | S65355   |    | S65355 nonselectiv |
| 29     | 1110.2 | 25.8  | 1551   | 6  | E05930   |    | E05930 DNA sequenc |
| 30     | 1104.8 | 25.7  | 2115   | 10 | BC026553 |    | BC026553 Mus muscu |
| 31     | 1099.2 | 25.6  | 1958   | 6  | AX305434 |    | AX305434 Sequence  |
| 32     | 1099.2 | 25.6  | 1958   | 10 | MMU32329 |    | U32329 Mus musculu |
| 33     | 1091   | 25.4  | 1892   | 10 | RNETBREC |    | X57764 Rat mRNA fo |

|      |        |      |        |    |          |                    |
|------|--------|------|--------|----|----------|--------------------|
| 34   | 1091   | 25.4 | 1965   | 6  | E03623   | E03623 DNA encodin |
| 35   | 1086.6 | 25.3 | 1311   | 4  | AF038900 | AF038900 Equus cab |
| 36   | 1070.4 | 24.9 | 1321   | 6  | AR207426 | AR207426 Sequence  |
| 37   | 1067.6 | 24.8 | 1314   | 4  | AF276427 | AF276427 Canis fam |
| 38   | 1042.8 | 24.2 | 1326   | 4  | AF245469 | AF245469 Oryctolag |
| c 39 | 931.8  | 21.7 | 135327 | 2  | AC118537 | AC118537 Felis cat |
| c 40 | 931.8  | 21.7 | 170121 | 2  | AC123546 | AC123546 Felis cat |
| c 41 | 922.2  | 21.4 | 192330 | 2  | AC122157 | AC122157 Canis fam |
| 42   | 746    | 17.3 | 1564   | 5  | AF472616 | AF472616 Gallus ga |
| 43   | 732.6  | 17.0 | 1041   | 5  | CCEDNRB  | X99295 C.coturnix  |
| 44   | 588    | 13.7 | 588    | 11 | G15922   | G15922 human STS C |
| 45   | 564.8  | 13.1 | 1520   | 5  | AF275636 | AF275636 Danio rer |

# ALIGNMENTS

## RESULT 1

ARI77880  
 LOCUS ARI77880 4301 bp DNA linear PAT 17-DEC-2001  
 DEFINITION Sequence 3 from patent US 6313276.  
 ACCESSION ARI77880  
 VERSION ARI77880.1 GI:17920235  
 KEYWORDS .  
 SOURCE Unknown.  
 ORGANISM Unknown.  
 Unclassified.  
 REFERENCE 1 (bases 1 to 4301)  
 AUTHORS Imura,H., Nakao,K. and Nakanishi,S.  
 TITLE Human endothelin receptor  
 JOURNAL Patent: US 6313276-A 3 06-NOV-2001;  
 FEATURES Location/Qualifiers  
 source 1. .4301  
 /organism="unknown"  
 /mol\_type="unassigned DNA"

## ORIGIN

Query Match 100.0%; Score 4301; DB 6; Length 4301;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 4301; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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| Qy | 1   | GAGACATTCCGGTGGGGGACTCTGGCCAGCCCGAGCAACGTGGATCCTGAGAGCACTCCC | 60  |
|    |     |  |     |
| Db | 1   | GAGACATTCCGGTGGGGGACTCTGGCCAGCCCGAGCAACGTGGATCCTGAGAGCACTCCC | 60  |
| Qy | 61  | AGGTAGGCATTTGCCCCGGTGGGACGCCTTGCCAGAGCAGTGTGTGGCAGGCCCCCGTGG | 120 |
|    |     |  |     |
| Db | 61  | AGGTAGGCATTTGCCCCGGTGGGACGCCTTGCCAGAGCAGTGTGTGGCAGGCCCCCGTGG | 120 |
| Qy | 121 | AGGATCAACACAGTGGCTGAACACTGGGAAGGAACTGGTACTTGGAGTCTGGACATCTGA | 180 |
|    |     |  |     |
| Db | 121 | AGGATCAACACAGTGGCTGAACACTGGGAAGGAACTGGTACTTGGAGTCTGGACATCTGA | 180 |
| Qy | 181 | AACTTGGCTCTGAAACTGCGGAGCGGCCACCGGACGCCTTCTGGAGCAGGTAGCAGCATG | 240 |
|    |     |  |     |
| Db | 181 | AACTTGGCTCTGAAACTGCGGAGCGGCCACCGGACGCCTTCTGGAGCAGGTAGCAGCATG | 240 |

Qy 241 CAGCCGCCTCCAAGTCTGTGCGGACGCGCCCTGGTTGCGCTGGTTCTTGCCTGCGGCCTG 300  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 241 CAGCCGCCTCCAAGTCTGTGCGGACGCGCCCTGGTTGCGCTGGTTCTTGCCTGCGGCCTG 300

Qy 301 TCGCGGATCTGGGGAGAGGAGAGAGGCTTCCCGCCTGACAGGGCCACTCCGCTTTTGCAA 360  
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 Db 301 TCGCGGATCTGGGGAGAGGAGAGAGGCTTCCCGCCTGACAGGGCCACTCCGCTTTTGCAA 360

Qy 361 ACCGCAGAGATAATGACGCCACCCACTAAGACCTTATGGCCCAAGGGTTCCAACGCCAGT 420  
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 Db 361 ACCGCAGAGATAATGACGCCACCCACTAAGACCTTATGGCCCAAGGGTTCCAACGCCAGT 420

Qy 421 CTGGCGCGGTTCGTTGGCACCTGCGGAGGTGCCTAAAGGAGACAGGACGGCAGGATCTCCG 480  
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 Db 421 CTGGCGCGGTTCGTTGGCACCTGCGGAGGTGCCTAAAGGAGACAGGACGGCAGGATCTCCG 480

Qy 481 CCACGCACCATCTCCCTCCCCGTGCCAAGGACCCATCGAGATCAAGGAGACTTTCAA 540  
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 Db 481 CCACGCACCATCTCCCTCCCCGTGCCAAGGACCCATCGAGATCAAGGAGACTTTCAA 540

Qy 541 TACATCAACACGGTTGTGTCTGCTTGTGTTCGTGCTGGGGATCATCGGGAACCTCCACA 600  
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 Db 541 TACATCAACACGGTTGTGTCTGCTTGTGTTCGTGCTGGGGATCATCGGGAACCTCCACA 600

Qy 601 CTTCTGAGAATTATCTACAAGAACAAGTGCATGCGAAACGGTCCCAATATCTTGATCGCC 660  
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 Db 601 CTTCTGAGAATTATCTACAAGAACAAGTGCATGCGAAACGGTCCCAATATCTTGATCGCC 660

Qy 661 AGCTTGGCTCTGGGAGACCTGCTGCACATCGTCATTGACATCCCTATCAATGTCTACAAG 720  
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 Db 661 AGCTTGGCTCTGGGAGACCTGCTGCACATCGTCATTGACATCCCTATCAATGTCTACAAG 720

Qy 721 CTGCTGGCAGAGGACTGGCCATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTTCATACAG 780  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 721 CTGCTGGCAGAGGACTGGCCATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTTCATACAG 780

Qy 781 AAAGCCTCCGTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATATCGA 840  
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 Db 781 AAAGCCTCCGTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATATCGA 840

Qy 841 GCTGTTGCTTCTTGGAGTAGAATTAAAGGAATTGGGGTTCCAAAATGGACAGCAGTAGAA 900  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 841 GCTGTTGCTTCTTGGAGTAGAATTAAAGGAATTGGGGTTCCAAAATGGACAGCAGTAGAA 900

Qy 901 ATTGTTTTGATTTGGGTGGTCTCTGTGGTTCTGGCTGTCCCTGAAGCCATAGGTTTTGAT 960  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 901 ATTGTTTTGATTTGGGTGGTCTCTGTGGTTCTGGCTGTCCCTGAAGCCATAGGTTTTGAT 960

Qy 961 ATAATTACGATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTTCAG 1020  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 961 ATAATTACGATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTTCAG 1020

Qy 1021 AAGACAGCTTTTCATGCAGTTTACAAGACAGCAAAGATTGGTGGCTGTTCAAGTTTCTAT 1080  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 1021 AAGACAGCTTTTCATGCAGTTTACAAGACAGCAAAGATTGGTGGCTGTTCAAGTTTCTAT 1080

Qy 1081 TTCTGCTTGCCATTGGCCATCACTGCATTTTTTTTATACACTAATGACCTGTGAAATGTTG 1140

|    |      |  |      |
|----|------|--|------|
| Db | 1081 | <br>TTCTGCTTGCCATTGGCCATCACTGCATTTTTTTATACACTAATGACCTGTGAAATGTTG | 1140 |
| Qy | 1141 | AGAAAGAAAAGTGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAAGTG     | 1200 |
| Db | 1141 | <br>AGAAAGAAAAGTGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAAGTG | 1200 |
| Qy | 1201 | GCCAAAACCGTCTTTTGCCTGGTCCTTGTCTTTGCCCTCTGCTGGCTTCCCCTTCACCTC     | 1260 |
| Db | 1201 | <br>GCCAAAACCGTCTTTTGCCTGGTCCTTGTCTTTGCCCTCTGCTGGCTTCCCCTTCACCTC | 1260 |
| Qy | 1261 | AGCAGGATTCTGAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGAACTTTTG     | 1320 |
| Db | 1261 | <br>AGCAGGATTCTGAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGAACTTTTG | 1320 |
| Qy | 1321 | AGCTTCTGTTGGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCCTGCATT      | 1380 |
| Db | 1321 | <br>AGCTTCTGTTGGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCCTGCATT  | 1380 |
| Qy | 1381 | AACCCAATTGCTCTGTATTTGGTGAGCAAAAGATTCAAAAAGTCTTTAAGTCATGCTTA      | 1440 |
| Db | 1381 | <br>AACCCAATTGCTCTGTATTTGGTGAGCAAAAGATTCAAAAAGTCTTTAAGTCATGCTTA  | 1440 |
| Qy | 1441 | TGCTGCTGGTGCCAGTCATTTGAAGAAAACAGTCCTTGGAGGAAAAGCAGTCGTGCTTA      | 1500 |
| Db | 1441 | <br>TGCTGCTGGTGCCAGTCATTTGAAGAAAACAGTCCTTGGAGGAAAAGCAGTCGTGCTTA  | 1500 |
| Qy | 1501 | AAGTTCAAAGCTAATGATCACGGATATGACAACTCCGTTCCAGTAATAAATACAGCTCA      | 1560 |
| Db | 1501 | <br>AAGTTCAAAGCTAATGATCACGGATATGACAACTCCGTTCCAGTAATAAATACAGCTCA  | 1560 |
| Qy | 1561 | TCTTGAAAGAAGAACTATTCAGTGTATTTTCTTTATATTGGACCGAAGTCATTAA          | 1620 |
| Db | 1561 | <br>TCTTGAAAGAAGAACTATTCAGTGTATTTTCTTTATATTGGACCGAAGTCATTAA      | 1620 |
| Qy | 1621 | AACAAAATGAAACATTTGCCAAAACAAAACAAAAAACTATGTATTTGCACAGCACACTAT     | 1680 |
| Db | 1621 | <br>AACAAAATGAAACATTTGCCAAAACAAAACAAAAAACTATGTATTTGCACAGCACACTAT | 1680 |
| Qy | 1681 | TAAAATATTAAGTGTAATTATTTTAACACTCACAGCTACATATGACATTTTATGAGCTGT     | 1740 |
| Db | 1681 | <br>TAAAATATTAAGTGTAATTATTTTAACACTCACAGCTACATATGACATTTTATGAGCTGT | 1740 |
| Qy | 1741 | TTACGGCATGGAAAGAAAATCAGTGGGAATTAAGAAAGCCTCGTCGTGAAAGCACTTAAT     | 1800 |
| Db | 1741 | <br>TTACGGCATGGAAAGAAAATCAGTGGGAATTAAGAAAGCCTCGTCGTGAAAGCACTTAAT | 1800 |
| Qy | 1801 | TTTTTACAGTTAGCACTTCAACATAGCTCTTAACAACCTCCAGGATATTCACACAACACT     | 1860 |
| Db | 1801 | <br>TTTTTACAGTTAGCACTTCAACATAGCTCTTAACAACCTCCAGGATATTCACACAACACT | 1860 |
| Qy | 1861 | TAGGCTTAAAAATGAGCTCACTCAGAATTTCTATTCTTTCTAAAAAGAGATTTATTTT       | 1920 |
| Db | 1861 | <br>TAGGCTTAAAAATGAGCTCACTCAGAATTTCTATTCTTTCTAAAAAGAGATTTATTTT   | 1920 |
| Qy | 1921 | AATCAATGGGACTCTGATATAAAGGAAGAATAAGTCACTGTAAAACAGAACTTTTAAATG     | 1980 |
|    |      |  |      |

Db 1921 AATCAATGGGACTCTGATATAAAGGAAGAATAAGTCACTGTAAACAGAACTTTTAAATG 1980

Qy 1981 AAGCTTAAATTACTCAATTTAAAATTTTAAAATCCTTTAAAACAACCTTTTCAATTAATAT 2040  
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Db 1981 AAGCTTAAATTACTCAATTTAAAATTTTAAAATCCTTTAAAACAACCTTTTCAATTAATAT 2040

Qy 2041 TATCACACTATTATCAGATTGTAATTAGATGCAAATGAGAGAGCAGTTTAGTTGTTGCAT 2100  
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Db 2041 TATCACACTATTATCAGATTGTAATTAGATGCAAATGAGAGAGCAGTTTAGTTGTTGCAT 2100

Qy 2101 TTTTCGGACACTGGAAACATTTAAATGATCAGGAGGGAGTAACAGAAAGAGCAAGGCTGT 2160  
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Db 2101 TTTTCGGACACTGGAAACATTTAAATGATCAGGAGGGAGTAACAGAAAGAGCAAGGCTGT 2160

Qy 2161 TTTTGAAAATCATTACACTTTTCTACTAGAAGCCCCAACCTCAGCATTCTGCAATATGTAAC 2220  
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Db 2161 TTTTGAAAATCATTACACTTTTCTACTAGAAGCCCCAACCTCAGCATTCTGCAATATGTAAC 2220

Qy 2221 CAACATGTCACAAACAAGCAGCATGTAACAGACTGGCACATGTGCCAGCTGAATTTAAAA 2280  
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Db 2221 CAACATGTCACAAACAAGCAGCATGTAACAGACTGGCACATGTGCCAGCTGAATTTAAAA 2280

Qy 2281 TATAATACTTTTAAAAAGAAAATTATTACATCCTTTACATTGAGTAAAGATCAAACCTCA 2340  
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Db 2281 TATAATACTTTTAAAAAGAAAATTATTACATCCTTTACATTGAGTAAAGATCAAACCTCA 2340

Qy 2341 CAAAGAGAAATAGAATGTTTGAAAGGCTATCCCAAAGACTTTTTTGAATCTGTCATTCA 2400  
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Db 2341 CAAAGAGAAATAGAATGTTTGAAAGGCTATCCCAAAGACTTTTTTGAATCTGTCATTCA 2400

Qy 2401 CATACCCTGTGAAGACAATACTATCTACAATTTTTTCAGGATTATTAAAATCTTCTTTTT 2460  
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Db 2401 CATACCCTGTGAAGACAATACTATCTACAATTTTTTCAGGATTATTAAAATCTTCTTTTT 2460

Qy 2461 TCACTATCGTAGCTTAAACTCTGTTTGGTTTTGTCATCTGTAAATACTTACCTACATACA 2520  
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Db 2461 TCACTATCGTAGCTTAAACTCTGTTTGGTTTTGTCATCTGTAAATACTTACCTACATACA 2520

Qy 2521 CTGCATGTAGATGATTAAATGAGGGCAGGCCCTGTGCTCATAGCTTTACGATGGAGAGAT 2580  
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Db 2521 CTGCATGTAGATGATTAAATGAGGGCAGGCCCTGTGCTCATAGCTTTACGATGGAGAGAT 2580

Qy 2581 GCCAGTGACCTCATAATAAAGACTGTGAACTGCCTGGTGCAGTGTCCACATGACAAAGGG 2640  
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Db 2581 GCCAGTGACCTCATAATAAAGACTGTGAACTGCCTGGTGCAGTGTCCACATGACAAAGGG 2640

Qy 2641 GCAGGTAGCACCCCTCTCTACCCATGCTGTGGTTAAAATGGTTTCTAGCATATGTATAAT 2700  
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Db 2641 GCAGGTAGCACCCCTCTCTACCCATGCTGTGGTTAAAATGGTTTCTAGCATATGTATAAT 2700

Qy 2701 GCTATAGTTAAAATACTATTTTTTCAAAATCATACAGATTAGTACATTTAACAGCTACCTG 2760  
 |||

Db 2701 GCTATAGTTAAAATACTATTTTTTCAAAATCATACAGATTAGTACATTTAACAGCTACCTG 2760

Qy 2761 TAAAGCTTATTACTAATTTTTGTATTATTTTTGTAAATAGCCAATAGAAAAGTTTGCTTG 2820  
 |||

Db 2761 TAAAGCTTATTACTAATTTTTGTATTATTTTTGTAAATAGCCAATAGAAAAGTTTGCTTG 2820

|    |      |  |      |
|----|------|--|------|
| Qy | 2821 | ACATGGTGCTTTTCTTTTCATCTAGAGGCAAACTGCTTTTTGAGACCGTAAGAACCTCTT   | 2880 |
|    |      |  |      |
| Db | 2821 | ACATGGTGCTTTTCTTTTCATCTAGAGGCAAACTGCTTTTTGAGACCGTAAGAACCTCTT   | 2880 |
| Qy | 2881 | AGCTTTGTGCGTTCCTGCCTAATTTTATATCTTCTAAGCAAAGTGCCTTAGGATAGCTT    | 2940 |
|    |      |  |      |
| Db | 2881 | AGCTTTGTGCGTTCCTGCCTAATTTTATATCTTCTAAGCAAAGTGCCTTAGGATAGCTT    | 2940 |
| Qy | 2941 | GGGATGAGATGTGTGTGAAAGTATGTACAAGAGAAAACGGAAGAGAGAGGAAATGAGGTG   | 3000 |
|    |      |  |      |
| Db | 2941 | GGGATGAGATGTGTGTGAAAGTATGTACAAGAGAAAACGGAAGAGAGAGGAAATGAGGTG   | 3000 |
| Qy | 3001 | GGGTTGGAGGAAACCCATGGGGACAGATTCCCATCTTAGCCTAACGTTTCGTCATTGCCT   | 3060 |
|    |      |  |      |
| Db | 3001 | GGGTTGGAGGAAACCCATGGGGACAGATTCCCATCTTAGCCTAACGTTTCGTCATTGCCT   | 3060 |
| Qy | 3061 | CGTCACATCAATGCAAAAGGTCTGATTTTGTTCAGCAAAACACAGTGCAATGTTCTCA     | 3120 |
|    |      |  |      |
| Db | 3061 | CGTCACATCAATGCAAAAGGTCTGATTTTGTTCAGCAAAACACAGTGCAATGTTCTCA     | 3120 |
| Qy | 3121 | GAGTGACTTTCGAAATAAATTGGGCCCAAGAGCTTTAACTCGGTCTTAAATATGCCCCA    | 3180 |
|    |      |  |      |
| Db | 3121 | GAGTGACTTTCGAAATAAATTGGGCCCAAGAGCTTTAACTCGGTCTTAAATATGCCCCA    | 3180 |
| Qy | 3181 | ATTTTTACTTTGTTTTCTTTTAATAGGCTGGGCCACATGTTGGAAATAAGCTAGTAATG    | 3240 |
|    |      |  |      |
| Db | 3181 | ATTTTTACTTTGTTTTCTTTTAATAGGCTGGGCCACATGTTGGAAATAAGCTAGTAATG    | 3240 |
| Qy | 3241 | TTGTTTTCTGTCAATATTGAATGTGATGGTACAGTAAACCAAACCAACAATGTGGCCA     | 3300 |
|    |      |  |      |
| Db | 3241 | TTGTTTTCTGTCAATATTGAATGTGATGGTACAGTAAACCAAACCAACAATGTGGCCA     | 3300 |
| Qy | 3301 | GAAAGAAAGAGCAATAATAATTAATTCACACACCATATGGATTCTATTTATAAATCACCC   | 3360 |
|    |      |  |      |
| Db | 3301 | GAAAGAAAGAGCAATAATAATTAATTCACACACCATATGGATTCTATTTATAAATCACCC   | 3360 |
| Qy | 3361 | ACAAACTTGTTCTTTAATTTTCATCCCAATCACTTTTTTCAGAGGCCTGTTATCATAGAAGT | 3420 |
|    |      |  |      |
| Db | 3361 | ACAAACTTGTTCTTTAATTTTCATCCCAATCACTTTTTTCAGAGGCCTGTTATCATAGAAGT | 3420 |
| Qy | 3421 | CATTTTAGACTCTCAATTTTAAATTAATTTGAATCACTAATATTTTCACAGTTTATTAA    | 3480 |
|    |      |  |      |
| Db | 3421 | CATTTTAGACTCTCAATTTTAAATTAATTTGAATCACTAATATTTTCACAGTTTATTAA    | 3480 |
| Qy | 3481 | TATATTTAATTTCTATTTAAATTTTAGATTATTTTATTACCATGTACTGAATTTTACA     | 3540 |
|    |      |  |      |
| Db | 3481 | TATATTTAATTTCTATTTAAATTTTAGATTATTTTATTACCATGTACTGAATTTTACA     | 3540 |
| Qy | 3541 | TCCTGATACCCTTTCTCTTCTCCATGTCAGTATCATGTTCTCTAATTATCTTGCCAAATTT  | 3600 |
|    |      |  |      |
| Db | 3541 | TCCTGATACCCTTTCTCTTCTCCATGTCAGTATCATGTTCTCTAATTATCTTGCCAAATTT  | 3600 |
| Qy | 3601 | TGAAACTACACACAAAAAGCATACTTGCAATTATTTATAATAAAATTGCATTTCAGTGGCTT | 3660 |
|    |      |  |      |
| Db | 3601 | TGAAACTACACACAAAAAGCATACTTGCAATTATTTATAATAAAATTGCATTTCAGTGGCTT | 3660 |

Qy 3661 TTTAAAAAAATGTTTGATTCAAAACTTTAACATACTGATAAGTAAGAAACAATTATAAT 3720  
 |||  
 Db 3661 TTTAAAAAAATGTTTGATTCAAAACTTTAACATACTGATAAGTAAGAAACAATTATAAT 3720  
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 Qy 3721 TTCTTTACATACTCAAAACCAAGATAGAAAAAGGTGCTATCGTTCAACTTCAAAACATGT 3780  
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 Db 3721 TTCTTTACATACTCAAAACCAAGATAGAAAAAGGTGCTATCGTTCAACTTCAAAACATGT 3780  
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 Qy 3781 TTCCTAGTATTAAGGACTTTAATATAGCAACAGACAAAATTATTGTTAACATGGATGTTA 3840  
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 Db 3781 TTCCTAGTATTAAGGACTTTAATATAGCAACAGACAAAATTATTGTTAACATGGATGTTA 3840  
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 Db 3841 CAGCTCAAAAGATTTATAAAAGATTTTAACCTATTTTCTCCCTTATTATCCACTGCTAAT 3900  
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 Qy 3901 GTGGATGTATGTTCAAACACCTTTTAGTATTGATAGCTTACATATGGCCAAAGGAATACA 3960  
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 Db 3901 GTGGATGTATGTTCAAACACCTTTTAGTATTGATAGCTTACATATGGCCAAAGGAATACA 3960  
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 Db 3961 GTTTATAGCAAAACATGGGTATGCTGTAGCTAACTTTATAAAAGTGTAATATAACAATGT 4020  
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 Qy 4021 AAAAAATTATATATCTGGGAGGATTTTTTGGTTGCCTAAAGTGGCTATAGTTACTGATTT 4080  
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 Db 4021 AAAAAATTATATATCTGGGAGGATTTTTTGGTTGCCTAAAGTGGCTATAGTTACTGATTT 4080  
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 Qy 4201 CAAGTGGACATTATTTATGTTAAATATACAATTATCAAGCAAGTATGAAGTTATTCAATT 4260  
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 Db 4201 CAAGTGGACATTATTTATGTTAAATATACAATTATCAAGCAAGTATGAAGTTATTCAATT 4260  
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 Qy 4261 AAAATGCCACATTTCTGGTCTCTGGGAAAAAAAAAAAAAAAAA 4301  
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 Db 4261 AAAATGCCACATTTCTGGTCTCTGGGAAAAAAAAAAAAAAAAA 4301  
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# RESULT 2

E07650

LOCUS E07650 4301 bp RNA linear PAT 29-SEP-1997

DEFINITION cDNA encoding endothelin receptor, ETB-receptor.

ACCESSION E07650

VERSION E07650.1 GI:2175785

KEYWORDS JP 1994157595-A/2.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 4301)



AUTHORS Imura,H., Nakao,I. and Nakanishi,S.  
 TITLE HUMAN ENDOTHELIN RECEPTOR  
 JOURNAL Patent: JP 1994157595-A 2 03-JUN-1994;  
 SHIONOGI & CO LTD  
 COMMENT OS Homo sapiens (human)  
 PN JP 1994157595-A/2  
 PD 03-JUN-1994  
 PF 12-JUL-1991 JP 1991172828  
 PI IMURA HIROO, NAKAO ICHIKAZU, NAKANISHI SHIGETADA PC  
 C07K13/00,C12N5/10,C12N15/12,C12P21/02,(C12N5/10,C12R1:91), PC  
 (C12P21/02,  
 PC C12R1:91);  
 CC strandedness: Double;  
 CC topology: Linear;  
 CC hypothetical: No;  
 CC anti-sense: No;  
 FH Key Location/Qualifiers  
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 FT /tissue\_type='placenta'  
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# ORIGIN

Query Match 100.0%; Score 4301; DB 6; Length 4301;  
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 Matches 4301; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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| Qy | 1   | GAGACATTCCGGTGGGGGACTCTGGCCAGCCCCGAGCAACGTGGATCCTGAGAGCACTCCC | 60  |
|    |     |   |     |
| Db | 1   | GAGACATTCCGGTGGGGGACTCTGGCCAGCCCCGAGCAACGTGGATCCTGAGAGCACTCCC | 60  |
| Qy | 61  | AGGTAGGCATTTGCCCCGGTGGGACGCCTTGCCAGAGCAGTGTGTGGCAGGCCCCCGTGG  | 120 |
|    |     |   |     |
| Db | 61  | AGGTAGGCATTTGCCCCGGTGGGACGCCTTGCCAGAGCAGTGTGTGGCAGGCCCCCGTGG  | 120 |
| Qy | 121 | AGGATCAACACAGTGGCTGAACACTGGGAAGGAACTGGTACTTGGAGTCTGGACATCTGA  | 180 |
|    |     |   |     |
| Db | 121 | AGGATCAACACAGTGGCTGAACACTGGGAAGGAACTGGTACTTGGAGTCTGGACATCTGA  | 180 |
| Qy | 181 | AACTTGGCTCTGAAACTGCGGAGCGGCCACCGGACGCCTTCTGGAGCAGGTAGCAGCATG  | 240 |
|    |     |   |     |
| Db | 181 | AACTTGGCTCTGAAACTGCGGAGCGGCCACCGGACGCCTTCTGGAGCAGGTAGCAGCATG  | 240 |

|    |      |  |      |
|----|------|--|------|
| Qy | 241  | CAGCCGCCTCCAAGTCTGTGCGGACGCGCCCTGGTTGCGCTGGTTCTTGCCCTGCGGCCTG  | 300  |
|    |      |  |      |
| Db | 241  | CAGCCGCCTCCAAGTCTGTGCGGACGCGCCCTGGTTGCGCTGGTTCTTGCCCTGCGGCCTG  | 300  |
| Qy | 301  | TCGCGGATCTGGGGAGAGGAGAGAGGCTTCCCGCCTGACAGGGCCACTCCGCTTTTGCAA   | 360  |
|    |      |  |      |
| Db | 301  | TCGCGGATCTGGGGAGAGGAGAGAGGCTTCCCGCCTGACAGGGCCACTCCGCTTTTGCAA   | 360  |
| Qy | 361  | ACCGCAGAGATAATGACGCCACCCACTAAGACCTTATGGCCCAAGGGTTCCAACGCCAGT   | 420  |
|    |      |  |      |
| Db | 361  | ACCGCAGAGATAATGACGCCACCCACTAAGACCTTATGGCCCAAGGGTTCCAACGCCAGT   | 420  |
| Qy | 421  | CTGGCGCGGTTCGTTGGCACCTGCGGAGGTGCCTAAAGGAGACAGGACGGCAGGATCTCCG  | 480  |
|    |      |  |      |
| Db | 421  | CTGGCGCGGTTCGTTGGCACCTGCGGAGGTGCCTAAAGGAGACAGGACGGCAGGATCTCCG  | 480  |
| Qy | 481  | CCACGCACCATCTCCCCCTCCCCCGTGCCAAGGACCCATCGAGATCAAGGAGACTTTCAAA  | 540  |
|    |      |  |      |
| Db | 481  | CCACGCACCATCTCCCCCTCCCCCGTGCCAAGGACCCATCGAGATCAAGGAGACTTTCAAA  | 540  |
| Qy | 541  | TACATCAACACGGTTGTGTCCTGCCTTGTGTTTCGTGCTGGGGATCATCGGGAACCTCCACA | 600  |
|    |      |  |      |
| Db | 541  | TACATCAACACGGTTGTGTCCTGCCTTGTGTTTCGTGCTGGGGATCATCGGGAACCTCCACA | 600  |
| Qy | 601  | CTTCTGAGAATTATCTACAAGAACAAGTGCATGCGAAACGGTCCCAATATCTTGATCGCC   | 660  |
|    |      |  |      |
| Db | 601  | CTTCTGAGAATTATCTACAAGAACAAGTGCATGCGAAACGGTCCCAATATCTTGATCGCC   | 660  |
| Qy | 661  | AGCTTGGCTCTGGGAGACCTGCTGCACATCGTCATTGACATCCCTATCAATGTCTACAAG   | 720  |
|    |      |  |      |
| Db | 661  | AGCTTGGCTCTGGGAGACCTGCTGCACATCGTCATTGACATCCCTATCAATGTCTACAAG   | 720  |
| Qy | 721  | CTGCTGGCAGAGGACTGGCCATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTCATACAG   | 780  |
|    |      |  |      |
| Db | 721  | CTGCTGGCAGAGGACTGGCCATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTCATACAG   | 780  |
| Qy | 781  | AAAGCCTCCGTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATATCGA   | 840  |
|    |      |  |      |
| Db | 781  | AAAGCCTCCGTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATATCGA   | 840  |
| Qy | 841  | GCTGTTGCTTCTTGGAGTAGAATTAAAGGAATTGGGGTTCCAAAATGGACAGCAGTAGAA   | 900  |
|    |      |  |      |
| Db | 841  | GCTGTTGCTTCTTGGAGTAGAATTAAAGGAATTGGGGTTCCAAAATGGACAGCAGTAGAA   | 900  |
| Qy | 901  | ATTGTTTTGATTTGGGTGGTCTCTGTGGTTCTGGCTGTCCCTGAAGCCATAGGTTTTGAT   | 960  |
|    |      |  |      |
| Db | 901  | ATTGTTTTGATTTGGGTGGTCTCTGTGGTTCTGGCTGTCCCTGAAGCCATAGGTTTTGAT   | 960  |
| Qy | 961  | ATAATTACGATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTTCAG   | 1020 |
|    |      |  |      |
| Db | 961  | ATAATTACGATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTTCAG   | 1020 |
| Qy | 1021 | AAGACAGCTTTCATGCAGTTTTACAAGACAGCAAAAGATTGGTGGCTGTTTCAGTTTCTAT  | 1080 |
|    |      |  |      |
| Db | 1021 | AAGACAGCTTTCATGCAGTTTTACAAGACAGCAAAAGATTGGTGGCTGTTTCAGTTTCTAT  | 1080 |

|    |      |  |      |
|----|------|--|------|
| Qy | 1081 | TTCTGCTTGCCATTGGCCATCACTGCATTTTTTTATACACTAATGACCTGTGAAATGTTG   | 1140 |
|    |      |  |      |
| Db | 1081 | TTCTGCTTGCCATTGGCCATCACTGCATTTTTTTATACACTAATGACCTGTGAAATGTTG   | 1140 |
| Qy | 1141 | AGAAAGAAAAGTGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAAGTG   | 1200 |
|    |      |  |      |
| Db | 1141 | AGAAAGAAAAGTGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAAGTG   | 1200 |
| Qy | 1201 | GCCAAAACCGTCTTTTGCCTGGTCCTTGTCTTTGCCCTCTGCTGGCTTCCCCTTCACCTC   | 1260 |
|    |      |  |      |
| Db | 1201 | GCCAAAACCGTCTTTTGCCTGGTCCTTGTCTTTGCCCTCTGCTGGCTTCCCCTTCACCTC   | 1260 |
| Qy | 1261 | AGCAGGATTCTGAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGAACTTTTG   | 1320 |
|    |      |  |      |
| Db | 1261 | AGCAGGATTCTGAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGAACTTTTG   | 1320 |
| Qy | 1321 | AGCTTCTGTTGGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCCTGCATT    | 1380 |
|    |      |  |      |
| Db | 1321 | AGCTTCTGTTGGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCCTGCATT    | 1380 |
| Qy | 1381 | AACCCAATTGCTCTGTATTTGGTGAGCAAAAGATTCAAAAAGTCTTTAAGTCATGCTTA    | 1440 |
|    |      |  |      |
| Db | 1381 | AACCCAATTGCTCTGTATTTGGTGAGCAAAAGATTCAAAAAGTCTTTAAGTCATGCTTA    | 1440 |
| Qy | 1441 | TGCTGCTGGTGCCAGTCATTTGAAGAAAAACAGTCCTTGGAGGAAAAGCAGTCGTGCTTA   | 1500 |
|    |      |  |      |
| Db | 1441 | TGCTGCTGGTGCCAGTCATTTGAAGAAAAACAGTCCTTGGAGGAAAAGCAGTCGTGCTTA   | 1500 |
| Qy | 1501 | AAGTTCAAAGCTAATGATCACGGATATGACAACTTCCGTTCCAGTAATAAATACAGCTCA   | 1560 |
|    |      |  |      |
| Db | 1501 | AAGTTCAAAGCTAATGATCACGGATATGACAACTTCCGTTCCAGTAATAAATACAGCTCA   | 1560 |
| Qy | 1561 | TCTTGAAAGAAGAACTATTCACTGTATTTTCACTTTTCTTTATATTGGACCGAAGTCATTAA | 1620 |
|    |      |  |      |
| Db | 1561 | TCTTGAAAGAAGAACTATTCACTGTATTTTCACTTTTCTTTATATTGGACCGAAGTCATTAA | 1620 |
| Qy | 1621 | AACAAAATGAAACATTTGCCAAAACAAAACAAAAAACTATGTATTTGCACAGCACACTAT   | 1680 |
|    |      |  |      |
| Db | 1621 | AACAAAATGAAACATTTGCCAAAACAAAACAAAAAACTATGTATTTGCACAGCACACTAT   | 1680 |
| Qy | 1681 | TAAAATATTAAGTGTAATTATTTTAACACTCACAGCTACATATGACATTTTATGAGCTGT   | 1740 |
|    |      |  |      |
| Db | 1681 | TAAAATATTAAGTGTAATTATTTTAACACTCACAGCTACATATGACATTTTATGAGCTGT   | 1740 |
| Qy | 1741 | TTACGGCATGGAAAGAAAATCAGTGGGAATTAAGAAAGCCTCGTCGTGAAAGCACTTAAT   | 1800 |
|    |      |  |      |
| Db | 1741 | TTACGGCATGGAAAGAAAATCAGTGGGAATTAAGAAAGCCTCGTCGTGAAAGCACTTAAT   | 1800 |
| Qy | 1801 | TTTTTACAGTTAGCACTTCAACATAGCTCTTAACAACCTCCAGGATATTCACACAACACT   | 1860 |
|    |      |  |      |
| Db | 1801 | TTTTTACAGTTAGCACTTCAACATAGCTCTTAACAACCTCCAGGATATTCACACAACACT   | 1860 |
| Qy | 1861 | TAGGCTTAAAAATGAGCTCACTCAGAATTTCTATTCTTTCTAAAAAGAGATTTATTTTAA   | 1920 |
|    |      |  |      |
| Db | 1861 | TAGGCTTAAAAATGAGCTCACTCAGAATTTCTATTCTTTCTAAAAAGAGATTTATTTTAA   | 1920 |
| Qy | 1921 | AATCAATGGGACTCTGATATAAAGGAAGAATAAGTCACTGTAAAAACAGAACTTTTAAATG  | 1980 |

|    |      |   |      |
|----|------|---|------|
| Db | 1921 | <br>AATCAATGGGACTCTGATATAAAGGAAGAATAAGTCACTGTAAACAGAAGCTTTTAAATG  | 1980 |
| Qy | 1981 | AAGCTTAAATTACTCAATTTAAAATTTTAAAATCCTTTAAAACAAGCTTTTCAATTAATAT     | 2040 |
| Db | 1981 | <br>AAGCTTAAATTACTCAATTTAAAATTTTAAAATCCTTTAAAACAAGCTTTTCAATTAATAT | 2040 |
| Qy | 2041 | TATCACACTATTATCAGATTGTAATTAGATGCAAATGAGAGAGCAGTTTAGTTGTTGCAT      | 2100 |
| Db | 2041 | <br>TATCACACTATTATCAGATTGTAATTAGATGCAAATGAGAGAGCAGTTTAGTTGTTGCAT  | 2100 |
| Qy | 2101 | TTTTCGGACACTGGAAACATTTAAATGATCAGGAGGGAGTAACAGAAAGAGCAAGGCTGT      | 2160 |
| Db | 2101 | <br>TTTTCGGACACTGGAAACATTTAAATGATCAGGAGGGAGTAACAGAAAGAGCAAGGCTGT  | 2160 |
| Qy | 2161 | TTTGTGAAAATCATTACACTTTCACTAGAAGCCCAAACCTCAGCATTCTGCAATATGTAAC     | 2220 |
| Db | 2161 | <br>TTTGTGAAAATCATTACACTTTCACTAGAAGCCCAAACCTCAGCATTCTGCAATATGTAAC | 2220 |
| Qy | 2221 | CAACATGTCACAAACAAGCAGCATGTAACAGACTGGCACATGTGCCAGCTGAATTTAAAA      | 2280 |
| Db | 2221 | <br>CAACATGTCACAAACAAGCAGCATGTAACAGACTGGCACATGTGCCAGCTGAATTTAAAA  | 2280 |
| Qy | 2281 | TATAATACTTTTAAAAAGAAAATTATTACATCCTTTACATTAGTAAAGATCAAACCTCA       | 2340 |
| Db | 2281 | <br>TATAATACTTTTAAAAAGAAAATTATTACATCCTTTACATTAGTAAAGATCAAACCTCA   | 2340 |
| Qy | 2341 | CAAAGAGAAATAGAATGTTTGAAAGGCTATCCCAAAGACTTTTTTGAATCTGTCATTCA       | 2400 |
| Db | 2341 | <br>CAAAGAGAAATAGAATGTTTGAAAGGCTATCCCAAAGACTTTTTTGAATCTGTCATTCA   | 2400 |
| Qy | 2401 | CATACCCTGTGAAGACAATACTATCTACAATTTTTTCAGGATTATTTAAATCTTCTTTTT      | 2460 |
| Db | 2401 | <br>CATACCCTGTGAAGACAATACTATCTACAATTTTTTCAGGATTATTTAAATCTTCTTTTT  | 2460 |
| Qy | 2461 | TCACTATCGTAGCTTAAACTCTGTTTGGTTTTGTCATCTGTAAATACTTACCTACATACA      | 2520 |
| Db | 2461 | <br>TCACTATCGTAGCTTAAACTCTGTTTGGTTTTGTCATCTGTAAATACTTACCTACATACA  | 2520 |
| Qy | 2521 | CTGCATGTAGATGATTAAATGAGGGCAGGCCCTGTGCTCATAGCTTTACGATGGAGAGAT      | 2580 |
| Db | 2521 | <br>CTGCATGTAGATGATTAAATGAGGGCAGGCCCTGTGCTCATAGCTTTACGATGGAGAGAT  | 2580 |
| Qy | 2581 | GCCAGTGACCTCATAATAAGACTGTGAACTGCCTGGTGCAGTGTCCACATGACAAAGGG       | 2640 |
| Db | 2581 | <br>GCCAGTGACCTCATAATAAGACTGTGAACTGCCTGGTGCAGTGTCCACATGACAAAGGG   | 2640 |
| Qy | 2641 | GCAGGTAGCACCCCTCTCTACCCATGCTGTGGTTAAAATGGTTTCTAGCATATGTATAAT      | 2700 |
| Db | 2641 | <br>GCAGGTAGCACCCCTCTCTACCCATGCTGTGGTTAAAATGGTTTCTAGCATATGTATAAT  | 2700 |
| Qy | 2701 | GCTATAGTTAAAATACTATTTTTTCAAAATCATACAGATTAGTACATTTAACAGCTACCTG     | 2760 |
| Db | 2701 | <br>GCTATAGTTAAAATACTATTTTTTCAAAATCATACAGATTAGTACATTTAACAGCTACCTG | 2760 |
| Qy | 2761 | TAAAGCTTATTACTAATTTTTGTATTATTTTTGTAAATAGCCAATAGAAAAGTTTGCTTG      | 2820 |
|    |      |   |      |

Db 2761 TAAAGCTTATTACTAATTTTTGTATTATTTTTGTAAATAGCCAATAGAAAAGTTTGCTTG 2820  
 Qy 2821 ACATGGTGCTTTTCTTTTCATCTAGAGGCAAACTGCTTTTTGAGACCGTAAGAACCTCTT 2880  
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 Db 2821 ACATGGTGCTTTTCTTTTCATCTAGAGGCAAACTGCTTTTTGAGACCGTAAGAACCTCTT 2880  
 Qy 2881 AGCTTTGTGCGTTCCTGCCTAATTTTTATATCTTCTAAGCAAAGTGCCTTAGGATAGCTT 2940  
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 Qy 2941 GGGATGAGATGTGTGTGAAAGTATGTACAAGAGAAAACGGAAGAGAGAGGAAATGAGGTG 3000  
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 Db 2941 GGGATGAGATGTGTGTGAAAGTATGTACAAGAGAAAACGGAAGAGAGAGGAAATGAGGTG 3000  
 Qy 3001 GGGTTGGAGGAAACCCATGGGGACAGATTCCCATTCCTTAGCCTAACGTTTCGTCATTGCCT 3060  
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 Qy 3181 ATTTTTACTTTGTTTTCTTTTAATAGGCTGGGCCACATGTTGGAAATAAGCTAGTAATG 3240  
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 Qy 3301 GAAAGAAAGAGCAATAATAATTAATTACACACCATATGGATTCTATTTATAAATCACCC 3360  
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 Db 3301 GAAAGAAAGAGCAATAATAATTAATTACACACCATATGGATTCTATTTATAAATCACCC 3360  
 Qy 3361 ACAAACTTGTTCTTTAATTTTCATCCCAATCACTTTTTTCAGAGGCCTGTTATCATAGAAGT 3420  
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 Db 3361 ACAAACTTGTTCTTTAATTTTCATCCCAATCACTTTTTTCAGAGGCCTGTTATCATAGAAGT 3420  
 Qy 3421 CATTTTAGACTCTCAATTTTAAATTAATTTGAATCACTAATATTTTCACAGTTTATTAA 3480  
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 Db 3421 CATTTTAGACTCTCAATTTTAAATTAATTTGAATCACTAATATTTTCACAGTTTATTAA 3480  
 Qy 3481 TATATTTAATTTCTATTTAAATTTTAGATTATTTTATTACCATGTACTGAATTTTACA 3540  
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 Db 3481 TATATTTAATTTCTATTTAAATTTTAGATTATTTTATTACCATGTACTGAATTTTACA 3540  
 Qy 3541 TCCTGATACCCTTTCCTTCTCCATGTCAGTATCATGTTCTCTAATTATCTTGCCAAATTT 3600  
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 Db 3541 TCCTGATACCCTTTCCTTCTCCATGTCAGTATCATGTTCTCTAATTATCTTGCCAAATTT 3600  
 Qy 3601 TGAAACTACACACAAAAAGCATACTTGCAATTATTTATAATAAAATTGCATTTCAGTGGCTT 3660  
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 Db 3601 TGAAACTACACACAAAAAGCATACTTGCAATTATTTATAATAAAATTGCATTTCAGTGGCTT 3660

|    |      |  |      |
|----|------|--|------|
| Qy | 3661 | TTTAAAAAAATGTTTGATTCAAACCTTTAACATACTGATAAGTAAGAAACAATTATAAT  | 3720 |
|    |      |  |      |
| Db | 3661 | TTTAAAAAAATGTTTGATTCAAACCTTTAACATACTGATAAGTAAGAAACAATTATAAT  | 3720 |
| Qy | 3721 | TTCTTTACATACTCAAACCAAGATAGAAAAAGGTGCTATCGTTCAACTTCAAACATGT   | 3780 |
|    |      |  |      |
| Db | 3721 | TTCTTTACATACTCAAACCAAGATAGAAAAAGGTGCTATCGTTCAACTTCAAACATGT   | 3780 |
| Qy | 3781 | TTCCTAGTATTAAGGACTTTAATATAGCAACAGACAAAATTATTGTTAACATGGATGTTA | 3840 |
|    |      |  |      |
| Db | 3781 | TTCCTAGTATTAAGGACTTTAATATAGCAACAGACAAAATTATTGTTAACATGGATGTTA | 3840 |
| Qy | 3841 | CAGCTCAAAGATTTATAAAAGATTTTAACCTATTTTCTCCCTTATTATCCACTGCTAAT  | 3900 |
|    |      |  |      |
| Db | 3841 | CAGCTCAAAGATTTATAAAAGATTTTAACCTATTTTCTCCCTTATTATCCACTGCTAAT  | 3900 |
| Qy | 3901 | GTGGATGTATGTTCAAACACCTTTTAGTATTGATAGCTTACATATGGCCAAAGGAATACA | 3960 |
|    |      |  |      |
| Db | 3901 | GTGGATGTATGTTCAAACACCTTTTAGTATTGATAGCTTACATATGGCCAAAGGAATACA | 3960 |
| Qy | 3961 | GTTTATAGCAAACATGGGTATGCTGTAGCTAACTTTATAAAAGTGTAATATAACAATGT  | 4020 |
|    |      |  |      |
| Db | 3961 | GTTTATAGCAAACATGGGTATGCTGTAGCTAACTTTATAAAAGTGTAATATAACAATGT  | 4020 |
| Qy | 4021 | AAAAAATTATATATCTGGGAGGATTTTTTGGTTGCCTAAAGTGGCTATAGTTACTGATTT | 4080 |
|    |      |  |      |
| Db | 4021 | AAAAAATTATATATCTGGGAGGATTTTTTGGTTGCCTAAAGTGGCTATAGTTACTGATTT | 4080 |
| Qy | 4081 | TTTATTATGTAAGCAAACCAATAAAATTTAAGTTTTTTTAACTACCTTATTTTTTC     | 4140 |
|    |      |  |      |
| Db | 4081 | TTTATTATGTAAGCAAACCAATAAAATTTAAGTTTTTTTAACTACCTTATTTTTTC     | 4140 |
| Qy | 4141 | ACTGTACAGACACTAATTCATTAAATACTAATTGATTGTTTAAAAGAAATATAAATGTGA | 4200 |
|    |      |  |      |
| Db | 4141 | ACTGTACAGACACTAATTCATTAAATACTAATTGATTGTTTAAAAGAAATATAAATGTGA | 4200 |
| Qy | 4201 | CAAGTGGACATTATTTATGTTAAATATACAATTATCAAGCAAGTATGAAGTTATTCAATT | 4260 |
|    |      |  |      |
| Db | 4201 | CAAGTGGACATTATTTATGTTAAATATACAATTATCAAGCAAGTATGAAGTTATTCAATT | 4260 |
| Qy | 4261 | AAAATGCCACATTTCTGGTCTCTGGGAAAAAAAAAAAAAAAAA                  | 4301 |
|    |      |  |      |
| Db | 4261 | AAAATGCCACATTTCTGGTCTCTGGGAAAAAAAAAAAAAAAAA                  | 4301 |

# RESULT 3

HUMETR

LOCUS HUMETR 4286 bp mRNA linear PRI 18-DEC-2002

DEFINITION Homo sapiens ETR mRNA for endothelin receptor, complete cds.

ACCESSION D90402

VERSION D90402.1 GI:219651

KEYWORDS .

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 4286)  
 AUTHORS Ogawa,Y., Nakao,K., Arai,H., Nakagawa,O., Hosoda,K., Suga,S.,  
 Nakanishi,S. and Imura,H.  
 TITLE Molecular cloning of a non-isopeptide-selective human endothelin  
 receptor  
 JOURNAL Biochem. Biophys. Res. Commun. 178 (1), 248-255 (1991)  
 MEDLINE 91298956  
 PUBMED 1648908  
 COMMENT Data kindly submitted in computer readable form by: Kazuwa Nakao  
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 Japan  
 Phone: 81-75-751-3170  
 Fax: 81-75-771-9452.

FEATURES Location/Qualifiers  
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# ORIGIN

Query Match 99.7%; Score 4286; DB 9; Length 4286;  
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 Matches 4286; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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|----|-----|---|-----|
| Qy | 1   | GAGACATTCCGGTGGGGGACTCTGGCCAGCCCGAGCAACGTGGATCCTGAGAGCACTCCC  | 60  |
|    |     |   |     |
| Db | 1   | GAGACATTCCGGTGGGGGACTCTGGCCAGCCCGAGCAACGTGGATCCTGAGAGCACTCCC  | 60  |
| Qy | 61  | AGGTAGGCATTTGCCCCGGTGGGACGCCCTTGCCAGAGCAGTGTGTGGCAGGCCCCCGTGG | 120 |
|    |     |   |     |
| Db | 61  | AGGTAGGCATTTGCCCCGGTGGGACGCCCTTGCCAGAGCAGTGTGTGGCAGGCCCCCGTGG | 120 |
| Qy | 121 | AGGATCAACACAGTGGCTGAACACTGGGAAGGAACTGGTACTTGGAGTCTGGACATCTGA  | 180 |
|    |     |   |     |
| Db | 121 | AGGATCAACACAGTGGCTGAACACTGGGAAGGAACTGGTACTTGGAGTCTGGACATCTGA  | 180 |

Qy 181 AACTTGGCTCTGAAACTGCGGAGCGGCCACCGGACGCCTTCTGGAGCAGGTAGCAGCATG 240  
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 Db 181 AACTTGGCTCTGAAACTGCGGAGCGGCCACCGGACGCCTTCTGGAGCAGGTAGCAGCATG 240

Qy 241 CAGCCGCCTCCAAGTCTGTGCGGACGCGCCCTGGTTGCGCTGGTTCTTGCCTGCGGCCTG 300  
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 Db 241 CAGCCGCCTCCAAGTCTGTGCGGACGCGCCCTGGTTGCGCTGGTTCTTGCCTGCGGCCTG 300

Qy 301 TCGCGGATCTGGGGAGAGGAGAGAGGCTTCCCGCCTGACAGGGCCACTCCGCTTTTGCAA 360  
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 Db 301 TCGCGGATCTGGGGAGAGGAGAGAGGCTTCCCGCCTGACAGGGCCACTCCGCTTTTGCAA 360

Qy 361 ACCGCAGAGATAATGACGCCACCCACTAAGACCTTATGGCCCAAGGGTTCCAACGCCAGT 420  
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Qy 421 CTGGCGCGGTTCGTTGGCACCTGCGGAGGTGCCTAAAGGAGACAGGACGGCAGGATCTCCG 480  
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Qy 481 CCACGCACCATCTCCCCTCCCCCGTGCCAAGGACCCATCGAGATCAAGGAGACTTTCAA 540  
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 Db 661 AGCTTGGCTCTGGGAGACCTGCTGCACATCGTCATTGACATCCCTATCAATGTCTACAAG 720

Qy 721 CTGCTGGCAGAGGACTGGCCATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTTCATACAG 780  
 |||  
 Db 721 CTGCTGGCAGAGGACTGGCCATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTTCATACAG 780

Qy 781 AAAGCCTCCGTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATATCGA 840  
 |||  
 Db 781 AAAGCCTCCGTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATATCGA 840

Qy 841 GCTGTTGCTTCTTGGAGTAGAATTAAAGGAATTGGGGTTCCAAAATGGACAGCAGTAGAA 900  
 |||  
 Db 841 GCTGTTGCTTCTTGGAGTAGAATTAAAGGAATTGGGGTTCCAAAATGGACAGCAGTAGAA 900

Qy 901 ATTGTTTTGATTTGGGTGGTCTCTGTGGTTCTGGCTGTCCCTGAAGCCATAGGTTTTGAT 960  
 |||  
 Db 901 ATTGTTTTGATTTGGGTGGTCTCTGTGGTTCTGGCTGTCCCTGAAGCCATAGGTTTTGAT 960

Qy 961 ATAATTACGATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTTCAG 1020  
 |||  
 Db 961 ATAATTACGATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTTCAG 1020

Qy 1021 AAGACAGCTTTCATGCAGTTTTACAAGACAGCAAAAGATTGGTGGCTGTTCAGTTTCTAT 1080



|    |      |  |      |
|----|------|--|------|
| Db | 1021 | <br>AAGACAGCTTTTCATGCAGTTTACAAAGACAGCAAAAGATTGGTGGCTGTTTCAGTTTCTAT | 1080 |
| Qy | 1081 | TTCTGCTTGCCATTGGCCATCACTGCATTTTTTTATACACTAATGACCTGTGAAATGTTG       | 1140 |
| Db | 1081 | <br>TTCTGCTTGCCATTGGCCATCACTGCATTTTTTTATACACTAATGACCTGTGAAATGTTG   | 1140 |
| Qy | 1141 | AGAAAGAAAAGTGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAAGTG       | 1200 |
| Db | 1141 | <br>AGAAAGAAAAGTGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAAGTG   | 1200 |
| Qy | 1201 | GCCAAAACCGTCTTTTGCCTGGTCCTTGTCTTTGCCCTCTGCTGGCTTCCCCTTCACCTC       | 1260 |
| Db | 1201 | <br>GCCAAAACCGTCTTTTGCCTGGTCCTTGTCTTTGCCCTCTGCTGGCTTCCCCTTCACCTC   | 1260 |
| Qy | 1261 | AGCAGGATTCTGAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGAACTTTTG       | 1320 |
| Db | 1261 | <br>AGCAGGATTCTGAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGAACTTTTG   | 1320 |
| Qy | 1321 | AGCTTTCTGTTGGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCCTGCATT       | 1380 |
| Db | 1321 | <br>AGCTTTCTGTTGGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCCTGCATT   | 1380 |
| Qy | 1381 | AACCCAATTGCTCTGTATTTGGTGAGCAAAAGATTCAAAAAGTCTTTAAGTCATGCTTA        | 1440 |
| Db | 1381 | <br>AACCCAATTGCTCTGTATTTGGTGAGCAAAAGATTCAAAAAGTCTTTAAGTCATGCTTA    | 1440 |
| Qy | 1441 | TGCTGCTGGTGCCAGTCATTTGAAGAAAACAGTCCTTGGAGGAAAAGCAGTCGTGCTTA        | 1500 |
| Db | 1441 | <br>TGCTGCTGGTGCCAGTCATTTGAAGAAAACAGTCCTTGGAGGAAAAGCAGTCGTGCTTA    | 1500 |
| Qy | 1501 | AAGTTCAAAGCTAATGATCACGGATATGACAACTCCGTTCCAGTAATAAATACAGCTCA        | 1560 |
| Db | 1501 | <br>AAGTTCAAAGCTAATGATCACGGATATGACAACTCCGTTCCAGTAATAAATACAGCTCA    | 1560 |
| Qy | 1561 | TCTTGAAAGAAGAAGTATTCACTGTATTTTCTTTTATATTGGACCGAAGTCATTAA           | 1620 |
| Db | 1561 | <br>TCTTGAAAGAAGAAGTATTCACTGTATTTTCTTTTATATTGGACCGAAGTCATTAA       | 1620 |
| Qy | 1621 | AACAAAATGAAACATTTGCCAAAACAAAACAAAAGTATGTATTTGCACAGCACACTAT         | 1680 |
| Db | 1621 | <br>AACAAAATGAAACATTTGCCAAAACAAAACAAAAGTATGTATTTGCACAGCACACTAT     | 1680 |
| Qy | 1681 | TAAAATATTAAGTGTAATTATTTTAACTCACAGCTACATATGACATTTTATGAGCTGT         | 1740 |
| Db | 1681 | <br>TAAAATATTAAGTGTAATTATTTTAACTCACAGCTACATATGACATTTTATGAGCTGT     | 1740 |
| Qy | 1741 | TTACGGCATGGAAAGAAAATCAGTGGGAATTAAGAAAGCCTCGTCGTGAAAGCACTTAAT       | 1800 |
| Db | 1741 | <br>TTACGGCATGGAAAGAAAATCAGTGGGAATTAAGAAAGCCTCGTCGTGAAAGCACTTAAT   | 1800 |
| Qy | 1801 | TTTTTACAGTTAGCACTTCAACATAGCTCTTAACAAGTCCAGGATATTCACACAACACT        | 1860 |
| Db | 1801 | <br>TTTTTACAGTTAGCACTTCAACATAGCTCTTAACAAGTCCAGGATATTCACACAACACT    | 1860 |
| Qy | 1861 | TAGGCTTAAAAATGAGCTCACTCAGAATTTCTATTCTTTCTAAAAAGAGATTTATTTTAA       | 1920 |
|    |      |  |      |

|    |      |   |      |
|----|------|---|------|
| Db | 1861 | TAGGCTTAAAAATGAGCTCACTCAGAATTTCTATTCTTTCTAAAAAGAGATTTATTTTTTA | 1920 |
| Qy | 1921 | AATCAATGGGACTCTGATATAAAGGAAGAATAAGTCACTGTAAACAGAACTTTTAAATG   | 1980 |
|    |      |   |      |
| Db | 1921 | AATCAATGGGACTCTGATATAAAGGAAGAATAAGTCACTGTAAACAGAACTTTTAAATG   | 1980 |
| Qy | 1981 | AAGCTTAAATTACTCAATTTAAAATTTTAAAATCCTTTAAAACAACCTTTTCAATTAATAT | 2040 |
|    |      |   |      |
| Db | 1981 | AAGCTTAAATTACTCAATTTAAAATTTTAAAATCCTTTAAAACAACCTTTTCAATTAATAT | 2040 |
| Qy | 2041 | TATCACACTATTATCAGATTGTAATTAGATGCAAATGAGAGAGCAGTTTAGTTGTTGCAT  | 2100 |
|    |      |   |      |
| Db | 2041 | TATCACACTATTATCAGATTGTAATTAGATGCAAATGAGAGAGCAGTTTAGTTGTTGCAT  | 2100 |
| Qy | 2101 | TTTTCGGACACTGGAAACATTTAAATGATCAGGAGGGAGTAACAGAAAGAGCAAGGCTGT  | 2160 |
|    |      |   |      |
| Db | 2101 | TTTTCGGACACTGGAAACATTTAAATGATCAGGAGGGAGTAACAGAAAGAGCAAGGCTGT  | 2160 |
| Qy | 2161 | TTTTGAAAATCATTACACTTTCACTAGAAGCCCAAACCTCAGCATTCTGCAATATGTAAC  | 2220 |
|    |      |   |      |
| Db | 2161 | TTTTGAAAATCATTACACTTTCACTAGAAGCCCAAACCTCAGCATTCTGCAATATGTAAC  | 2220 |
| Qy | 2221 | CAACATGTCACAAACAAGCAGCATGTAACAGACTGGCACATGTGCCAGCTGAATTTAAAA  | 2280 |
|    |      |   |      |
| Db | 2221 | CAACATGTCACAAACAAGCAGCATGTAACAGACTGGCACATGTGCCAGCTGAATTTAAAA  | 2280 |
| Qy | 2281 | TATAATACTTTTAAAAAGAAAATTATTACATCCTTTACATTCAAGTAAAGATCAAACCTCA | 2340 |
|    |      |   |      |
| Db | 2281 | TATAATACTTTTAAAAAGAAAATTATTACATCCTTTACATTCAAGTAAAGATCAAACCTCA | 2340 |
| Qy | 2341 | CAAAGAGAAATAGAATGTTTGAAAGGCTATCCCAAAGACTTTTTTGAATCTGTCATTCA   | 2400 |
|    |      |   |      |
| Db | 2341 | CAAAGAGAAATAGAATGTTTGAAAGGCTATCCCAAAGACTTTTTTGAATCTGTCATTCA   | 2400 |
| Qy | 2401 | CATACCCTGTGAAGACAATACTATCTACAATTTTTTCAGGATTATTTAAATCTTCTTTTT  | 2460 |
|    |      |   |      |
| Db | 2401 | CATACCCTGTGAAGACAATACTATCTACAATTTTTTCAGGATTATTTAAATCTTCTTTTT  | 2460 |
| Qy | 2461 | TCATATCGTAGCTTAAACTCTGTTTGGTTTTGTCATCTGTAAATACTTACCTACATACA   | 2520 |
|    |      |   |      |
| Db | 2461 | TCATATCGTAGCTTAAACTCTGTTTGGTTTTGTCATCTGTAAATACTTACCTACATACA   | 2520 |
| Qy | 2521 | CTGCATGTAGATGATTAAATGAGGGCAGGCCCTGTGCTCATAGCTTTACGATGGAGAGAT  | 2580 |
|    |      |   |      |
| Db | 2521 | CTGCATGTAGATGATTAAATGAGGGCAGGCCCTGTGCTCATAGCTTTACGATGGAGAGAT  | 2580 |
| Qy | 2581 | GCCAGTGACCTCATAATAAGACTGTGAACTGCCTGGTGCAGTGTCCACATGACAAAGGG   | 2640 |
|    |      |   |      |
| Db | 2581 | GCCAGTGACCTCATAATAAGACTGTGAACTGCCTGGTGCAGTGTCCACATGACAAAGGG   | 2640 |
| Qy | 2641 | GCAGGTAGCACCCCTCTCTCACCCATGCTGTGGTTAAAATGGTTTCTAGCATATGTATAAT | 2700 |
|    |      |   |      |
| Db | 2641 | GCAGGTAGCACCCCTCTCTCACCCATGCTGTGGTTAAAATGGTTTCTAGCATATGTATAAT | 2700 |
| Qy | 2701 | GCTATAGTTAAAATACTATTTTTCAAATCATACAGATTAGTACATTTAACAGCTACCTG   | 2760 |
|    |      |   |      |
| Db | 2701 | GCTATAGTTAAAATACTATTTTTCAAATCATACAGATTAGTACATTTAACAGCTACCTG   | 2760 |

|    |      |  |      |
|----|------|--|------|
| Qy | 2761 | TAAAGCTTATTACTAATTTTTGTATTATTTTGTAAATAGCCAATAGAAAAGTTTGCTTG    | 2820 |
|    |      |  |      |
| Db | 2761 | TAAAGCTTATTACTAATTTTTGTATTATTTTGTAAATAGCCAATAGAAAAGTTTGCTTG    | 2820 |
| Qy | 2821 | ACATGGTGCTTTTCTTTCATCTAGAGGCCAAAAGTGGCTTTTGAGACCGTAAGAACCTCTT  | 2880 |
|    |      |  |      |
| Db | 2821 | ACATGGTGCTTTTCTTTCATCTAGAGGCCAAAAGTGGCTTTTGAGACCGTAAGAACCTCTT  | 2880 |
| Qy | 2881 | AGCTTTGTGCGTTCCTGCCTAATTTTTATATCTTCTAAGCAAAGTGCCTTAGGATAGCTT   | 2940 |
|    |      |  |      |
| Db | 2881 | AGCTTTGTGCGTTCCTGCCTAATTTTTATATCTTCTAAGCAAAGTGCCTTAGGATAGCTT   | 2940 |
| Qy | 2941 | GGGATGAGATGTGTGTGAAAGTATGTACAAGAGAAAACGGAAGAGAGAGGAAATGAGGTG   | 3000 |
|    |      |  |      |
| Db | 2941 | GGGATGAGATGTGTGTGAAAGTATGTACAAGAGAAAACGGAAGAGAGAGGAAATGAGGTG   | 3000 |
| Qy | 3001 | GGGTTGGAGGAAACCCATGGGGACAGATTCCCATTCTTAGCCTAACGTTTCGTCATTGCCT  | 3060 |
|    |      |  |      |
| Db | 3001 | GGGTTGGAGGAAACCCATGGGGACAGATTCCCATTCTTAGCCTAACGTTTCGTCATTGCCT  | 3060 |
| Qy | 3061 | CGTCACATCAATGCAAAAGGTCCTGATTTTGTTCAGCAAAACACAGTGCAATGTTCTCA    | 3120 |
|    |      |  |      |
| Db | 3061 | CGTCACATCAATGCAAAAGGTCCTGATTTTGTTCAGCAAAACACAGTGCAATGTTCTCA    | 3120 |
| Qy | 3121 | GAGTGACTTTCGAAATAAATTGGGCCCAAGAGCTTTAACTCGGTCTTAAAATATGCCCAA   | 3180 |
|    |      |  |      |
| Db | 3121 | GAGTGACTTTCGAAATAAATTGGGCCCAAGAGCTTTAACTCGGTCTTAAAATATGCCCAA   | 3180 |
| Qy | 3181 | ATTTTTACTTTGTTTTCTTTTAATAGGCTGGGCCACATGTTGGAAATAAGCTAGTAATG    | 3240 |
|    |      |  |      |
| Db | 3181 | ATTTTTACTTTGTTTTCTTTTAATAGGCTGGGCCACATGTTGGAAATAAGCTAGTAATG    | 3240 |
| Qy | 3241 | TTGTTTTCTGTCAATATTGAATGTGATGGTACAGTAAACCAAAACCCAACAATGTGGCCA   | 3300 |
|    |      |  |      |
| Db | 3241 | TTGTTTTCTGTCAATATTGAATGTGATGGTACAGTAAACCAAAACCCAACAATGTGGCCA   | 3300 |
| Qy | 3301 | GAAAGAAAGAGCAATAATAATTAATTACACACCATATGGATTCTATTTATAAATCACCC    | 3360 |
|    |      |  |      |
| Db | 3301 | GAAAGAAAGAGCAATAATAATTAATTACACACCATATGGATTCTATTTATAAATCACCC    | 3360 |
| Qy | 3361 | ACAAACTTGTTCTTTAATTTTCATCCCAATCACTTTTTTCAGAGGCCTGTTATCATAGAAGT | 3420 |
|    |      |  |      |
| Db | 3361 | ACAAACTTGTTCTTTAATTTTCATCCCAATCACTTTTTTCAGAGGCCTGTTATCATAGAAGT | 3420 |
| Qy | 3421 | CATTTTAGACTCTCAATTTTAAATTAATTTTGAATCACTAATATTTTCACAGTTTATTAA   | 3480 |
|    |      |  |      |
| Db | 3421 | CATTTTAGACTCTCAATTTTAAATTAATTTTGAATCACTAATATTTTCACAGTTTATTAA   | 3480 |
| Qy | 3481 | TATATTTAATTTCTATTTAAATTTTAGATTATTTTATTACCATGTACTGAATTTTACA     | 3540 |
|    |      |  |      |
| Db | 3481 | TATATTTAATTTCTATTTAAATTTTAGATTATTTTATTACCATGTACTGAATTTTACA     | 3540 |
| Qy | 3541 | TCCTGATACCCTTTCCTTCTCCATGTCAGTATCATGTTCTCTAATTATCTTGCCAAATTT   | 3600 |
|    |      |  |      |
| Db | 3541 | TCCTGATACCCTTTCCTTCTCCATGTCAGTATCATGTTCTCTAATTATCTTGCCAAATTT   | 3600 |

Qy 3601 TGAAACTACACACAAAAAGCATACTTGCATTATTTATAATAAAATTGCATTTCAGTGGCTT 3660  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 3601 TGAAACTACACACAAAAAGCATACTTGCATTATTTATAATAAAATTGCATTTCAGTGGCTT 3660  
 Qy 3661 TTTAAAAAAATGTTTGATTCAAAACTTTAACATACTGATAAGTAAGAAACAATTATAAT 3720  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 3661 TTTAAAAAAATGTTTGATTCAAAACTTTAACATACTGATAAGTAAGAAACAATTATAAT 3720  
 Qy 3721 TTCTTTACATACTCAAAACCAAGATAGAAAAAGGTGCTATCGTTCAACTTCAAAACATGT 3780  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 3721 TTCTTTACATACTCAAAACCAAGATAGAAAAAGGTGCTATCGTTCAACTTCAAAACATGT 3780  
 Qy 3781 TTCCTAGTATTAAGGACTTTAATATAGCAACAGACAAAATTATTGTTAACATGGATGTTA 3840  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 3781 TTCCTAGTATTAAGGACTTTAATATAGCAACAGACAAAATTATTGTTAACATGGATGTTA 3840  
 Qy 3841 CAGCTCAAAAGATTTATAAAAGATTTTAACCTATTTTCTCCCTTATTATCCACTGCTAAT 3900  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 3841 CAGCTCAAAAGATTTATAAAAGATTTTAACCTATTTTCTCCCTTATTATCCACTGCTAAT 3900  
 Qy 3901 GTGGATGTATGTTCAAACACCTTTTAGTATTGATAGCTTACATATGGCCAAAGGAATACA 3960  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 3901 GTGGATGTATGTTCAAACACCTTTTAGTATTGATAGCTTACATATGGCCAAAGGAATACA 3960  
 Qy 3961 GTTTATAGCAAAACATGGGTATGCTGTAGCTAACTTTATAAAAGTGTAATATAACAATGT 4020  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 3961 GTTTATAGCAAAACATGGGTATGCTGTAGCTAACTTTATAAAAGTGTAATATAACAATGT 4020  
 Qy 4021 AAAAAATTATATATCTGGGAGGATTTTTTGGTTGCCTAAAGTGGCTATAGTTACTGATTT 4080  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 4021 AAAAAATTATATATCTGGGAGGATTTTTTGGTTGCCTAAAGTGGCTATAGTTACTGATTT 4080  
 Qy 4081 TTTATTATGTAAGCAAAACCAATAAAAATTTAAGTTTTTTTAACAACCTACCTTATTTTTTC 4140  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 4081 TTTATTATGTAAGCAAAACCAATAAAAATTTAAGTTTTTTTAACAACCTACCTTATTTTTTC 4140  
 Qy 4141 ACTGTACAGACACTAATTCATTAAATACTAATTGATTGTTTAAAAGAAATATAAATGTGA 4200  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 4141 ACTGTACAGACACTAATTCATTAAATACTAATTGATTGTTTAAAAGAAATATAAATGTGA 4200  
 Qy 4201 CAAGTGGACATTATTTATGTTAAATATACAATTATCAAGCAAGTATGAAGTTATTCAATT 4260  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 4201 CAAGTGGACATTATTTATGTTAAATATACAATTATCAAGCAAGTATGAAGTTATTCAATT 4260  
 Qy 4261 AAAATGCCACATTTCTGGTCTCTGGG 4286  
 ||||||||||||||||||||||||||||  
 Db 4261 AAAATGCCACATTTCTGGTCTCTGGG 4286

RESULT 4

AX548828

LOCUS

AX548828

4286 bp

DNA

linear

PAT 26-NOV-2002

DEFINITION

Sequence 113 from Patent WO02061087.

ACCESSION

AX548828

VERSION

AX548828.1 GI:25813723

KEYWORDS

.

SOURCE

Homo sapiens (human)

ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1

AUTHORS Burmer, G.C., Roush, C.L. and Brown, J.P.

TITLE Antigenic peptides, such as for G protein-coupled receptors  
(GPCRs), antibodies thereto, and systems for identifying such  
antigenic peptides

JOURNAL Patent: WO 02061087-A 113 08-AUG-2002;  
Lifespan Biosciences, Inc. (US)

FEATURES Location/Qualifiers

source 1. .4286  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

# ORIGIN

Query Match 99.6%; Score 4284.4; DB 6; Length 4286;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 4285; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

|    |     |  |     |
|----|-----|--|-----|
| Qy | 1   | GAGACATTCCGGTGGGGGACTCTGGCCAGCCCAGCAACGTGGATCCTGAGAGCACTCCC  | 60  |
|    |     |  |     |
| Db | 1   | GAGACATTCCGGTGGGGGACTCTGGCCAGCCCAGCAACGTGGATCCTGAGAGCACTCCC  | 60  |
| Qy | 61  | AGGTAGGCATTTGCCCCGGTGGGACGCCTTGCCAGAGCAGTGTGTGGCAGGCCCCCGTGG | 120 |
|    |     |  |     |
| Db | 61  | AGGTAGGCATTTGCCCCGGTGGGACGCCTTGCCAGAGCAGTGTGTGGCAGGCCCCCGTGG | 120 |
| Qy | 121 | AGGATCAACACAGTGGCTGAACACTGGGAAGGAACTGGTACTTGGAGTCTGGACATCTGA | 180 |
|    |     |  |     |
| Db | 121 | AGGATCAACACAGTGGCTGAACACTGGGAAGGAACTGGTACTTGGAGTCTGGACATCTGA | 180 |
| Qy | 181 | AACTTGCTCTGAAACTGCGGAGCGGCCACCGACGCCTTCTGGAGCAGGTAGCAGCATG   | 240 |
|    |     |  |     |
| Db | 181 | AACTTGCTCTGAAACTGCGCAGCGGCCACCGACGCCTTCTGGAGCAGGTAGCAGCATG   | 240 |
| Qy | 241 | CAGCCGCCTCCAAGTCTGTGCGGACGCGCCCTGGTTGCGCTGGTTCTTGCCTGCGGCCTG | 300 |
|    |     |  |     |
| Db | 241 | CAGCCGCCTCCAAGTCTGTGCGGACGCGCCCTGGTTGCGCTGGTTCTTGCCTGCGGCCTG | 300 |
| Qy | 301 | TCGCGGATCTGGGGAGAGGAGAGAGGCTTCCCGCCTGACAGGGCCACTCCGCTTTTGCAA | 360 |
|    |     |  |     |
| Db | 301 | TCGCGGATCTGGGGAGAGGAGAGAGGCTTCCCGCCTGACAGGGCCACTCCGCTTTTGCAA | 360 |
| Qy | 361 | ACCGCAGAGATAATGACGCCACCCACTAAGACCTTATGGCCCAAGGGTTCCAACGCCAGT | 420 |
|    |     |  |     |
| Db | 361 | ACCGCAGAGATAATGACGCCACCCACTAAGACCTTATGGCCCAAGGGTTCCAACGCCAGT | 420 |
| Qy | 421 | CTGGCGCGGTCGTTGGCACCTGCGGAGGTGCCTAAAGGAGACAGGACGGCAGGATCTCCG | 480 |
|    |     |  |     |
| Db | 421 | CTGGCGCGGTCGTTGGCACCTGCGGAGGTGCCTAAAGGAGACAGGACGGCAGGATCTCCG | 480 |
| Qy | 481 | CCACGCACCATCTCCCCTCCCCCGTGCCAAGGACCCATCGAGATCAAGGAGACTTTCAA  | 540 |
|    |     |  |     |
| Db | 481 | CCACGCACCATCTCCCCTCCCCCGTGCCAAGGACCCATCGAGATCAAGGAGACTTTCAA  | 540 |

|    |      |  |      |
|----|------|--|------|
| Qy | 541  | TACATCAACACGGTTGTGTCTGCCTTGTGTTTCGTGCTGGGGATCATCGGGAACCTCCACA  | 600  |
| Db | 541  | TACATCAACACGGTTGTGTCTGCCTTGTGTTTCGTGCTGGGGATCATCGGGAACCTCCACA  | 600  |
| Qy | 601  | CTTCTGAGAATTATCTACAAGAACAAGTGCATGCGAAACGGTCCCAATATCTTGATCGCC   | 660  |
| Db | 601  | CTTCTGAGAATTATCTACAAGAACAAGTGCATGCGAAACGGTCCCAATATCTTGATCGCC   | 660  |
| Qy | 661  | AGCTTGGCTCTGGGAGACCTGCTGCACATCGTCATTGACATCCCTATCAATGTCTACAAG   | 720  |
| Db | 661  | AGCTTGGCTCTGGGAGACCTGCTGCACATCGTCATTGACATCCCTATCAATGTCTACAAG   | 720  |
| Qy | 721  | CTGCTGGCAGAGGACTGGCCATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTCATACAG   | 780  |
| Db | 721  | CTGCTGGCAGAGGACTGGCCATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTCATACAG   | 780  |
| Qy | 781  | AAAGCCTCCGTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATATCGA   | 840  |
| Db | 781  | AAAGCCTCCGTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATATCGA   | 840  |
| Qy | 841  | GCTGTTGCTTCTTGGAGTAGAATTAAGGAATTGGGGTTCCAAAATGGACAGCAGTAGAA    | 900  |
| Db | 841  | GCTGTTGCTTCTTGGAGTAGAATTAAGGAATTGGGGTTCCAAAATGGACAGCAGTAGAA    | 900  |
| Qy | 901  | ATTGTTTTGATTTGGGTGGTCTCTGTGGTCTGGCTGTCCCTGAAGCCATAGGTTTTGAT    | 960  |
| Db | 901  | ATTGTTTTGATTTGGGTGGTCTCTGTGGTCTGGCTGTCCCTGAAGCCATAGGTTTTGAT    | 960  |
| Qy | 961  | ATAATTACGATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTTTCAG  | 1020 |
| Db | 961  | ATAATTACGATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTTTCAG  | 1020 |
| Qy | 1021 | AAGACAGCTTTCATGCAGTTTTTACAAGACAGCAAAAGATTGGTGGCTGTTTCAGTTTCTAT | 1080 |
| Db | 1021 | AAGACAGCTTTCATGCAGTTTTTACAAGACAGCAAAAGATTGGTGGCTGTTTCAGTTTCTAT | 1080 |
| Qy | 1081 | TTCTGCTTGCCATTGGCCATCACTGCATTTTTTTTATACACTAATGACCTGTGAAATGTTG  | 1140 |
| Db | 1081 | TTCTGCTTGCCATTGGCCATCACTGCATTTTTTTTATACACTAATGACCTGTGAAATGTTG  | 1140 |
| Qy | 1141 | AGAAAGAAAAGTGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAAGTG   | 1200 |
| Db | 1141 | AGAAAGAAAAGTGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAAGTG   | 1200 |
| Qy | 1201 | GCCAAAACCGTCTTTTGCCTGGTCCTTGTCTTTGCCCTCTGCTGGCTTCCCCTTCACCTC   | 1260 |
| Db | 1201 | GCCAAAACCGTCTTTTGCCTGGTCCTTGTCTTTGCCCTCTGCTGGCTTCCCCTTCACCTC   | 1260 |
| Qy | 1261 | AGCAGGATTCTGAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGAACTTTTG   | 1320 |
| Db | 1261 | AGCAGGATTCTGAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGAACTTTTG   | 1320 |
| Qy | 1321 | AGCTTTCTGTTGGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCTGCATT    | 1380 |
| Db | 1321 | AGCTTTCTGTTGGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCTGCATT    | 1380 |
| Qy | 1381 | AACCCAATTGCTCTGTATTTGGTGAGCAAAAGATTCAAAAACCTGCTTTAAGTCATGCTTA  | 1440 |

|    |      |   |      |
|----|------|---|------|
| Db | 1381 | <br>AACCCAATTGCTCTGTATTTGGTGAGCAAAAGATTCAAAACTGCTTTAAGTCATGCTTA   | 1440 |
| Qy | 1441 | TGCTGCTGGTGCCAGTCATTTGAAGAAAAACAGTCCTTGGAGGAAAAGCAGTCGTGCTTA      | 1500 |
| Db | 1441 | <br>TGCTGCTGGTGCCAGTCATTTGAAGAAAAACAGTCCTTGGAGGAAAAGCAGTCGTGCTTA  | 1500 |
| Qy | 1501 | AAGTTCAAAGCTAATGATCACGGATATGACAACTTCCGTTCCAGTAATAAATACAGCTCA      | 1560 |
| Db | 1501 | <br>AAGTTCAAAGCTAATGATCACGGATATGACAACTTCCGTTCCAGTAATAAATACAGCTCA  | 1560 |
| Qy | 1561 | TCTTGAAAGAAGAACTATTCAGTGTATTTCAATTTCTTTATATTGGACCGAAGTCATTAA      | 1620 |
| Db | 1561 | <br>TCTTGAAAGAAGAACTATTCAGTGTATTTCAATTTCTTTATATTGGACCGAAGTCATTAA  | 1620 |
| Qy | 1621 | AACAAAATGAAACATTTGCCAAAACAAAACAAAAAATATGTATTTGCACAGCACACTAT       | 1680 |
| Db | 1621 | <br>AACAAAATGAAACATTTGCCAAAACAAAACAAAAAATATGTATTTGCACAGCACACTAT   | 1680 |
| Qy | 1681 | TAAAATATTAAGTGTAATTATTTTAACACTCACAGCTACATATGACATTTTATGAGCTGT      | 1740 |
| Db | 1681 | <br>TAAAATATTAAGTGTAATTATTTTAACACTCACAGCTACATATGACATTTTATGAGCTGT  | 1740 |
| Qy | 1741 | TTACGGCATGGAAAGAAAATCAGTGGGAATTAAGAAAGCCTCGTCGTGAAAGCACTTAAT      | 1800 |
| Db | 1741 | <br>TTACGGCATGGAAAGAAAATCAGTGGGAATTAAGAAAGCCTCGTCGTGAAAGCACTTAAT  | 1800 |
| Qy | 1801 | TTTTTACAGTTAGCACTTCAACATAGCTCTTAACAACCTCCAGGATATTCACACAACACT      | 1860 |
| Db | 1801 | <br>TTTTTACAGTTAGCACTTCAACATAGCTCTTAACAACCTCCAGGATATTCACACAACACT  | 1860 |
| Qy | 1861 | TAGGCTTAAAAATGAGCTCACTCAGAATTTCTATTCTTTCTAAAAAGAGATTTATTTTTTA     | 1920 |
| Db | 1861 | <br>TAGGCTTAAAAATGAGCTCACTCAGAATTTCTATTCTTTCTAAAAAGAGATTTATTTTTTA | 1920 |
| Qy | 1921 | AATCAATGGGACTCTGATATAAAGGAAGAATAAGTCACTGTAAAACAGAACTTTTAAATG      | 1980 |
| Db | 1921 | <br>AATCAATGGGACTCTGATATAAAGGAAGAATAAGTCACTGTAAAACAGAACTTTTAAATG  | 1980 |
| Qy | 1981 | AAGCTTAAATTACTCAATTTAAATTTTAAATCCTTTAAACAACCTTTTCAATTAATAT        | 2040 |
| Db | 1981 | <br>AAGCTTAAATTACTCAATTTAAATTTTAAATCCTTTAAACAACCTTTTCAATTAATAT    | 2040 |
| Qy | 2041 | TATCACACTATTATCAGATTGTAATTAGATGCAAATGAGAGAGCAGTTTAGTTGTTGCAT      | 2100 |
| Db | 2041 | <br>TATCACACTATTATCAGATTGTAATTAGATGCAAATGAGAGAGCAGTTTAGTTGTTGCAT  | 2100 |
| Qy | 2101 | TTTTCGGACACTGGAAACATTTAAATGATCAGGAGGGAGTAACAGAAAGAGCAAGGCTGT      | 2160 |
| Db | 2101 | <br>TTTTCGGACACTGGAAACATTTAAATGATCAGGAGGGAGTAACAGAAAGAGCAAGGCTGT  | 2160 |
| Qy | 2161 | TTTTGAAAATCATTACACTTTCACTAGAAGCCCAAACCTCAGCATTCTGCAATATGTAAC      | 2220 |
| Db | 2161 | <br>TTTTGAAAATCATTACACTTTCACTAGAAGCCCAAACCTCAGCATTCTGCAATATGTAAC  | 2220 |
| Qy | 2221 | CAACATGTCACAAACAAGCAGCATGTAACAGACTGGCACATGTGCCAGCTGAATTTAAAA      | 2280 |
|    |      |   |      |

|    |      |   |      |
|----|------|---|------|
| Db | 2221 | CAACATGTCACAAACAAGCAGCATGTAACAGACTGGCACATGTGCCAGCTGAATTTAAAA  | 2280 |
| Qy | 2281 | TATAATACTTTTAAAAAGAAAATTATTACATCCTTTACATTCAAGTTAAGATCAAACCTCA | 2340 |
|    |      |   |      |
| Db | 2281 | TATAATACTTTTAAAAAGAAAATTATTACATCCTTTACATTCAAGTTAAGATCAAACCTCA | 2340 |
| Qy | 2341 | CAAAGAGAAATAGAATGTTTGAAAGGCTATCCCAAAGACTTTTTTGAATCTGTCATTCA   | 2400 |
|    |      |   |      |
| Db | 2341 | CAAAGAGAAATAGAATGTTTGAAAGGCTATCCCAAAGACTTTTTTGAATCTGTCATTCA   | 2400 |
| Qy | 2401 | CATACCCTGTGAAGACAATACTATCTACAATTTTTTCAGGATTATTAATCTTCTTTTT    | 2460 |
|    |      |   |      |
| Db | 2401 | CATACCCTGTGAAGACAATACTATCTACAATTTTTTCAGGATTATTAATCTTCTTTTT    | 2460 |
| Qy | 2461 | TCACTATCGTAGCTTAAACTCTGTTTGGTTTTGTCATCTGTAAATACTTACCTACATACA  | 2520 |
|    |      |   |      |
| Db | 2461 | TCACTATCGTAGCTTAAACTCTGTTTGGTTTTGTCATCTGTAAATACTTACCTACATACA  | 2520 |
| Qy | 2521 | CTGCATGTAGATGATTAAATGAGGGCAGGCCCTGTGCTCATAGCTTTACGATGGAGAGAT  | 2580 |
|    |      |   |      |
| Db | 2521 | CTGCATGTAGATGATTAAATGAGGGCAGGCCCTGTGCTCATAGCTTTACGATGGAGAGAT  | 2580 |
| Qy | 2581 | GCCAGTGACCTCATAATAAAGACTGTGAAGTGCCTGGTGCAGTGTCCACATGACAAAGGG  | 2640 |
|    |      |   |      |
| Db | 2581 | GCCAGTGACCTCATAATAAAGACTGTGAAGTGCCTGGTGCAGTGTCCACATGACAAAGGG  | 2640 |
| Qy | 2641 | GCAGGTAGCACCCCTCTCTCACCCTGCTGTGGTTAAATGGTTTCTAGCATATGTATAAT   | 2700 |
|    |      |   |      |
| Db | 2641 | GCAGGTAGCACCCCTCTCTCACCCTGCTGTGGTTAAATGGTTTCTAGCATATGTATAAT   | 2700 |
| Qy | 2701 | GCTATAGTTAAAATACTATTTTTCAAATCATAACAGATTAGTACATTTAACAGCTACCTG  | 2760 |
|    |      |   |      |
| Db | 2701 | GCTATAGTTAAAATACTATTTTTCAAATCATAACAGATTAGTACATTTAACAGCTACCTG  | 2760 |
| Qy | 2761 | TAAAGCTTATTACTAATTTTTGTATTATTTTTGTAAATAGCCAATAGAAAAGTTTGCTTG  | 2820 |
|    |      |   |      |
| Db | 2761 | TAAAGCTTATTACTAATTTTTGTATTATTTTTGTAAATAGCCAATAGAAAAGTTTGCTTG  | 2820 |
| Qy | 2821 | ACATGGTGCTTTTCTTTTCATCTAGAGGCAAACTGCTTTTTGAGACCGTAAGAACCTCTT  | 2880 |
|    |      |   |      |
| Db | 2821 | ACATGGTGCTTTTCTTTTCATCTAGAGGCAAACTGCTTTTTGAGACCGTAAGAACCTCTT  | 2880 |
| Qy | 2881 | AGCTTTGTGCGTTCCTGCCTAATTTTTATATCTTCTAAGCAAAGTGCCTTAGGATAGCTT  | 2940 |
|    |      |   |      |
| Db | 2881 | AGCTTTGTGCGTTCCTGCCTAATTTTTATATCTTCTAAGCAAAGTGCCTTAGGATAGCTT  | 2940 |
| Qy | 2941 | GGGATGAGATGTGTGTGAAAGTATGTACAAGAGAAAACGGAAGAGAGAGGAAATGAGGTG  | 3000 |
|    |      |   |      |
| Db | 2941 | GGGATGAGATGTGTGTGAAAGTATGTACAAGAGAAAACGGAAGAGAGAGGAAATGAGGTG  | 3000 |
| Qy | 3001 | GGGTTGGAGGAAACCCATGGGGACAGATTCCCATTCTTAGCCTAACGTTTCGTCATTGCCT | 3060 |
|    |      |   |      |
| Db | 3001 | GGGTTGGAGGAAACCCATGGGGACAGATTCCCATTCTTAGCCTAACGTTTCGTCATTGCCT | 3060 |
| Qy | 3061 | CGTCACATCAATGCAAAAGGTCCTGATTTTGTTCAGCAAAACACAGTGCAATGTTCTCA   | 3120 |
|    |      |   |      |
| Db | 3061 | CGTCACATCAATGCAAAAGGTCCTGATTTTGTTCAGCAAAACACAGTGCAATGTTCTCA   | 3120 |



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|----|------|---|------|
| Qy | 3121 | GAGTGACTTTCGAAATAAATTGGGCCCAAGAGCTTTAACTCGGTCTTAAATATGCCCCA   | 3180 |
|    |      |   |      |
| Db | 3121 | GAGTGACTTTCGAAATAAATTGGGCCCAAGAGCTTTAACTCGGTCTTAAATATGCCCCA   | 3180 |
| Qy | 3181 | ATTTTACTTTGTTTTCTTTAATAGGCTGGGCCACATGTTGGAAATAAGCTAGTAATG     | 3240 |
|    |      |   |      |
| Db | 3181 | ATTTTACTTTGTTTTCTTTAATAGGCTGGGCCACATGTTGGAAATAAGCTAGTAATG     | 3240 |
| Qy | 3241 | TTGTTTTCTGTCAATATTGAATGTGATGGTACAGTAAACCAAAACCAACAATGTGGCCA   | 3300 |
|    |      |   |      |
| Db | 3241 | TTGTTTTCTGTCAATATTGAATGTGATGGTACAGTAAACCAAAACCAACAATGTGGCCA   | 3300 |
| Qy | 3301 | GAAAGAAAGAGCAATAATAATTAATTCACACACCATATGGATTCTATTTATAAATCACCC  | 3360 |
|    |      |   |      |
| Db | 3301 | GAAAGAAAGAGCAATAATAATTAATTCACACACCATATGGATTCTATTTATAAATCACCC  | 3360 |
| Qy | 3361 | ACAAACTTGTCTTTAATTTTCATCCCAATCACTTTTTTCAGAGGCCTGTTATCATAGAAGT | 3420 |
|    |      |   |      |
| Db | 3361 | ACAAACTTGTCTTTAATTTTCATCCCAATCACTTTTTTCAGAGGCCTGTTATCATAGAAGT | 3420 |
| Qy | 3421 | CATTTTAGACTCTCAATTTTAAATTAATTTTGAATCACTAATATTTTCACAGTTTATTAA  | 3480 |
|    |      |   |      |
| Db | 3421 | CATTTTAGACTCTCAATTTTAAATTAATTTTGAATCACTAATATTTTCACAGTTTATTAA  | 3480 |
| Qy | 3481 | TATATTTAATTTCTATTTAAATTTTAGATTATTTTATTACCATGTACTGAATTTTACA    | 3540 |
|    |      |   |      |
| Db | 3481 | TATATTTAATTTCTATTTAAATTTTAGATTATTTTATTACCATGTACTGAATTTTACA    | 3540 |
| Qy | 3541 | TCCTGATACCCTTTCCTTCTCCATGTCAGTATCATGTTCTCTAATTATCTTGCCAAATTT  | 3600 |
|    |      |   |      |
| Db | 3541 | TCCTGATACCCTTTCCTTCTCCATGTCAGTATCATGTTCTCTAATTATCTTGCCAAATTT  | 3600 |
| Qy | 3601 | TGAAACTACACACAAAAAGCATACTTGCATTATTTATAATAAAATTGCATTCACTGGCTT  | 3660 |
|    |      |   |      |
| Db | 3601 | TGAAACTACACACAAAAAGCATACTTGCATTATTTATAATAAAATTGCATTCACTGGCTT  | 3660 |
| Qy | 3661 | TTTAAAAAAATGTTTGATTCAAACTTTAACATACTGATAAGTAAGAAACAATTATAAT    | 3720 |
|    |      |   |      |
| Db | 3661 | TTTAAAAAAATGTTTGATTCAAACTTTAACATACTGATAAGTAAGAAACAATTATAAT    | 3720 |
| Qy | 3721 | TTCTTTACATACTCAAACCAAGATAGAAAAAGGTGCTATCGTTCAACTTCAAACATGT    | 3780 |
|    |      |   |      |
| Db | 3721 | TTCTTTACATACTCAAACCAAGATAGAAAAAGGTGCTATCGTTCAACTTCAAACATGT    | 3780 |
| Qy | 3781 | TTCCTAGTATTAAGGACTTTAATATAGCAACAGACAAAATTATTGTTAACATGGATGTTA  | 3840 |
|    |      |   |      |
| Db | 3781 | TTCCTAGTATTAAGGACTTTAATATAGCAACAGACAAAATTATTGTTAACATGGATGTTA  | 3840 |
| Qy | 3841 | CAGCTCAAAAGATTTATAAAAGATTTTAACCTATTTTCTCCCTTATTATCCACTGCTAAT  | 3900 |
|    |      |   |      |
| Db | 3841 | CAGCTCAAAAGATTTATAAAAGATTTTAACCTATTTTCTCCCTTATTATCCACTGCTAAT  | 3900 |
| Qy | 3901 | GTGGATGTATGTTCAAACACCTTTTAGTATTGATAGCTTACATATGGCCAAAGGAATACA  | 3960 |
|    |      |   |      |
| Db | 3901 | GTGGATGTATGTTCAAACACCTTTTAGTATTGATAGCTTACATATGGCCAAAGGAATACA  | 3960 |

Qy 3961 GTTTATAGCAAAACATGGGTATGCTGTAGCTAACTTTATAAAAGTGTAATATAACAATGT 4020  
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 Db 3961 GTTTATAGCAAAACATGGGTATGCTGTAGCTAACTTTATAAAAGTGTAATATAACAATGT 4020  
 Qy 4021 AAAAAATTATATATCTGGGAGGATTTTTTGGTTGCCTAAAGTGGCTATAGTTACTGATTT 4080  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 4021 AAAAAATTATATATCTGGGAGGATTTTTTGGTTGCCTAAAGTGGCTATAGTTACTGATTT 4080  
 Qy 4081 TTTATTATGTAAGCAAAACCAATAAAAAATTTAAGTTTTTTTAACTACCTTATTTTTC 4140  
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 Db 4081 TTTATTATGTAAGCAAAACCAATAAAAAATTTAAGTTTTTTTAACTACCTTATTTTTC 4140  
 Qy 4141 ACTGTACAGACACTAATTCATTAAATACTAATTGATTGTTTAAAAGAAATATAAATGTGA 4200  
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 Db 4141 ACTGTACAGACACTAATTCATTAAATACTAATTGATTGTTTAAAAGAAATATAAATGTGA 4200  
 Qy 4201 CAAGTGGACATTATTTATGTTAAATATACAATTATCAAGCAAGTATGAAGTTATTCAATT 4260  
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 Db 4201 CAAGTGGACATTATTTATGTTAAATATACAATTATCAAGCAAGTATGAAGTTATTCAATT 4260  
 Qy 4261 AAAATGCCACATTTCTGGTCTCTGGG 4286  
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 Db 4261 AAAATGCCACATTTCTGGTCTCTGGG 4286

RESULT 5

AX587707

LOCUS AX587707 4286 bp DNA linear PAT 10-JAN-2003

DEFINITION Sequence 177 from Patent WO0246467.

ACCESSION AX587707

VERSION AX587707.1 GI:28212378

KEYWORDS .

SOURCE synthetic construct

ORGANISM synthetic construct

artificial sequences.

REFERENCE 1

AUTHORS Bertucci,F., Houlgatte,R., Birnbaum,D., Nguyen,C., Viens,P. and Fert,V.

TITLE Gene expression profiling of primary breast carcinomas using arrays of candidate genes

JOURNAL Patent: WO 0246467-A 177 13-JUN-2002;  
 Ipsogen (FR)

FEATURES Location/Qualifiers

source 1. .4286

/organism="synthetic construct"

/mol\_type="unassigned DNA"

/db\_xref="taxon:32630"

/note="primer"

misc\_feature 1. .4286

/note="endothelin receptor type b (EDNRB) gene."

ORIGIN

Query Match 99.6%; Score 4284.4; DB 6; Length 4286;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 4285; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GAGACATTCCGGTGGGGGACTCTGCCAGCCCGAGCAACGTGGATCCTGAGAGCACTCCC 60

|    |     |   |     |
|----|-----|---|-----|
| Db | 1   |   | 60  |
| Qy | 61  | AGGTAGGCATTTGCCCCGGTGGGACGCCTTGCCAGAGCAGTGTGTGGCAGGCCCCCGTGG  | 120 |
| Db | 61  | AGGTAGGCATTTGCCCCGGTGGGACGCCTTGCCAGAGCAGTGTGTGGCAGGCCCCCGTGG  | 120 |
| Qy | 121 | AGGATCAACACAGTGGCTGAACACTGGGAAGGAACTGGTACTTGGAGTCTGGACATCTGA  | 180 |
| Db | 121 | AGGATCAACACAGTGGCTGAACACTGGGAAGGAACTGGTACTTGGAGTCTGGACATCTGA  | 180 |
| Qy | 181 | AACTTGGCTCTGAAACTGCGGAGCGGCCACCGACGCCTTCTGGAGCAGGTAGCAGCATG   | 240 |
| Db | 181 | AACTTGGCTCTGAAACTGCGGAGCGGCCACCGACGCCTTCTGGAGCAGGTAGCAGCATG   | 240 |
| Qy | 241 | CAGCCGCCTCCAAGTCTGTGCGGACGCGCCCTGGTTGCGCTGGTTCTTGCTGCGGCCCTG  | 300 |
| Db | 241 | CAGCCGCCTCCAAGTCTGTGCGGACGCGCCCTGGTTGCGCTGGTTCTTGCTGCGGCCCTG  | 300 |
| Qy | 301 | TCGCGGATCTGGGGAGAGGAGAGAGGCTTCCCGCCTGACAGGGCCACTCCGCTTTTGCAA  | 360 |
| Db | 301 | TCGCGGATCTGGGGAGAGGAGAGAGGCTTCCCGCCTGACAGGGCCACTCCGCTTTTGCAA  | 360 |
| Qy | 361 | ACCGCAGAGATAATGACGCCACCCACTAAGACCTTATGGCCCAAGGGTTCCAACGCCAGT  | 420 |
| Db | 361 | ACCGCAGAGATAATGACGCCACCCACTAAGACCTTATGGCCCAAGGGTTCCAACGCCAGT  | 420 |
| Qy | 421 | CTGGCGCGGTTCGTTGGCACCTGCGGAGGTGCCTAAAGGAGACAGGACGGCAGGATCTCCG | 480 |
| Db | 421 | CTGGCGCGGTTCGTTGGCACCTGCGGAGGTGCCTAAAGGAGACAGGACGGCAGGATCTCCG | 480 |
| Qy | 481 | CCACGCACCATCTCCCCTCCCCGTGCCAAGGACCCATCGAGATCAAGGAGACTTTCAA    | 540 |
| Db | 481 | CCACGCACCATCTCCCCTCCCCGTGCCAAGGACCCATCGAGATCAAGGAGACTTTCAA    | 540 |
| Qy | 541 | TACATCAACACGGTTGTGTCCTGCCTTGTGTTTCGTGCTGGGGATCATCGGGAACCTCACA | 600 |
| Db | 541 | TACATCAACACGGTTGTGTCCTGCCTTGTGTTTCGTGCTGGGGATCATCGGGAACCTCACA | 600 |
| Qy | 601 | CTTCTGAGAATTATCTACAAGAACAAGTGCATGCGAAACGGTCCCAATATCTTGATCGCC  | 660 |
| Db | 601 | CTTCTGAGAATTATCTACAAGAACAAGTGCATGCGAAACGGTCCCAATATCTTGATCGCC  | 660 |
| Qy | 661 | AGCTTGGCTCTGGGAGACCTGCTGCACATCGTCATTGACATCCCTATCAATGTCTACAAG  | 720 |
| Db | 661 | AGCTTGGCTCTGGGAGACCTGCTGCACATCGTCATTGACATCCCTATCAATGTCTACAAG  | 720 |
| Qy | 721 | CTGCTGGCAGAGGACTGGCCATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTCATACAG  | 780 |
| Db | 721 | CTGCTGGCAGAGGACTGGCCATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTCATACAG  | 780 |
| Qy | 781 | AAAGCCTCCGTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATATCGA  | 840 |
| Db | 781 | AAAGCCTCCGTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATATCGA  | 840 |
| Qy | 841 | GCTGTTGCTTCTTGGAGTAGAATTAAAGGAATTGGGGTTCCAAAATGGACAGCAGTAGAA  | 900 |

Db 841 GCTGTTGCTTCTTGGAGTAGAATTAAAGGAATTGGGGTTCCAAAATGGACAGCAGTAGAA 900

Qy 901 ATTGTTTTGATTTGGGTGGTCTCTGTGGTTCTGGCTGTCCCTGAAGCCATAGGTTTTGAT 960  
 |||

Db 901 ATTGTTTTGATTTGGGTGGTCTCTGTGGTTCTGGCTGTCCCTGAAGCCATAGGTTTTGAT 960

Qy 961 ATAATTACGATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTTCAG 1020  
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Db 961 ATAATTACGATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTTCAG 1020

Qy 1021 AAGACAGCTTTTCATGCAGTTTTACAAGACAGCAAAAGATTGGTGGCTGTTTCAGTTTCTAT 1080  
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Db 1021 AAGACAGCTTTTCATGCAGTTTTACAAGACAGCAAAAGATTGGTGGCTGTTTCAGTTTCTAT 1080

Qy 1081 TTCTGCTTGCCATTGGCCATCACTGCATTTTTTTATACACTAATGACCTGTGAAATGTTG 1140  
 |||

Db 1081 TTCTGCTTGCCATTGGCCATCACTGCATTTTTTTATACACTAATGACCTGTGAAATGTTG 1140

Qy 1141 AGAAAGAAAAGTGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAAGTG 1200  
 |||

Db 1141 AGAAAGAAAAGTGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAAGTG 1200

Qy 1201 GCCAAAACCGTCTTTTGCCTGGTCCTTGTCTTTGCCCTCTGCTGGCTTCCCCTTCACCTC 1260  
 |||

Db 1201 GCCAAAACCGTCTTTTGCCTGGTCCTTGTCTTTGCCCTCTGCTGGCTTCCCCTTCACCTC 1260

Qy 1261 AGCAGGATTCTGAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGAACTTTTG 1320  
 |||

Db 1261 AGCAGGATTCTGAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGAACTTTTG 1320

Qy 1321 AGCTTTCTGTTGGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCCTGCATT 1380  
 |||

Db 1321 AGCTTTCTGTTGGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCCTGCATT 1380

Qy 1381 AACCCAATTGCTCTGTATTTGGTGAGCAAAAGATTCAAAAAGTCTTTAAGTCATGCTTA 1440  
 |||

Db 1381 AACCCAATTGCTCTGTATTTGGTGAGCAAAAGATTCAAAAAGTCTTTAAGTCATGCTTA 1440

Qy 1441 TGCTGCTGGTGCCAGTCATTTGAAGAAAAACAGTCCTTGGAGGAAAAGCAGTCGTGCTTA 1500  
 |||

Db 1441 TGCTGCTGGTGCCAGTCATTTGAAGAAAAACAGTCCTTGGAGGAAAAGCAGTCGTGCTTA 1500

Qy 1501 AAGTTCAAAGCTAATGATCACGGATATGACAACCTCCGTTCCAGTAATAAATACAGCTCA 1560  
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Db 1501 AAGTTCAAAGCTAATGATCACGGATATGACAACCTCCGTTCCAGTAATAAATACAGCTCA 1560

Qy 1561 TCTTGAAAGAAGAACTATTCACTGTATTTCAATTTCTTTATATTGGACCGAAGTCATTAA 1620  
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Db 1561 TCTTGAAAGAAGAACTATTCACTGTATTTCAATTTCTTTATATTGGACCGAAGTCATTAA 1620

Qy 1621 AACAAAATGAAACATTTGCCAAAACAAAACAAAAAACTATGTATTTGCACAGCACACTAT 1680  
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Db 1621 AACAAAATGAAACATTTGCCAAAACAAAACAAAAAACTATGTATTTGCACAGCACACTAT 1680

Qy 1681 TAAAATATTAAGTGTAATTATTTTAACTACAGCTACATATGACATTTTATGAGCTGT 1740  
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Db 1681 TAAAATATTAAGTGTAATTATTTTAACTACAGCTACATATGACATTTTATGAGCTGT 1740

|    |      |  |      |
|----|------|--|------|
| Qy | 1741 | TTACGGCATGGAAAGAAAATCAGTGGGAATTAAGAAAGCCTCGTCGTGAAAGCACTTAAT   | 1800 |
|    |      |  |      |
| Db | 1741 | TTACGGCATGGAAAGAAAATCAGTGGGAATTAAGAAAGCCTCGTCGTGAAAGCACTTAAT   | 1800 |
| Qy | 1801 | TTTTTACAGTTAGCACTTCAACATAGCTCTTAACAACTTCCAGGATATTCACACAACACT   | 1860 |
|    |      |  |      |
| Db | 1801 | TTTTTACAGTTAGCACTTCAACATAGCTCTTAACAACTTCCAGGATATTCACACAACACT   | 1860 |
| Qy | 1861 | TAGGCTTAAAAATGAGCTCACTCAGAATTTCTATTCTTTCTAAAAAGAGATTATTTTTTA   | 1920 |
|    |      |  |      |
| Db | 1861 | TAGGCTTAAAAATGAGCTCACTCAGAATTTCTATTCTTTCTAAAAAGAGATTATTTTTTA   | 1920 |
| Qy | 1921 | AATCAATGGGACTCTGATATAAAGGAAGAATAAGTCACTGTAAAACAGAACTTTTAAATG   | 1980 |
|    |      |  |      |
| Db | 1921 | AATCAATGGGACTCTGATATAAAGGAAGAATAAGTCACTGTAAAACAGAACTTTTAAATG   | 1980 |
| Qy | 1981 | AAGCTTAAATTACTCAATTTAAATTTTAAATCCTTTAAACAACCTTTTCAATTAATAT     | 2040 |
|    |      |  |      |
| Db | 1981 | AAGCTTAAATTACTCAATTTAAATTTTAAATCCTTTAAACAACCTTTTCAATTAATAT     | 2040 |
| Qy | 2041 | TATCACACTATTATCAGATTGTAATTAGATGCAAATGAGAGAGCAGTTTAGTTGTTGCAT   | 2100 |
|    |      |  |      |
| Db | 2041 | TATCACACTATTATCAGATTGTAATTAGATGCAAATGAGAGAGCAGTTTAGTTGTTGCAT   | 2100 |
| Qy | 2101 | TTTTCGGACACTGGAAACATTTAAATGATCAGGAGGGAGTAACAGAAAGAGCAAGGCTGT   | 2160 |
|    |      |  |      |
| Db | 2101 | TTTTCGGACACTGGAAACATTTAAATGATCAGGAGGGAGTAACAGAAAGAGCAAGGCTGT   | 2160 |
| Qy | 2161 | TTTTGAAAATCATTACACTTTCCTAGTAGAAGCCCAAACCTCAGCATTCTGCAATATGTAAC | 2220 |
|    |      |  |      |
| Db | 2161 | TTTTGAAAATCATTACACTTTCCTAGTAGAAGCCCAAACCTCAGCATTCTGCAATATGTAAC | 2220 |
| Qy | 2221 | CAACATGTCACAAACAAGCAGCATGTAACAGACTGGCACATGTGCCAGCTGAATTTAAAA   | 2280 |
|    |      |  |      |
| Db | 2221 | CAACATGTCACAAACAAGCAGCATGTAACAGACTGGCACATGTGCCAGCTGAATTTAAAA   | 2280 |
| Qy | 2281 | TATAATACTTTTAAAAAGAAAATTATTACATCCTTTACATTAGTTAAGATCAAACCTCA    | 2340 |
|    |      |  |      |
| Db | 2281 | TATAATACTTTTAAAAAGAAAATTATTACATCCTTTACATTAGTTAAGATCAAACCTCA    | 2340 |
| Qy | 2341 | CAAAGAGAAATAGAATGTTTGAAAGGCTATCCCAAAGACTTTTTTGAATCTGTCATTCA    | 2400 |
|    |      |  |      |
| Db | 2341 | CAAAGAGAAATAGAATGTTTGAAAGGCTATCCCAAAGACTTTTTTGAATCTGTCATTCA    | 2400 |
| Qy | 2401 | CATACCCTGTGAAGACAATACTATCTACAATTTTTTCAGGATTATTAAATCTTCTTTTT    | 2460 |
|    |      |  |      |
| Db | 2401 | CATACCCTGTGAAGACAATACTATCTACAATTTTTTCAGGATTATTAAATCTTCTTTTT    | 2460 |
| Qy | 2461 | TCATATCGTAGCTTAAACTCTGTTTGGTTTTGTCATCTGTAAATACTTACCTACATACA    | 2520 |
|    |      |  |      |
| Db | 2461 | TCATATCGTAGCTTAAACTCTGTTTGGTTTTGTCATCTGTAAATACTTACCTACATACA    | 2520 |
| Qy | 2521 | CTGCATGTAGATGATTAAATGAGGGCAGGCCCTGTGCTCATAGCTTTACGATGGAGAGAT   | 2580 |
|    |      |  |      |
| Db | 2521 | CTGCATGTAGATGATTAAATGAGGGCAGGCCCTGTGCTCATAGCTTTACGATGGAGAGAT   | 2580 |

Qy 2581 GCCAGTGACCTCATAATAAAGACTGTGAACTGCCTGGTGCAGTGTCCACATGACAAAGGG 2640  
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 Db 2581 GCCAGTGACCTCATAATAAAGACTGTGAACTGCCTGGTGCAGTGTCCACATGACAAAGGG 2640

Qy 2641 GCAGGTAGCACCTCTCTCACCCATGCTGTGGTTAAAATGGTTTCTAGCATATGTATAAT 2700  
 |||  
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 |||  
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 Db 3001 GGGTTGGAGGAAACCCATGGGGACAGATTCCCATTCTTAGCCTAACGTTTCGTCAATTGCCT 3060

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 |||  
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Qy 3241 TTGTTTTCTGTCAATATTGAATGTGATGGTACAGTAAACCAAACCAACAATGTGGCCA 3300  
 |||  
 Db 3241 TTGTTTTCTGTCAATATTGAATGTGATGGTACAGTAAACCAAACCAACAATGTGGCCA 3300

Qy 3301 GAAAGAAAGAGCAATAATAATTAATTCACACACCATATGGATTCTATTTATAAATCACCC 3360  
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 |||  
 Db 3361 ACAAACTTGTTCTTTAATTTTCATCCCAATCACTTTTTTCAGAGGCCTGTTATCATAGAAGT 3420

Qy 3421 CATTTTAGACTCTCAATTTTAAATTAATTTTGAATCACTAATATTTTCACAGTTTATTAA 3480

|    |      |  |  |      |
|----|------|--|--|------|
| Db | 3421 |  | CATTTTAGACTCTCAATTTTAAATTAATTTTGAATCACTAATATTTTCACAGTTTATTAA   | 3480 |
| Qy | 3481 |  | TATATTTAATTTCTATTTAAATTTTAGATTATTTTATTACCATGTACTGAATTTTACA     | 3540 |
| Db | 3481 |  | TATATTTAATTTCTATTTAAATTTTAGATTATTTTATTACCATGTACTGAATTTTACA     | 3540 |
| Qy | 3541 |  | TCCTGATACCCCTTTCCTTCTCCATGTCAGTATCATGTTCTCTAATTATCTTGCCAAATTT  | 3600 |
| Db | 3541 |  | TCCTGATACCCCTTTCCTTCTCCATGTCAGTATCATGTTCTCTAATTATCTTGCCAAATTT  | 3600 |
| Qy | 3601 |  | TGAAACTACACACAAAAAGCATACTTGCATTATTTATAATAAAATTGCATTCAGTGGCTT   | 3660 |
| Db | 3601 |  | TGAAACTACACACAAAAAGCATACTTGCATTATTTATAATAAAATTGCATTCAGTGGCTT   | 3660 |
| Qy | 3661 |  | TTTAAAAAAATGTTTGATTCAAACCTTTAACATACTGATAAGTAAGAAACAATTATAAT    | 3720 |
| Db | 3661 |  | TTTAAAAAAATGTTTGATTCAAACCTTTAACATACTGATAAGTAAGAAACAATTATAAT    | 3720 |
| Qy | 3721 |  | TTCTTTACATACTCAAACCAAGATAGAAAAAGGTGCTATCGTTCAACTCAAACATGT      | 3780 |
| Db | 3721 |  | TTCTTTACATACTCAAACCAAGATAGAAAAAGGTGCTATCGTTCAACTCAAACATGT      | 3780 |
| Qy | 3781 |  | TTCCTAGTATTAAGGACTTTAATATAGCAACAGACAAAATTATTGTTAACATGGATGTTA   | 3840 |
| Db | 3781 |  | TTCCTAGTATTAAGGACTTTAATATAGCAACAGACAAAATTATTGTTAACATGGATGTTA   | 3840 |
| Qy | 3841 |  | CAGCTCAAAGATTTATAAAAGATTTTAACCTATTTTCTCCCTTATTATCCACTGCTAAT    | 3900 |
| Db | 3841 |  | CAGCTCAAAGATTTATAAAAGATTTTAACCTATTTTCTCCCTTATTATCCACTGCTAAT    | 3900 |
| Qy | 3901 |  | GTGGATGTATGTTCAAACACCTTTTAGTATTGATAGCTTACATATGGCCAAAGGAATACA   | 3960 |
| Db | 3901 |  | GTGGATGTATGTTCAAACACCTTTTAGTATTGATAGCTTACATATGGCCAAAGGAATACA   | 3960 |
| Qy | 3961 |  | GTTTATAGCAAACATGGGTATGCTGTAGCTAACTTTATAAAAGTGTAATATAACAATGT    | 4020 |
| Db | 3961 |  | GTTTATAGCAAACATGGGTATGCTGTAGCTAACTTTATAAAAGTGTAATATAACAATGT    | 4020 |
| Qy | 4021 |  | AAAAAATTATATATCTGGGAGGATTTTTTGGTTGCCTAAAGTGGCTATAGTTACTGATTT   | 4080 |
| Db | 4021 |  | AAAAAATTATATATCTGGGAGGATTTTTTGGTTGCCTAAAGTGGCTATAGTTACTGATTT   | 4080 |
| Qy | 4081 |  | TTTATTATGTAAGCAAAACCAATAAAAAATTTAAGTTTTTTTAAACAACTACCTTATTTTTC | 4140 |
| Db | 4081 |  | TTTATTATGTAAGCAAAACCAATAAAAAATTTAAGTTTTTTTAAACAACTACCTTATTTTTC | 4140 |
| Qy | 4141 |  | ACTGTACAGACACTAATTCATTAAATACTAATTGATTGTTTAAAAGAAATATAAATGTGA   | 4200 |
| Db | 4141 |  | ACTGTACAGACACTAATTCATTAAATACTAATTGATTGTTTAAAAGAAATATAAATGTGA   | 4200 |
| Qy | 4201 |  | CAAGTGGACATTATTTATGTTAAATATACAATTATCAAGCAAGTATGAAGTTATTCAATT   | 4260 |
| Db | 4201 |  | CAAGTGGACATTATTTATGTTAAATATACAATTATCAAGCAAGTATGAAGTTATTCAATT   | 4260 |
| Qy | 4261 |  | AAAATGCCACATTTCTGGTCTCTGGG                                     | 4286 |
|    |      |  |  |      |

Db 4261 AAAATGCCACATTTCTGGTCTCTGGG 4286

RESULT 6

S57283

LOCUS S57283 4286 bp mRNA linear PRI 18-MAR-2002

DEFINITION Homo sapiens endothelin ET-B receptor mRNA, complete cds.

ACCESSION S57283

VERSION S57283.1 GI:298321

KEYWORDS .

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 4286)

AUTHORS Arai,H., Nakao,K., Hosoda,K., Ogawa,Y., Nakagawa,O., Komatsu,Y. and  
Imura,H.

TITLE Molecular cloning of human endothelin receptors and their  
expression in vascular endothelial cells and smooth muscle cells

JOURNAL Jpn. Circ. J. 56 Suppl 5, 1303-1307 (1992)

MEDLINE 93180293

PUBMED 1291713

REMARK GenBank staff at the National Library of Medicine created this  
entry [NCBI gibbsq 128424] from the original journal article.  
This sequence comes from Fig. 5.

FEATURES

Location/Qualifiers

source

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CDS

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ORIGIN

Query Match 99.6%; Score 4284.4; DB 9; Length 4286;  
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Matches 4285; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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|||||  
Db 1 GAGACATTCCGGTGGGGGACTCTGGCCAGCCCAGCAACGTGGATCCTGAGAGCACTCCC 60  
Qy 61 AGGTAGGCATTTGCCCCGGTGGGACGCCTTGCCAGAGCAGTGTGTGGCAGGCCCCCGTGG 120  
|||||



|    |     |   |     |
|----|-----|---|-----|
| Db | 61  | AGGTAGGCATTTGCCCCGGTGGGACGCCTTGCCAGAGCAGTGTGTGGCAGGCCCCCCGTGG | 120 |
| Qy | 121 | AGGATCAACACAGTGGCTGAACACTGGGAAGGAACTGGTACTTGGAGTCTGGACATCTGA  | 180 |
|    |     |   |     |
| Db | 121 | AGGATCAACACAGTGGCTGAACACTGGGAAGGAACTGGTACTTGGAGTCTGGACATCTGA  | 180 |
| Qy | 181 | AACTTGGCTCTGAAACTGCGGAGCGGCCACCGGACGCCTTCTGGAGCAGGTAGCAGCATG  | 240 |
|    |     |   |     |
| Db | 181 | AACTTGGCTCTGAAACTGCGCAGCGGCCACCGGACGCCTTCTGGAGCAGGTAGCAGCATG  | 240 |
| Qy | 241 | CAGCCGCCTCCAAGTCTGTGCGGACGCGCCCTGGTTGCGCTGGTTCTTGCCTGCGGCCTG  | 300 |
|    |     |   |     |
| Db | 241 | CAGCCGCCTCCAAGTCTGTGCGGACGCGCCCTGGTTGCGCTGGTTCTTGCCTGCGGCCTG  | 300 |
| Qy | 301 | TCGCGGATCTGGGGAGAGGAGAGAGGCTTCCCGCCTGACAGGGCCACTCCGCTTTTGCAA  | 360 |
|    |     |   |     |
| Db | 301 | TCGCGGATCTGGGGAGAGGAGAGAGGCTTCCCGCCTGACAGGGCCACTCCGCTTTTGCAA  | 360 |
| Qy | 361 | ACCGCAGAGATAATGACGCCACCCACTAAGACCTTATGGCCCAAGGGTTCCAACGCCAGT  | 420 |
|    |     |   |     |
| Db | 361 | ACCGCAGAGATAATGACGCCACCCACTAAGACCTTATGGCCCAAGGGTTCCAACGCCAGT  | 420 |
| Qy | 421 | CTGGCGCGGTTCGTTGGCACCTGCGGAGGTGCCTAAAGGAGACAGGACGGCAGGATCTCCG | 480 |
|    |     |   |     |
| Db | 421 | CTGGCGCGGTTCGTTGGCACCTGCGGAGGTGCCTAAAGGAGACAGGACGGCAGGATCTCCG | 480 |
| Qy | 481 | CCACGCACCATCTCCCCCTCCCCCGTGCCAAGGACCCATCGAGATCAAGGAGACTTTCAA  | 540 |
|    |     |   |     |
| Db | 481 | CCACGCACCATCTCCCCCTCCCCCGTGCCAAGGACCCATCGAGATCAAGGAGACTTTCAA  | 540 |
| Qy | 541 | TACATCAACACGGTTGTGTCCTGCCTTGTGTTTCGTGCTGGGGATCATCGGGAACCTCACA | 600 |
|    |     |   |     |
| Db | 541 | TACATCAACACGGTTGTGTCCTGCCTTGTGTTTCGTGCTGGGGATCATCGGGAACCTCACA | 600 |
| Qy | 601 | CTTCTGAGAATTATCTACAAGAACAAGTGCATGCGAAACGGTCCCAATATCTTGATCGCC  | 660 |
|    |     |   |     |
| Db | 601 | CTTCTGAGAATTATCTACAAGAACAAGTGCATGCGAAACGGTCCCAATATCTTGATCGCC  | 660 |
| Qy | 661 | AGCTTGGCTCTGGGAGACCTGCTGCACATCGTCATTGACATCCCTATCAATGTCTACAAG  | 720 |
|    |     |   |     |
| Db | 661 | AGCTTGGCTCTGGGAGACCTGCTGCACATCGTCATTGACATCCCTATCAATGTCTACAAG  | 720 |
| Qy | 721 | CTGCTGGCAGAGGACTGGCCATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTCATACAG  | 780 |
|    |     |   |     |
| Db | 721 | CTGCTGGCAGAGGACTGGCCATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTCATACAG  | 780 |
| Qy | 781 | AAAGCCTCCGTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATATCGA  | 840 |
|    |     |   |     |
| Db | 781 | AAAGCCTCCGTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATATCGA  | 840 |
| Qy | 841 | GCTGTTGCTTCTTGGAGTAGAATTAAAGGAATTGGGGTTCCAAAATGGACAGCAGTAGAA  | 900 |
|    |     |   |     |
| Db | 841 | GCTGTTGCTTCTTGGAGTAGAATTAAAGGAATTGGGGTTCCAAAATGGACAGCAGTAGAA  | 900 |
| Qy | 901 | ATTGTTTTGATTTGGGTGGTCTCTGTGGTTCTGGCTGTCCCTGAAGCCATAGGTTTTGAT  | 960 |
|    |     |   |     |
| Db | 901 | ATTGTTTTGATTTGGGTGGTCTCTGTGGTTCTGGCTGTCCCTGAAGCCATAGGTTTTGAT  | 960 |

|    |      |   |      |
|----|------|---|------|
| Qy | 961  | ATAATTACGATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTTCAG  | 1020 |
|    |      |   |      |
| Db | 961  | ATAATTACGATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTTCAG  | 1020 |
| Qy | 1021 | AAGACAGCTTTCATGCAGTTTTACAAGACAGCAAAAGATTGGTGGCTGTTCAAGTTTCTAT | 1080 |
|    |      |   |      |
| Db | 1021 | AAGACAGCTTTCATGCAGTTTTACAAGACAGCAAAAGATTGGTGGCTGTTCAAGTTTCTAT | 1080 |
| Qy | 1081 | TTCTGCTTGCCATTGGCCATCACTGCATTTTTTTATACACTAATGACCTGTGAAATGTTG  | 1140 |
|    |      |   |      |
| Db | 1081 | TTCTGCTTGCCATTGGCCATCACTGCATTTTTTTATACACTAATGACCTGTGAAATGTTG  | 1140 |
| Qy | 1141 | AGAAAGAAAAGTGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAAGTG  | 1200 |
|    |      |   |      |
| Db | 1141 | AGAAAGAAAAGTGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAAGTG  | 1200 |
| Qy | 1201 | GCCAAAACCGTCTTTTGCCTGGTCCTTGTCTTTGCCCTCTGCTGGCTTCCCCTTCACCTC  | 1260 |
|    |      |   |      |
| Db | 1201 | GCCAAAACCGTCTTTTGCCTGGTCCTTGTCTTTGCCCTCTGCTGGCTTCCCCTTCACCTC  | 1260 |
| Qy | 1261 | AGCAGGATTCTGAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGAACCTTTTG | 1320 |
|    |      |   |      |
| Db | 1261 | AGCAGGATTCTGAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGAACCTTTTG | 1320 |
| Qy | 1321 | AGCTTTCTGTTGGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCCTGCATT  | 1380 |
|    |      |   |      |
| Db | 1321 | AGCTTTCTGTTGGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCCTGCATT  | 1380 |
| Qy | 1381 | AACCCAATTGCTCTGTATTTGGTGAGCAAAAGATTCAAAAAGTCTTTAAGTCATGCTTA   | 1440 |
|    |      |   |      |
| Db | 1381 | AACCCAATTGCTCTGTATTTGGTGAGCAAAAGATTCAAAAAGTCTTTAAGTCATGCTTA   | 1440 |
| Qy | 1441 | TGCTGCTGGTGCCAGTCATTTGAAGAAAAACAGTCCTTGGAGGAAAAGCAGTCGTGCTTA  | 1500 |
|    |      |   |      |
| Db | 1441 | TGCTGCTGGTGCCAGTCATTTGAAGAAAAACAGTCCTTGGAGGAAAAGCAGTCGTGCTTA  | 1500 |
| Qy | 1501 | AAGTTCAAAGCTAATGATCACGGATATGACAACCTCCGTTCCAGTAATAAATACAGCTCA  | 1560 |
|    |      |   |      |
| Db | 1501 | AAGTTCAAAGCTAATGATCACGGATATGACAACCTCCGTTCCAGTAATAAATACAGCTCA  | 1560 |
| Qy | 1561 | TCTTGAAAGAAGAACTATTCACTGTATTTTCAATTTCTTTATATTGGACCGAAGTCATTAA | 1620 |
|    |      |   |      |
| Db | 1561 | TCTTGAAAGAAGAACTATTCACTGTATTTTCAATTTCTTTATATTGGACCGAAGTCATTAA | 1620 |
| Qy | 1621 | AACAAAATGAAACATTTGCCAAAACAAAACAAAAAATATGTATTTGCACAGCACACTAT   | 1680 |
|    |      |   |      |
| Db | 1621 | AACAAAATGAAACATTTGCCAAAACAAAACAAAAAATATGTATTTGCACAGCACACTAT   | 1680 |
| Qy | 1681 | TAAAATATTAAGTGTAATTATTTTAACACTCACAGCTACATATGACATTTTATGAGCTGT  | 1740 |
|    |      |   |      |
| Db | 1681 | TAAAATATTAAGTGTAATTATTTTAACACTCACAGCTACATATGACATTTTATGAGCTGT  | 1740 |
| Qy | 1741 | TTACGGCATGGAAAGAAAATCAGTGGGAATTAAGAAAGCCTCGTCGTGAAAGCACTTAAT  | 1800 |
|    |      |   |      |
| Db | 1741 | TTACGGCATGGAAAGAAAATCAGTGGGAATTAAGAAAGCCTCGTCGTGAAAGCACTTAAT  | 1800 |

|    |      |   |      |
|----|------|---|------|
| Qy | 1801 | TTTTTACAGTTAGCACTTCAACATAGCTCTTAACAACCTCCAGGATATTCACACAACACT  | 1860 |
|    |      |   |      |
| Db | 1801 | TTTTTACAGTTAGCACTTCAACATAGCTCTTAACAACCTCCAGGATATTCACACAACACT  | 1860 |
| Qy | 1861 | TAGGCTTAAAAATGAGCTCACTCAGAATTTCTATTCTTTCTAAAAAGAGATTTATTTT    | 1920 |
|    |      |   |      |
| Db | 1861 | TAGGCTTAAAAATGAGCTCACTCAGAATTTCTATTCTTTCTAAAAAGAGATTTATTTT    | 1920 |
| Qy | 1921 | AATCAATGGGACTCTGATATAAAGGAAGAATAAGTCACTGTAAACAGAACTTTTAAATG   | 1980 |
|    |      |   |      |
| Db | 1921 | AATCAATGGGACTCTGATATAAAGGAAGAATAAGTCACTGTAAACAGAACTTTTAAATG   | 1980 |
| Qy | 1981 | AAGCTTAAATTACTCAATTTAAAATTTTAAAATCCTTTAAAACAACCTTTTCAATTAATAT | 2040 |
|    |      |   |      |
| Db | 1981 | AAGCTTAAATTACTCAATTTAAAATTTTAAAATCCTTTAAAACAACCTTTTCAATTAATAT | 2040 |
| Qy | 2041 | TATCACACTATTATCAGATTGTAATTAGATGCAATGAGAGAGCAGTTTAGTTGTTGCAT   | 2100 |
|    |      |   |      |
| Db | 2041 | TATCACACTATTATCAGATTGTAATTAGATGCAATGAGAGAGCAGTTTAGTTGTTGCAT   | 2100 |
| Qy | 2101 | TTTTCGGACACTGGAAACATTTAAATGATCAGGAGGGAGTAACAGAAAGAGCAAGGCTGT  | 2160 |
|    |      |   |      |
| Db | 2101 | TTTTCGGACACTGGAAACATTTAAATGATCAGGAGGGAGTAACAGAAAGAGCAAGGCTGT  | 2160 |
| Qy | 2161 | TTTTGAAAATCATTACACTTTTCACTAGAAGCCCAAACCTCAGCATTCTGCAATATGTAAC | 2220 |
|    |      |   |      |
| Db | 2161 | TTTTGAAAATCATTACACTTTTCACTAGAAGCCCAAACCTCAGCATTCTGCAATATGTAAC | 2220 |
| Qy | 2221 | CAACATGTCACAAACAAGCAGCATGTAACAGACTGGCACATGTGCCAGCTGAATTTAAAA  | 2280 |
|    |      |   |      |
| Db | 2221 | CAACATGTCACAAACAAGCAGCATGTAACAGACTGGCACATGTGCCAGCTGAATTTAAAA  | 2280 |
| Qy | 2281 | TATAATACTTTTAAAAAGAAAATTATTACATCCTTTACATTAGTTAAGATCAAACCTCA   | 2340 |
|    |      |   |      |
| Db | 2281 | TATAATACTTTTAAAAAGAAAATTATTACATCCTTTACATTAGTTAAGATCAAACCTCA   | 2340 |
| Qy | 2341 | CAAAGAGAAATAGAATGTTTGAAAGGCTATCCCAAAGACTTTTTTGAATCTGTCATTCA   | 2400 |
|    |      |   |      |
| Db | 2341 | CAAAGAGAAATAGAATGTTTGAAAGGCTATCCCAAAGACTTTTTTGAATCTGTCATTCA   | 2400 |
| Qy | 2401 | CATACCCTGTGAAGACAATACTATCTACAATTTTTTCAGGATTATTTAAATCTTCTTTT   | 2460 |
|    |      |   |      |
| Db | 2401 | CATACCCTGTGAAGACAATACTATCTACAATTTTTTCAGGATTATTTAAATCTTCTTTT   | 2460 |
| Qy | 2461 | TCACTATCGTAGCTTAACTCTGTTTGGTTTTGTCATCTGTAAATACTTACCTACATACA   | 2520 |
|    |      |   |      |
| Db | 2461 | TCACTATCGTAGCTTAACTCTGTTTGGTTTTGTCATCTGTAAATACTTACCTACATACA   | 2520 |
| Qy | 2521 | CTGCATGTAGATGATTAAATGAGGGCAGGCCCTGTGCTCATAGCTTTACGATGGAGAGAT  | 2580 |
|    |      |   |      |
| Db | 2521 | CTGCATGTAGATGATTAAATGAGGGCAGGCCCTGTGCTCATAGCTTTACGATGGAGAGAT  | 2580 |
| Qy | 2581 | GCCAGTGACCTCATAATAAAGACTGTGAACTGCCTGGTGCAGTGTCCACATGACAAAGGG  | 2640 |
|    |      |   |      |
| Db | 2581 | GCCAGTGACCTCATAATAAAGACTGTGAACTGCCTGGTGCAGTGTCCACATGACAAAGGG  | 2640 |
| Qy | 2641 | GCAGGTAGCACCCCTCTCTACCCATGCTGTGGTTAAAATGGTTTCTAGCATATGTATAAT  | 2700 |

|    |      |  |  |      |
|----|------|--|--|------|
| Db | 2641 |  | GCAGGTAGCACCTCTCTACCCATGCTGTGGTTAAAATGGTTTCTAGCATATGTATAAT     | 2700 |
| Qy | 2701 |  | GCTATAGTTAAAATACTATTTTTCAAATCATACAGATTAGTACATTTAACAGCTACCTG    | 2760 |
| Db | 2701 |  | GCTATAGTTAAAATACTATTTTTCAAATCATACAGATTAGTACATTTAACAGCTACCTG    | 2760 |
| Qy | 2761 |  | TAAAGCTTATTACTAATTTTTGTATTATTTTTGTAAATAGCCAATAGAAAAGTTTGCTTG   | 2820 |
| Db | 2761 |  | TAAAGCTTATTACTAATTTTTGTATTATTTTTGTAAATAGCCAATAGAAAAGTTTGCTTG   | 2820 |
| Qy | 2821 |  | ACATGGTGCTTTTCTTTCATCTAGAGGCAAACTGCTTTTGAGACCGTAAGAACCTCTT     | 2880 |
| Db | 2821 |  | ACATGGTGCTTTTCTTTCATCTAGAGGCAAACTGCTTTTGAGACCGTAAGAACCTCTT     | 2880 |
| Qy | 2881 |  | AGCTTTGTGCGTTCCTGCCTAATTTTTATATCTTCTAAGCAAAGTGCCTTAGGATAGCTT   | 2940 |
| Db | 2881 |  | AGCTTTGTGCGTTCCTGCCTAATTTTTATATCTTCTAAGCAAAGTGCCTTAGGATAGCTT   | 2940 |
| Qy | 2941 |  | GGGATGAGATGTGTGTGAAAGTATGTACAAGAGAAAACGGAAGAGAGAGGAAATGAGGTG   | 3000 |
| Db | 2941 |  | GGGATGAGATGTGTGTGAAAGTATGTACAAGAGAAAACGGAAGAGAGAGGAAATGAGGTG   | 3000 |
| Qy | 3001 |  | GGGTTGGAGGAAACCCATGGGGACAGATTCCCATTCTTAGCCTAACGTTTCGTCATTGCCT  | 3060 |
| Db | 3001 |  | GGGTTGGAGGAAACCCATGGGGACAGATTCCCATTCTTAGCCTAACGTTTCGTCATTGCCT  | 3060 |
| Qy | 3061 |  | CGTCACATCAATGCAAAAGGTCCTGATTTTGTTCAGCAAAACACAGTGCAATGTTCTCA    | 3120 |
| Db | 3061 |  | CGTCACATCAATGCAAAAGGTCCTGATTTTGTTCAGCAAAACACAGTGCAATGTTCTCA    | 3120 |
| Qy | 3121 |  | GAGTGACTTTCGAAATAAATTGGGCCCAAGAGCTTTAACTCGGTCTTAAAATATGCCCAA   | 3180 |
| Db | 3121 |  | GAGTGACTTTCGAAATAAATTGGGCCCAAGAGCTTTAACTCGGTCTTAAAATATGCCCAA   | 3180 |
| Qy | 3181 |  | ATTTTTACTTTGTTTTCTTTTAATAGGCTGGGCCACATGTTGGAAATAAGCTAGTAATG    | 3240 |
| Db | 3181 |  | ATTTTTACTTTGTTTTCTTTTAATAGGCTGGGCCACATGTTGGAAATAAGCTAGTAATG    | 3240 |
| Qy | 3241 |  | TTGTTTTCTGTCAATATTGAATGTGATGGTACAGTAAACCAAAACCCAACAATGTGGCCA   | 3300 |
| Db | 3241 |  | TTGTTTTCTGTCAATATTGAATGTGATGGTACAGTAAACCAAAACCCAACAATGTGGCCA   | 3300 |
| Qy | 3301 |  | GAAAGAAAGAGCAATAATAATTAATTCACACACCATATGGATTCTATTTATAAATCACCC   | 3360 |
| Db | 3301 |  | GAAAGAAAGAGCAATAATAATTAATTCACACACCATATGGATTCTATTTATAAATCACCC   | 3360 |
| Qy | 3361 |  | ACAAACTTGTTCTTTAATTTTCATCCCAATCACTTTTTTCAGAGGCCTGTTATCATAGAAGT | 3420 |
| Db | 3361 |  | ACAAACTTGTTCTTTAATTTTCATCCCAATCACTTTTTTCAGAGGCCTGTTATCATAGAAGT | 3420 |
| Qy | 3421 |  | CATTTTAGACTCTCAATTTTAAATTAATTTGAATCACTAATATTTTCACAGTTTATTAA    | 3480 |
| Db | 3421 |  | CATTTTAGACTCTCAATTTTAAATTAATTTGAATCACTAATATTTTCACAGTTTATTAA    | 3480 |
| Qy | 3481 |  | TATATTTAATTTCTATTTAAATTTTAGATTATTTTATTACCATGTACTGAATTTTACA     | 3540 |
|    |      |  |  |      |

Db 3481 TATATTTAATTTCTATTTAAATTTTAGATTATTTTTATTACCATGTACTGAATTTTTTACA 3540

Qy 3541 TCCTGATACCCTTTTCCTTCTCCATGTCAGTATCATGTTCTCTAATTATCTTGCCAAATTT 3600  
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Db 3541 TCCTGATACCCTTTTCCTTCTCCATGTCAGTATCATGTTCTCTAATTATCTTGCCAAATTT 3600

Qy 3601 TGAAACTACACACAAAAAGCATACTTGCATTATTTATAATAAAATTGCATTTCAGTGGCTT 3660  
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Db 3601 TGAAACTACACACAAAAAGCATACTTGCATTATTTATAATAAAATTGCATTTCAGTGGCTT 3660

Qy 3661 TTTAAAAAAATGTTTGATTCAAAACTTTAACATACTGATAAGTAAGAAACAATTATAAT 3720  
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Db 3661 TTTAAAAAAATGTTTGATTCAAAACTTTAACATACTGATAAGTAAGAAACAATTATAAT 3720

Qy 3721 TTCTTTACATACTCAAACCAAGATAGAAAAAGGTGCTATCGTTCAACTTCAAACATGT 3780  
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Db 3721 TTCTTTACATACTCAAACCAAGATAGAAAAAGGTGCTATCGTTCAACTTCAAACATGT 3780

Qy 3781 TTCCTAGTATTAAGGACTTTAATATAGCAACAGACAAAATTATTGTTAACATGGATGTTA 3840  
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Db 3781 TTCCTAGTATTAAGGACTTTAATATAGCAACAGACAAAATTATTGTTAACATGGATGTTA 3840

Qy 3841 CAGCTCAAAGATTTATAAAAGATTTTAACCTATTTTCTCCCTTATTATCCACTGCTAAT 3900  
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Db 3841 CAGCTCAAAGATTTATAAAAGATTTTAACCTATTTTCTCCCTTATTATCCACTGCTAAT 3900

Qy 3901 GTGGATGTATGTTCAAACACCTTTTAGTATTGATAGCTTACATATGGCCAAAGGAATACA 3960  
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Db 3901 GTGGATGTATGTTCAAACACCTTTTAGTATTGATAGCTTACATATGGCCAAAGGAATACA 3960

Qy 3961 GTTTATAGCAAACATGGGTATGCTGTAGCTAACTTTATAAAAGTGTAATATAACAATGT 4020  
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Db 3961 GTTTATAGCAAACATGGGTATGCTGTAGCTAACTTTATAAAAGTGTAATATAACAATGT 4020

Qy 4021 AAAAAATTATATATCTGGGAGGATTTTTTGGTTGCCTAAAGTGGCTATAGTTACTGATTT 4080  
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Db 4021 AAAAAATTATATATCTGGGAGGATTTTTTGGTTGCCTAAAGTGGCTATAGTTACTGATTT 4080

Qy 4081 TTTATTATGTAAGCAAACCAATAAAAATTTAAGTTTTTTTAACTACCTTATTTTTTC 4140  
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Qy 4141 ACTGTACAGACACTAATTCATTAAATACTAATTGATTGTTTAAAGAAATATAAATGTGA 4200  
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Db 4141 ACTGTACAGACACTAATTCATTAAATACTAATTGATTGTTTAAAGAAATATAAATGTGA 4200

Qy 4201 CAAGTGGACATTATTTATGTTAAATATACAATTATCAAGCAAGTATGAAGTTATTCAATT 4260  
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Db 4201 CAAGTGGACATTATTTATGTTAAATATACAATTATCAAGCAAGTATGAAGTTATTCAATT 4260

Qy 4261 AAAATGCCACATTTCTGGTCTCTGGG 4286  
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Db 4261 AAAATGCCACATTTCTGGTCTCTGGG 4286

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 and exon 7.  
 ACCESSION D13168  
 VERSION D13168.1 GI:285924  
 KEYWORDS .  
 SEGMENT 7 of 7  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 2972)  
 AUTHORS Arai,H., Nakao,K., Takaya,K., Hosoda,K., Ogawa,Y., Nakanishi,S. and  
 Imura,H.  
 TITLE The human endothelin-B receptor gene. Structural organization and  
 chromosomal assignment  
 JOURNAL J. Biol. Chem. 268 (5), 3463-3470 (1993)  
 MEDLINE 93155196  
 PUBMED 8429023  
 REFERENCE 2 (bases 1 to 2972)  
 AUTHORS Arai,H.  
 TITLE Direct Submission  
 JOURNAL Submitted (02-SEP-1992) Hiroshi Arai, Kyoto University School of  
 Medicine, Second Division, Department of Medicine; 54 Shogoin,  
 Kawahara-cho, Sakyo-ku, Kyoto, Kyoto 606, Japan  
 (Tel:81-75-751-3170, Fax:81-75-771-9452)  
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 D13167.1:11. .119,11. .2865)  
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 KLLAEDWPFGAEMCKLV PFIQKASVGITVLSLCALSIDRYRAVASWSRIKGIGVPKWT  
 AVEIVLIWVSVVLAVPEAIGFDIITMDYKGSYLRLCLLHPVQKTA FMQFYKTAKDWW  
 LFSFYFCLPLAITAFFYTLMTCEMLRKKSGMQIALNDHLKQRREVAKTVFCLVLVFAL  
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 exon 11. .2865  
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 /product="endothelin-B receptor"

/note="G protein-coupled receptor"  
/number=7  
/evidence=experimental

ORIGIN

Query Match 66.4%; Score 2857; DB 9; Length 2972;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2857; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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| Qy | 1430 | AGTCATGCTTATGCTGCTGGTGCCAGTCATTTGAAGAAAAACAGTCCTTGGAGGAAAAGC | 1489 |
|    |      |  |      |
| Db | 9    | AGTCATGCTTATGCTGCTGGTGCCAGTCATTTGAAGAAAAACAGTCCTTGGAGGAAAAGC | 68   |
| Qy | 1490 | AGTCGTGCTTAAAGTTCAAAGCTAATGATCACGGATATGACAACTTCCGTTCCAGTAATA | 1549 |
|    |      |  |      |
| Db | 69   | AGTCGTGCTTAAAGTTCAAAGCTAATGATCACGGATATGACAACTTCCGTTCCAGTAATA | 128  |
| Qy | 1550 | AATACAGCTCATCTTGAAAGAAGAACTATTCAGTGTATTTTCTTTATATTGGACC      | 1609 |
|    |      |  |      |
| Db | 129  | AATACAGCTCATCTTGAAAGAAGAACTATTCAGTGTATTTTCTTTATATTGGACC      | 188  |
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|    |      |  |      |
| Db | 189  | GAAGTCATTAAAAACAAATGAAACATTTGCCAAAACAAAACAAAAAACTATGTATTTGCA | 248  |
| Qy | 1670 | CAGCACACTATTAAATATTAAGTGTAAATATTTTAACTCACAGCTACATATGACATT    | 1729 |
|    |      |  |      |
| Db | 249  | CAGCACACTATTAAATATTAAGTGTAAATATTTTAACTCACAGCTACATATGACATT    | 308  |
| Qy | 1730 | TTATGAGCTGTTTACGGCATGGAAAGAAAATCAGTGGGAATTAAGAAAGCCTCGTCGTGA | 1789 |
|    |      |  |      |
| Db | 309  | TTATGAGCTGTTTACGGCATGGAAAGAAAATCAGTGGGAATTAAGAAAGCCTCGTCGTGA | 368  |
| Qy | 1790 | AAGCACTTAATTTTTTACAGTTAGCACTTCAACATAGCTCTTAACAACCTCCAGGATATT | 1849 |
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| Db | 369  | AAGCACTTAATTTTTTACAGTTAGCACTTCAACATAGCTCTTAACAACCTCCAGGATATT | 428  |
| Qy | 1850 | CACACAACACTTAGGCTTAAAAATGAGCTCACTCAGAATTTCTATTCTTTCTAAAAAGAG | 1909 |
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| Db | 429  | CACACAACACTTAGGCTTAAAAATGAGCTCACTCAGAATTTCTATTCTTTCTAAAAAGAG | 488  |
| Qy | 1910 | ATTTATTTTTTAAATCAATGGGACTCTGATATAAAGGAAGAATAAGTCACTGTAAACAGA | 1969 |
|    |      |  |      |
| Db | 489  | ATTTATTTTTTAAATCAATGGGACTCTGATATAAAGGAAGAATAAGTCACTGTAAACAGA | 548  |
| Qy | 1970 | ACTTTTAAATGAAGCTTAAATTACTCAATTTAAATTTTAAATCCTTTAAACAACCTTT   | 2029 |
|    |      |  |      |
| Db | 549  | ACTTTTAAATGAAGCTTAAATTACTCAATTTAAATTTTAAATCCTTTAAACAACCTTT   | 608  |
| Qy | 2030 | TCAATTAATATTATCACACTATTATCAGATTGTAATTAGATGCAATGAGAGAGCAGTTT  | 2089 |
|    |      |  |      |
| Db | 609  | TCAATTAATATTATCACACTATTATCAGATTGTAATTAGATGCAATGAGAGAGCAGTTT  | 668  |
| Qy | 2090 | AGTTGTTGCATTTTTCGGACACTGGAAACATTTAAATGATCAGGAGGGAGTAACAGAAAG | 2149 |
|    |      |  |      |
| Db | 669  | AGTTGTTGCATTTTTCGGACACTGGAAACATTTAAATGATCAGGAGGGAGTAACAGAAAG | 728  |

Qy 2150 AGCAAGGCTGTTTTTAAAATCATTACACTTTCTACTAGAAGCCCAAACCTCAGCATTCTG 2209  
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 Db 729 AGCAAGGCTGTTTTTAAAATCATTACACTTTCTACTAGAAGCCCAAACCTCAGCATTCTG 788

Qy 2210 CAATATGTAACCAACATGTCACAAACAAGCAGCATGTAACAGACTGGCACATGTGCCAGC 2269  
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 Db 789 CAATATGTAACCAACATGTCACAAACAAGCAGCATGTAACAGACTGGCACATGTGCCAGC 848

Qy 2270 TGAATTTAAAATATAATACTTTTAAAAAGAAAATTATTACATCCTTTACATTAGTTAAG 2329  
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Qy 2330 ATCAAACCTCACAAAGAGAAATAGAATGTTTGAAAGGCTATCCCAAAGACTTTTTTGAA 2389  
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Qy 2390 TCTGTCATTACATACCCTGTGAAGACAATACTATCTACAATTTTTTCAGGATTATTAAA 2449  
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 Db 969 TCTGTCATTACATACCCTGTGAAGACAATACTATCTACAATTTTTTCAGGATTATTAAA 1028

Qy 2450 ATCTTCTTTTTTCACTATCGTAGCTTAACTCTGTTTGGTTTTGTCATCTGTAAATACTT 2509  
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 Db 1029 ATCTTCTTTTTTCACTATCGTAGCTTAACTCTGTTTGGTTTTGTCATCTGTAAATACTT 1088

Qy 2510 ACCTACATACACTGCATGTAGATGATTAAATGAGGGCAGGCCCTGTGCTCATAGCTTTAC 2569  
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Qy 2570 GATGGAGAGATGCCAGTGACCTCATAATAAAGACTGTGAAGTGCCTGGTGCAGTGTCCAC 2629  
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Qy 2690 ATATGTATAATGCTATAGTTAAATACTATTTTTCAAATCATACAGATTAGTACATTTA 2749  
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Qy 2810 AAGTTTGCTTGACATGGTGCTTTTCTTTCATCTAGAGGCAAACTGCTTTTTGAGACCGT 2869  
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 Db 1389 AAGTTTGCTTGACATGGTGCTTTTCTTTCATCTAGAGGCAAACTGCTTTTTGAGACCGT 1448

Qy 2870 AAGAACCTCTTAGCTTTGTGCGTTCCTGCCTAATTTTTATATCTTCTAAGCAAAGTGCCT 2929  
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 Db 1449 AAGAACCTCTTAGCTTTGTGCGTTCCTGCCTAATTTTTATATCTTCTAAGCAAAGTGCCT 1508

Qy 2930 TAGGATAGCTTGGGATGAGATGTGTGTGAAAGTATGTACAAGAGAAAACGGAAGAGAGAG 2989  
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 Db 1509 TAGGATAGCTTGGGATGAGATGTGTGTGAAAGTATGTACAAGAGAAAACGGAAGAGAGAG 1568

Qy 2990 GAAATGAGGTGGGGTTGGAGGAAACCCATGGGGACAGATTCCCATTCTTAGCCTAACGTT 3049



|    |      |  |  |      |
|----|------|--|--|------|
| Db | 1569 |  | GAAATGAGGTGGGGTTGGAGGAAACCCATGGGGACAGATTCCCATTCTTAGCCTAACGTT | 1628 |
| Qy | 3050 |  | CGTCATTGCCTCGTCACATCAATGCAAAGGTCCTGATTTTGTTCAGCAAAACACAGTG   | 3109 |
| Db | 1629 |  | CGTCATTGCCTCGTCACATCAATGCAAAGGTCCTGATTTTGTTCAGCAAAACACAGTG   | 1688 |
| Qy | 3110 |  | CAATGTTCTCAGAGTGACTTTTCAAATAAATTGGGCCCAAGAGCTTTAACTCGGTCTTAA | 3169 |
| Db | 1689 |  | CAATGTTCTCAGAGTGACTTTTCAAATAAATTGGGCCCAAGAGCTTTAACTCGGTCTTAA | 1748 |
| Qy | 3170 |  | AATATGCCCAAATTTTACTTTGTTTTCTTTTAAATAGGCTGGGCCACATGTTGGAAATA  | 3229 |
| Db | 1749 |  | AATATGCCCAAATTTTACTTTGTTTTCTTTTAAATAGGCTGGGCCACATGTTGGAAATA  | 1808 |
| Qy | 3230 |  | AGCTAGTAATGTTGTTTTCTGTCAATATTGAATGTGATGGTACAGTAAACCAAAACCCAA | 3289 |
| Db | 1809 |  | AGCTAGTAATGTTGTTTTCTGTCAATATTGAATGTGATGGTACAGTAAACCAAAACCCAA | 1868 |
| Qy | 3290 |  | CAATGTGGCCAGAAAGAAAGAGCAATAATAATTAATTCACACACCATATGGATTCTATTT | 3349 |
| Db | 1869 |  | CAATGTGGCCAGAAAGAAAGAGCAATAATAATTAATTCACACACCATATGGATTCTATTT | 1928 |
| Qy | 3350 |  | ATAAATCACCACAAACTTGTCTTTAATTTTCATCCCAATCACTTTTTTCAGAGGCCTGTT | 3409 |
| Db | 1929 |  | ATAAATCACCACAAACTTGTCTTTAATTTTCATCCCAATCACTTTTTTCAGAGGCCTGTT | 1988 |
| Qy | 3410 |  | ATCATAGAAGTCATTTTAGACTCTCAATTTTAAATTAATTTTGAATCACTAATATTTTCA | 3469 |
| Db | 1989 |  | ATCATAGAAGTCATTTTAGACTCTCAATTTTAAATTAATTTTGAATCACTAATATTTTCA | 2048 |
| Qy | 3470 |  | CAGTTTATTAATATATTTAATTTCTATTTAAATTTTAGATTATTTTTATTACCATGTACT | 3529 |
| Db | 2049 |  | CAGTTTATTAATATATTTAATTTCTATTTAAATTTTAGATTATTTTTATTACCATGTACT | 2108 |
| Qy | 3530 |  | GAATTTTACATCCTGATACCCTTTCCTTCTCCATGTCAGTATCATGTTCTCTAATTATC  | 3589 |
| Db | 2109 |  | GAATTTTACATCCTGATACCCTTTCCTTCTCCATGTCAGTATCATGTTCTCTAATTATC  | 2168 |
| Qy | 3590 |  | TTGCCAAATTTTGAACTACACACAAAAAGCATACTTGCATTATTTATAATAAAATTGCA  | 3649 |
| Db | 2169 |  | TTGCCAAATTTTGAACTACACACAAAAAGCATACTTGCATTATTTATAATAAAATTGCA  | 2228 |
| Qy | 3650 |  | TTCAGTGGCTTTTAAAAAAAATGTTTGATTCAAAACTTTAACATACTGATAAGTAAGAA  | 3709 |
| Db | 2229 |  | TTCAGTGGCTTTTAAAAAAAATGTTTGATTCAAAACTTTAACATACTGATAAGTAAGAA  | 2288 |
| Qy | 3710 |  | ACAATTATAATTTCTTTACATACTCAAACCAAGATAGAAAAAGGTGCTATCGTTCAACT  | 3769 |
| Db | 2289 |  | ACAATTATAATTTCTTTACATACTCAAACCAAGATAGAAAAAGGTGCTATCGTTCAACT  | 2348 |
| Qy | 3770 |  | TCAAAACATGTTTCTTAGTATTAAGGACTTTAATATAGCAACAGACAAAATTATTGTTAA | 3829 |
| Db | 2349 |  | TCAAAACATGTTTCTTAGTATTAAGGACTTTAATATAGCAACAGACAAAATTATTGTTAA | 2408 |
| Qy | 3830 |  | CATGGATGTTACAGCTCAAAGATTTATAAAAGATTTTAACTATTTTCTCCCTTATTAT   | 3889 |
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Db 2409 CATGGATGTTACAGCTCAAAGATTTATAAAAGATTTTAACCTATTTTCTCCCTTATTAT 2468

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Db 2529 AAAGGAATACAGTTTATAGCAAACATGGGTATGCTGTAGCTAACTTTATAAAAGTGTA 2588

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Qy 4070 GTTACTGATTTTTTATTATGTAAGCAAAACCAATAAAATTTAAGTTTTTTTAAACAACTA 4129  
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Db 2649 GTTACTGATTTTTTATTATGTAAGCAAAACCAATAAAATTTAAGTTTTTTTAAACAACTA 2708

Qy 4130 CCTTATTTTTCACTGTACAGACACTAATTCATTAAATACTAATTGATTGTTTAAAAGAAA 4189  
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Db 2709 CCTTATTTTTCACTGTACAGACACTAATTCATTAAATACTAATTGATTGTTTAAAAGAAA 2768

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Db 2769 TATAAATGTGACAAGTGGACATTATTTATGTTAAATATACAATTATCAAGCAAGTATGAA 2828

Qy 4250 GTTATTCAATTAAAATGCCACATTTCTGGTCTCTGGG 4286  
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Db 2829 GTTATTCAATTAAAATGCCACATTTCTGGTCTCTGGG 2865

# RESULT 8

AL139002/c

LOCUS AL139002 183337 bp DNA linear PRI 28-JAN-2001

DEFINITION Human DNA sequence from clone RP11-318G21 on chromosome 13q22.2-31.1, complete sequence.

ACCESSION AL139002

VERSION AL139002.18 GI:12597038

KEYWORDS HTG.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 183337)

AUTHORS Wall,M.

TITLE Direct Submission

JOURNAL Submitted (28-JAN-2001) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk

COMMENT On Jan 29, 2001 this sequence version replaced gi:12584355. During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above. This sequence has been finished according to sequence map criteria

as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annotated repeat sequence elements. Where the sequence is ambiguous, there is an annotation using the 'unsure' feature key. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at [http://www.sanger.ac.uk/Projects/C\\_elegans/wormpep](http://www.sanger.ac.uk/Projects/C_elegans/wormpep) This sequence was generated from part of bacterial clone contigs of human chromosome 13, constructed by the Sanger Centre Chromosome 13 Mapping Group. Further information can be found at <http://www.sanger.ac.uk/HGP/Chr13> RP11-318G21 is from the library RPCI-11.2 constructed by the group of Pieter de Jong. For further details see <http://www.chori.org/bacpac/home.htm> VECTOR: pBACe3.6 This sequence is the entire insert of clone RP11-318G21 The true left end of clone RP11-267I18 is at 125528 in this sequence.

| FEATURES      | Location/Qualifiers   |
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| repeat_region | 1216. .1308<br>/note="HAL1 repeat: matches 1475. .1563 of consensus"  |
| repeat_region | 1309. .1597<br>/note="AluJb repeat: matches 1. .297 of consensus"   |
| repeat_region | 1598. .2044<br>/note="HAL1 repeat: matches 1003. .1475 of consensus"  |
| repeat_region | 2148. .2276<br>/note="L2 repeat: matches 2620. .2749 of consensus"  |
| repeat_region | 2330. .2378<br>/note="L2 repeat: matches 2442. .2492 of consensus"  |
| repeat_region | 3915. .4224<br>/note="AluY repeat: matches 1. .306 of consensus"  |
| repeat_region | 4617. .4750<br>/note="67 copies 2 mer cc 61% conserved"   |
| repeat_region | 4648. .4727<br>/note="20 copies 4 mer cctt 78% conserved"   |
| repeat_region | 4729. .4784<br>/note="14 copies 4 mer tcct 78% conserved"   |
| repeat_region | 5431. .5736<br>/note="AluSx repeat: matches 1. .305 of consensus"   |
| repeat_region | 11990. .12273<br>/note="AluSx repeat: matches 9. .292 of consensus"   |
| repeat_region | 12589. .12809<br>/note="MIR repeat: matches 7. .234 of consensus"   |
| repeat_region | 13390. .13519<br>/note="L2 repeat: matches 2410. .2548 of consensus"  |
| repeat_region | 14630. .14978   |

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|---------------|---------------|--|
| repeat_region | 15092. .15580 | /note="THE1B repeat: matches 1. .360 of consensus"     |
| repeat_region | 15581. .16095 | /note="L1MB1 repeat: matches 5656. .6116 of consensus" |
| repeat_region | 16096. .16549 | /note="L1PA7 repeat: matches 5629. .6143 of consensus" |
| repeat_region | 16731. .16777 | /note="L1MB1 repeat: matches 5188. .5656 of consensus" |
| repeat_region | 16778. .17137 | /note="MIR repeat: matches 35. .78 of consensus"       |
| repeat_region | 17138. .17273 | /note="THE1C repeat: matches 1. .371 of consensus"     |
| repeat_region | 17374. .17484 | /note="MIR repeat: matches 78. .226 of consensus"      |
| repeat_region | 17485. .17777 | /note="MIR repeat: matches 26. .158 of consensus"      |
| repeat_region | 17778. .17815 | /note="AluSc repeat: matches 1. .290 of consensus"     |
| repeat_region | 18981. .19048 | /note="MIR repeat: matches 158. .191 of consensus"     |
| repeat_region | 19447. .19589 | /note="34 copies 2 mer tt 66% conserved"               |
| repeat_region | 19843. .20162 | /note="MIR repeat: matches 131. .262 of consensus"     |
| repeat_region | 20866. .21198 | /note="MER33 repeat: matches 1. .324 of consensus"     |
| repeat_region | 21742. .21878 | /note="MER44A repeat: matches 3. .333 of consensus"    |
| repeat_region | 22214. .22310 | /note="MIR repeat: matches 9. .154 of consensus"       |
| repeat_region | 22321. .22418 | /note="MIR repeat: matches 164. .260 of consensus"     |
| repeat_region | 22390. .22715 | /note="L1MB8 repeat: matches 6078. .6171 of consensus" |
| misc_feature  | 22419. .22730 | /note="Sequence from AC018674 sequenced by WUGSC."     |
| repeat_region | 22731. .23714 | /note="AluY repeat: matches 1. .311 of consensus"      |
| repeat_region | 23715. .24008 | /note="L1MB8 repeat: matches 5130. .6078 of consensus" |
| repeat_region | 24009. .24264 | /note="AluSg repeat: matches 1. .294 of consensus"     |
| repeat_region | 24265. .24569 | /note="L1MB8 repeat: matches 4884. .5130 of consensus" |
| repeat_region | 24570. .25577 | /note="AluY repeat: matches 1. .305 of consensus"      |
| repeat_region | 25582. .25635 | /note="L1MB8 repeat: matches 3786. .4884 of consensus" |
| repeat_region | 26221. .26571 | /note="27 copies 2 mer tt 70% conserved"               |
| repeat_region | 26572. .26750 | /note="MSTA repeat: matches 1. .347 of consensus"      |
| repeat_region | 26752. .27066 | /note="AluY repeat: matches 129. .307 of consensus"    |
| repeat_region | 27067. .27134 | /note="AluY repeat: matches 1. .311 of consensus"      |
| repeat_region |               | /note="MSTA repeat: matches 347. .371 of consensus"    |

|               |  |
|---------------|--|
| repeat_region | 27963. .28006<br>/note="22 copies 2 mer tt 75% conserved"                |
| repeat_region | 28916. .29282<br>/note="MER39 repeat: matches 13. .381 of consensus"     |
| repeat_region | 29282. .29517<br>/note="MER39b repeat: matches 327. .579 of consensus"   |
| repeat_region | 30210. .30526<br>/note="AluJo repeat: matches 1. .303 of consensus"      |
| repeat_region | 31423. .31572<br>/note="L1PA13 repeat: matches 6005. .6155 of consensus" |
| repeat_region | 31587. .31624<br>/note="19 copies 2 mer tt 86% conserved"                |
| repeat_region | 32103. .32181<br>/note="ORSL repeat: matches 390. .467 of consensus"     |
| repeat_region | 33878. .34312<br>/note="MER57A repeat: matches 1. .433 of consensus"     |
| repeat_region | 36673. .36768<br>/note="LTR37A repeat: matches 81. .172 of consensus"    |
| repeat_region | 36769. .37066<br>/note="AluSq repeat: matches 1. .296 of consensus"      |
| repeat_region | 37067. .37300<br>/note="LTR37A repeat: matches 172. .424 of consensus"   |
| repeat_region | 39470. .39501<br>/note="16 copies 2 mer tt 90% conserved"                |
| repeat_region | 41434. .42607<br>/note="L1M4 repeat: matches -258. .888 of consensus"    |
| repeat_region | 42744. .43220<br>/note="L1M4 repeat: matches 1085. .1580 of consensus"   |
| repeat_region | 43703. .44007<br>/note="AluJb repeat: matches 1. .305 of consensus"      |
| repeat_region | 44019. .44180<br>/note="L1MD1 repeat: matches 6044. .6211 of consensus"  |
| repeat_region | 44183. .44485<br>/note="AluJo repeat: matches 1. .300 of consensus"      |
| repeat_region | 44486. .44611<br>/note="L1MD2 repeat: matches 5949. .6066 of consensus"  |
| repeat_region | 45256. .45430<br>/note="MER5B repeat: matches 1. .178 of consensus"      |
| repeat_region | 45588. .45669<br>/note="MER5A repeat: matches 109. .188 of consensus"    |
| repeat_region | 46919. .47084<br>/note="MIR repeat: matches 94. .260 of consensus"       |
| repeat_region | 47873. .47902<br>/note="15 copies 2 mer tg 90% conserved"                |
| repeat_region | 49906. .49933<br>/note="7 copies 4 mer tgtg 96% conserved"               |
| repeat_region | 50452. .50507<br>/note="LTR37A repeat: matches 128. .184 of consensus"   |
| repeat_region | 51786. .51829<br>/note="MER74A repeat: matches 271. .309 of consensus"   |
| repeat_region | 51830. .52172<br>/note="THE1B repeat: matches 1. .364 of consensus"      |
| repeat_region | 52173. .52221<br>/note="MER74A repeat: matches 221. .271 of consensus"   |
| repeat_region | 52710. .53396<br>/note="L1MB7 repeat: matches 5451. .6171 of consensus"  |
| repeat_region | 53890. .53996  |

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repeat_region      /note="MIR repeat: matches 35. .152 of consensus"
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repeat_region      /note="19 copies 2 mer tt 84% conserved"
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                    /note="L1PA3 repeat: matches 4925. .6146 of consensus"

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Query Match          66.1%; Score 2841.8; DB 9; Length 183337;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2854; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

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Qy      1490 AGTCGTGCTTAAAGTTCAAAGCTAATGATCACGGATATGACAACTTCCGTTCCAGTAATA 1549
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Qy 2270 TGAATTTAAATATAATACTTTTAAAAAGAAAATTATTACATCCTTTACATTCAAGTTAAG 2329  
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Qy 2330 ATCAAACCTCACAAAGAGAAATAGAATGTTTGAAAGGCTATCCCAAAGACTTTTTTGAA 2389  
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Qy 2990 GAAATGAGGTGGGGTTGGAGGAAACCCATGGGGACAGATTCCCATTTCTTAGCCTAACGTT 3049  
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| Db | 70431 | CATGGATGTTACAGCTCAAAGATTTATAAAAGATTTTAACCTATTTCTCCCTTATTAT 70372    |
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| Qy | 3950  | AAAGGAATACAGTTTATAGCAAACATGGGTATGCTGTAGCTAACTTTATAAAAGTGTA 4009     |
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| Qy | 4010  | TATAACAATGTAAAAAATTATATATCTGGGAGGATTTTTTGGTTGCCTAAAGTGGCTATA 4069   |
| Db | 70251 | TATAACAATGTAAAAAATTATATATCTGGGAGGATTTTTTGGTTGCCTAAAGTGGCTATA 70192  |
| Qy | 4070  | GTTACTGATTTTTTTATTATGTAAGCAAAACCAATAAAATTTAAGTTTTTTTAAACAACTA 4129  |
| Db | 70191 | GTTACTGATTTTTTTATTATGTAAGCAAAACCAATAAAATTTAAGTTTTTTTAAACAACTA 70132 |
| Qy | 4130  | CCTTATTTTTTCACTGTACAGACACTAATTCATTAAATACTAATTGATTGTTTAAAAGAAA 4189  |
| Db | 70131 | CCTTATTTTTTCACTGTACAGACACTAATTCATTAAATACTAATTGATTGTTTAAAAGAAA 70072 |
| Qy | 4190  | TATAAATGTGACAAGTGGACATTATTTATGTTAAATATACAATTATCAAGCAAGTATGAA 4249   |
| Db | 70071 | TATAAATGTGACAAGTGGACATTATTTATGTTAAATATACAATTATCAAGCAAGTATGAA 70012  |
| Qy | 4250  | GTTATTCAATTAAAATGCCACATTTCTGGTCTCTGGG 4286                          |
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# RESULT 9

AC144750/c

LOCUS AC144750 201093 bp DNA linear HTG 04-JUN-2003

DEFINITION Pan troglodytes clone CH251-517B22, WORKING DRAFT SEQUENCE, 3 ordered pieces.

ACCESSION AC144750

VERSION AC144750.2 GI:31376422

KEYWORDS HTG; HTGS\_PHASE2; HTGS\_DRAFT.

SOURCE Pan troglodytes (chimpanzee)

ORGANISM Pan troglodytes

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.

REFERENCE 1 (bases 1 to 201093)

AUTHORS Antonellis,A., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B., Blakesley,R.W., Bouffard,G.G., Brinkley,C., Brooks,S., Cariaga,K., Chu,G., Coleman,B., Coleman,H., Engle,J., Granite,S., Guan,X., Gupta,J., Haghighi,P., Han,J., Hansen,N., Ho,S.-L., Hu,P., Hurle,B., Idol,J.R., Karlins,E., Kwong,P., Laric,P., Lee-Lin,S.-Q., Legaspi,R., Maduro,Q.L., Maduro,V.B., Margulies,E.H., Masiello,C., Maskeri,B., McDowell,J., Paguirigan,C., Pearson,R., Portnoy,M.E., Prasad,A., Reddix-Dugue,N., Schandler,K., Schueler,M.G., Shah,K., Sison,C., Stantripop,S., Thomas,J.W., Thomas,P.J., Tsipouri,V., Vogt,J.L., Wetherby,K.D., Wiggins,L., Young,A. and Green,E.D.

TITLE NISC Comparative Sequencing Initiative

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 201093)  
 AUTHORS Green,E.D.  
 TITLE Direct Submission  
 JOURNAL Submitted (15-MAY-2003) NIH Intramural Sequencing Center, 8717  
 Grovemont Circle, Gaithersburg, MD 20877, USA  
 REFERENCE 3 (bases 1 to 201093)  
 AUTHORS Green,E.D.  
 TITLE Direct Submission  
 JOURNAL Submitted (04-JUN-2003) NIH Intramural Sequencing Center, 8717  
 Grovemont Circle, Gaithersburg, MD 20877, USA  
 COMMENT On Jun 4, 2003 this sequence version replaced gi:30725907.

----- Genome Center  
 Center: NIH Intramural Sequencing Center  
 Center code: NISC  
 Web site: <http://www.nisc.nih.gov>  
 Contact: [nisc\\_zoo@nhgri.nih.gov](mailto:nisc_zoo@nhgri.nih.gov)  
 ----- Project Information  
 Center project name: esg  
 Center clone name: 517B22

The sequence data in this record represents an 'enhanced' version of a Phase 2 submission. Specifically, the indicated order and orientation of each sequence contig has been established using one or more of the following: read-pair data from individual subclones, overlaps with neighboring clones, alignment with available reference sequence (e.g., human), and/or confirmation by PCR testing. In addition, the sequence assembly is based on at least 8X average coverage in Q20 bases and has been reviewed to rule out gross misassemblies, the low-quality ends of sequence contigs have been trimmed away, and each base is associated with a Phrap-derived quality score.

----- Summary Statistics  
 Sequencing vector: plasmid; n/a; 100% of reads  
 Chemistry: Dye-terminator Big Dye; 100% of reads  
 Assembly program: Phrap; version 0.990319  
 Consensus quality: 200649 bases at least Q40  
 Consensus quality: 200775 bases at least Q30  
 Consensus quality: 200836 bases at least Q20  
 Insert size: 165000; agarose-fp  
 Insert size: 200893; sum-of-contigs  
 Quality coverage: 13.47x in Q20 bases; agarose-fp  
 Quality coverage: 11.07x in Q20 bases; sum-of-contigs

-----  
 \* NOTE: This is a 'working draft' sequence. It currently  
 \* consists of 3 contigs. Gaps between the contigs  
 \* are represented as runs of N. The order of the pieces  
 \* is believed to be correct as given, however the sizes  
 \* of the gaps between them are based on estimates that have  
 \* provided by the submittor.  
 \* This sequence will be replaced  
 \* by the finished sequence as soon as it is available and  
 \* the accession number will be preserved.  
 \* 1 107546: contig of 107546 bp in length  
 \* 107547 107646: gap of unknown length  
 \* 107647 153000: contig of 45354 bp in length  
 \* 153001 153100: gap of unknown length



Db 69297 CACACAACACTTAGGCTTAAAAATGAGCTCACTCAGAATTTTTATTCTTTCTAAAAAGAG 69238  
 Qy 1910 ATTTATTTTTTAAATCAATGGGACTCTGATATAAAGGAAGAATAAGTCACTGTAAAACAGA 1969  
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 Qy 2447 AAAATCTTCTTTTTTCACTATCGTAGCTTAAACTCTGTTTGGTTTTGTCATCTGTAAATA 2506  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 68699 AAAATCTTCTTCTTTCACTATCGTAGCTTAAACTCTGTTTGGTTTTGTCATCTGTAAATA 68640  
 Qy 2507 CTTACCTACATACACTGCATGTAGATGATTAAATGAGGGCAGGCCCTGTGCTCATAGCTT 2566  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 68639 CTTACCTACATACACTGCATGTAGATGATTAAATGAGGGCAGGCCCTGTGCTCATAGCTT 68580  
 Qy 2567 TACGATGGAGAGATGCCAGTGACCTCATAATAAAGACTGTGAACTGCCTGGTGCAGTGTC 2626  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 68579 TACGATGGAGAGATGCCAGTGACCTCATAATAAAGACTGTGAACTGCCTGGTGCAGTGTC 68520  
 Qy 2627 CACATGACAAAGGGGCAGGTAGCACCTCTCTCACCCTGCTGTGGTTAAAATGGTTTCT 2686  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 68519 CACATGACAAAGGGGCAGGTAGCACCTCTCTCACCCTGCTGTGGTTAAAATGGTTTCT 68460  
 Qy 2687 AGCATATGTATAATGCTATAGTTAAAATACTATTTTTCAAATCATACAGATTAGTACAT 2746  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 68459 AGCATATGTATAATGCTATAGTTAAAATACTATTTTTCAAATCATACAGATTAGTACAT 68400

|    |       |   |       |
|----|-------|---|-------|
| Qy | 2747  | TTAACAGCTACCTGTAAAGCTTATTACTAATTTTTGTATTATTTTTGTAAATAGCCAATA  | 2806  |
| Db | 68399 | TTAACAGCTACCTGTAAAGCTTATTACTAATTTTTGTATTATTTTTGTAAATAGCCAATA  | 68340 |
| Qy | 2807  | GAAAAGTTTGCTTGACATGGTGCTTTTCTTTCATCTAGAGGCAAACTGCTTTTTGAGAC   | 2866  |
| Db | 68339 | GAAAAGTTTGCTTGACATGGTGCTTTTCTTTCATCTAGAGGCAAACTGCTTTTTGAGAC   | 68280 |
| Qy | 2867  | CGTAAGAACCTCTTAGCTTTGTGCGTTCCTGCCTAATTTTTATATCTTCTAAGCAAAGTG  | 2926  |
| Db | 68279 | CGTAAGAACCTCTTAGCTTTGTGCGTTCCTGCCTAATTTTTATATCTTCTAAGCAAAGTG  | 68220 |
| Qy | 2927  | CCTTAGGATAGCTTGGGATGAGATGTGTGTGAAAGTATGTACAAGAGAAAACGGAAGAGA  | 2986  |
| Db | 68219 | CCTTAGGATAGCTTGGGATGAGATGTGTGTGAAAGTATGTACAAGAGAAAACGGAAGAGA  | 68160 |
| Qy | 2987  | GAGGAAATGAGGTGGGGTTGGAGGAAACCCATGGGGACAGATTCCCATCTTAGCCTAAC   | 3046  |
| Db | 68159 | GAGGAAATGAGGTGGGGTTGGAGGAAACCCATGGGGACAGATTCCCATCTTAGCCTAAC   | 68100 |
| Qy | 3047  | GTTTCGTCATTGCCTCGTCACATCAATGCAAAAGGTCCTGATTTTGTTCAGCAAAACACA  | 3106  |
| Db | 68099 | GTTTCGTCATTGCCTCGTCACATCAATGCAAAAGGTCCTGATTTTGTTCAGCAAAACACA  | 68040 |
| Qy | 3107  | GTGCAATGTTCTCAGAGTGACTTTCGAAATAAATTGGGCCCCAAGAGCTTTAACTCGGTCT | 3166  |
| Db | 68039 | GTGCAATGTTCTCAGAGTGACTTTCGAAATAAATTGGGCCCCAAGAGCTTTAACTCGGTCT | 67980 |
| Qy | 3167  | TAAAATATGCCCAAATTTTTACTTTGTTTTCTTTTAATAGGCTGGGCCACATGTTGGAA   | 3226  |
| Db | 67979 | TAAAATATGCCCAAATTTTTACTTTGTTTTCTTTTAATAGGCTGGGCCACATGTTGGAA   | 67920 |
| Qy | 3227  | ATAAGCTAGTAATGTTGTTTTCTGTCAATATTGAATGTGATGGTACAGTAAACCAAACC   | 3286  |
| Db | 67919 | ATAAGCTAGTAATGTTGTTTTCTGTCAATATTGAATGTGATGGTACAGTAAACCAAACC   | 67860 |
| Qy | 3287  | CAACAATGTGGCCAGAAAGAAAGAGCAATAATAATTAATTACACACCATATGGATTCTA   | 3346  |
| Db | 67859 | CAACAATGTGGCCAGAAAGAAAGAGCAATAATAATTAATTACACACCATATGGATTCTA   | 67800 |
| Qy | 3347  | TTTATAAATCACCCACAACTTGTTCTTTAATTTTCATCCCAATCACTTTTTCAGAGGCCT  | 3406  |
| Db | 67799 | TTTATAAATCACCCACAACTTGTTTTTTAATTTTCATCCCAATCACTTTTTCAGAGGCCT  | 67740 |
| Qy | 3407  | GTTATCATAGAAGTCATTTTAGACTCTCAATTTTAAATTAATTTTGAATCACTAATATTT  | 3466  |
| Db | 67739 | GTTATCATAGAAGACATTTTAGACTCTCAATTTTAAATTAATTTTGAATCACTAATATTT  | 67680 |
| Qy | 3467  | TCACAGTTTATTAATATATTTAATTTCTATTTAAATTTTAGATTATTTTATTACCATGT   | 3526  |
| Db | 67679 | TCACAGTTTATTAATATATTTAATTTCTATTTAAATTTTAGATTATTTTATTACCATGT   | 67620 |
| Qy | 3527  | ACTGAATTTTACATCCTGATACCCTTTCCTTCTCCATGTCAGTATCATGTTCTCTAATT   | 3586  |
| Db | 67619 | ACTGAATTTTACATCCTGATACCCTTTCCTTCTCCATGTCAGTATCATGTTCTCTAATT   | 67560 |

Qy 3587 ATCTTGCCAAATTTTGAAGTACACACAAAAGCATACTTGCATTATTTATAATAAAATT 3646  
 |||  
 Db 67559 ATCTTGCCAAATTTTGAAGTACACACAAAAGCATACTTGCATTATTTATAATAAAATT 67500  
 Qy 3647 GCATTCAGTGGCTTTTTAAAAAAATGTTTGATTCAAACCTTTAACATACTGATAAGTAA 3706  
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 Db 67499 GCATTCAGTGGCTTTTT-AAAAAATGTTTGATTCAAACCTTTAACATACTGATAAGTAA 67441  
 Qy 3707 GAAACAATTATAATTTCTTTACATACTCAAACCAAGATAGAAAAGGTGCTATCGTTCA 3766  
 |||  
 Db 67440 GAAACAATTATAATTTCTTTACATACTCAAACCAAGATAGAAAAGGTGCTATCGTTCA 67381  
 Qy 3767 ACTTCAAACATGTTTCCTAGTATTAAGGACTTTAATATAGCAACAGACAAAATTATTGT 3826  
 |||  
 Db 67380 ACTTCAAACATGTTTCCTAGTATTAAGGACTTTAATATAGCAACAGACAAAATTATTGT 67321  
 Qy 3827 TAACATGGATGTTACAGCTCAAAGATTTATAAAAGATTTTAACTATTTTCTCCCTTAT 3886  
 |||  
 Db 67320 TAACATGGATGTTACAGCTCAAAGATTTATAAAAGATTTTAACTATTTTCTCCCTTAT 67261  
 Qy 3887 TATCCACTGCTAATGTGGATGTATGTTCAAACACCTTTTAGTATTGATAGCTTACATATG 3946  
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 Db 67260 TATCCACTGCTAATGTGGATGTATGTTCAAACACCTTTTAGTATTGATAGCTTACATATG 67201  
 Qy 3947 GCCAAAGGAATACAGTTTATAGCAAACATGGGTATGCTGTAGCTAACTTTATAAAAGTG 4006  
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 Db 67200 GCCAAAGGAATACAGTTTATAGCAAACATGGGTATGCTGTAGCTAACTTTATAAAAGTG 67141  
 Qy 4007 TAATATAACAATGTAAAAAATTATATATCTGGGAGGATTTTTTGGTTGCCTAAAGTGGCT 4066  
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 Db 67140 TAATATAACAATGTAAAAAATTATATATCTGGGAGGATTTTTTGGTTGCCTAAAGTGGCT 67081  
 Qy 4067 ATAGTTACTGATTTTTTTATTATGTAAGCAAACCAATAAAAATTTAAGTTTTTTTAACAA 4126  
 |||  
 Db 67080 ATAGTTACTGATTTTTTTATTATGTAAGCAAACCAATAAAAATTTAAGTTTTTTTAACAA 67021  
 Qy 4127 CTACCTTATTTTTTCACTGTACAGACACTAATTCATTAAATACTAATTGATTGTTTAAAAG 4186  
 |||  
 Db 67020 CTACCTTATTTTTTCACTGTACAGACACTAATTCATTAAATACTAATTGATTGTTTAAAAG 66961  
 Qy 4187 AAATATAAATGTGACAAGTGGACATTATTTATGTTAAATATACAATTATCAAGCAAGTAT 4246  
 |||  
 Db 66960 AAATATAAATGTGACAAGTGGACATTATTTATGTTAAATATACAATTATCAAGCAAGTAT 66901  
 Qy 4247 GAAGTTATTCAATTAAAATGCCACATTTCTGGTCTCTGGG 4286  
 |||  
 Db 66900 GAAGTTATTCAATTAAAATGCCACATTTCTGGTCTCTGGG 66861

RESULT 10

G06417

LOCUS G06417 2720 bp DNA linear STS 19-OCT-1995

DEFINITION human STS WI-7149, sequence tagged site.

ACCESSION G06417

VERSION G06417.1 GI:859662

KEYWORDS STS; STS sequence; primer; sequence tagged site.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 2720)

AUTHORS Hudson, T.

TITLE Whitehead Institute/MIT Center for Genome Research; Physically  
 Mapped ESTs

JOURNAL Unpublished (1995)

COMMENT

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 Email: thudson@genome.wi.mit.edu

Primer A: ATGGAGAGATGCCAGTGACC  
 Primer B: TAGGCAGGAACGCACAAAG  
 STS size: 331  
 PCR Profile:

Presoak:  
 Denaturation:  
 Annealing: 56 degrees C  
 Polymerization:  
 PCR Cycles: 35  
 Thermal Cycler:

Protocol:

Template: 10 ng  
 Primer: each 5 pM  
 dNTPs: each 4 nM  
 Taq Polymerase: 0.025 units/ul  
 Total Vol: 20 ul

Buffer:

MgCl2: 1.5 mM  
 KCl: 50 mM  
 Tris-HCL: 10 mM  
 pH: 9.3

Prepared with primer pairs derived from D90402 -- Unigene.

FEATURES Location/Qualifiers

|             |  |
|-------------|--|
| source      | 1. .2720   |
|             | /organism="Homo sapiens"                                       |
|             | /mol_type="genomic DNA"  |
|             | /db_xref="taxon:9606"  |
|             | /map="710_D_4; 788_D_1; 795_F_4; 921_F_2; 940_G_8;<br>969_D_1" |
| STS         | 1005. .1335  |
| primer_bind | 1005. .1024  |
| primer_bind | complement(1317. .1335)  |

ORIGIN

Query Match 60.7%; Score 2610; DB 11; Length 2720;  
 Best Local Similarity 96.0%; Pred. No. 0;  
 Matches 2610; Conservative 0; Mismatches 110; Indels 0; Gaps 0;

|    |      |   |      |
|----|------|---|------|
| Qy | 1567 | AAGAAGAACTATTCACTGTATTTTCAATTTTCTTTATATTGGACCGAAGTCATTAAAAACAAA | 1626 |
|    |      |   |      |
| Db | 1    | AAGAAGAACTATTCACTGTATTTTCAATTTTCTTTATATTGGACCGAAGTCATTNNNNNNNNN | 60   |
|    |      |   |      |
| Qy | 1627 | ATGAAACATTTGCCAAAAACAAAACAAAAAACTATGTATTTGCACAGCACACTATTAAAAT   | 1686 |
|    |      |   |      |
| Db | 61   | NNNNNNNNNNNNNNNNNNNNNNNNNNNNNTATGTATTTGCACAGCACACTATTAAAAT      | 120  |
|    |      |   |      |
| Qy | 1687 | ATTAAGTGTAATTATTTTAACTCAGCTACATATGACATTTTATGAGCTGTTTACGG        | 1746 |
|    |      |   |      |
| Db | 121  | ATTAAGTGTAATTATTTTAACTCAGCTACATATGACATTTTATGAGCTGTTTACGG        | 180  |
|    |      |   |      |
| Qy | 1747 | CATGGAAAGAAAATCAGTGGAATTAAGAAAGCCTCGTCGTGAAAGCACTTAATTTTTTA     | 1806 |
|    |      |   |      |
| Db | 181  | CATGGAAAGAAAATCAGTGGAATTAAGAAAGCCTCGTCGTGAAAGCACTTAATTTTTTA     | 240  |
|    |      |   |      |
| Qy | 1807 | CAGTTAGCACTTCAACATAGCTCTTAACAACCTCCAGGATATTCACACAACACTTAGGCT    | 1866 |
|    |      |   |      |
| Db | 241  | CAGTTAGCACTTCAACATAGCTCTTAACAACCTCCAGGATATTCACACAACACTTAGGCT    | 300  |
|    |      |   |      |
| Qy | 1867 | TAAAAATGAGCTCACTCAGAATTTCTATTCTTTCTAAAAAGAGATTTATTTTTAAATCAA    | 1926 |
|    |      |   |      |
| Db | 301  | TAAAAATGAGCTCACTCAGAATTTCTATTCTTTCTAAAAAGAGATTTATTTTTAAATCAA    | 360  |
|    |      |   |      |
| Qy | 1927 | TGGGACTCTGATATAAAGGAAGAATAAGTCACTGTAAACAGAACTTTTAAATGAAGCTT     | 1986 |
|    |      |   |      |
| Db | 361  | TGGGACTCTGATATAAAGGAAGAATAAGTCACTGTAAACAGAACTTTTAAATGAAGCTT     | 420  |
|    |      |   |      |
| Qy | 1987 | AAATTACTCAATTTAAAAATTTTAAAAATCCTTTAAAACAACTTTTCAATTAATATTATCAC  | 2046 |
|    |      |   |      |
| Db | 421  | AAATTACTCAATTTAAAAATTTTAAAAATCCTTTAAAACAACTTTTCAATTAATATTATCAC  | 480  |
|    |      |   |      |
| Qy | 2047 | ACTATTATCAGATTGTAATTAGATGCAAATGAGAGAGCAGTTTAGTTGTTGCATTTTTTCG   | 2106 |
|    |      |   |      |
| Db | 481  | ACTATTATCAGATTGTAATTAGATGCAAATGAGAGAGCAGTTTAGTTGTTGCATTTTTTCG   | 540  |
|    |      |   |      |
| Qy | 2107 | GACACTGGAACATTTTAAATGATCAGGAGGGAGTAACAGAAAGAGCAAGGCTGTTTTTGA    | 2166 |
|    |      |   |      |
| Db | 541  | GACACTGGAACATTTTAAATGATCAGGAGGGAGTAACAGAAAGAGCAAGGCTGTTTTTGA    | 600  |
|    |      |   |      |
| Qy | 2167 | AAATCATTACACTTTTCTAGTAAGCCCCAACCTCAGCATTTCTGCAATATGTAACCAACAT   | 2226 |
|    |      |   |      |
| Db | 601  | AAATCATTACACTTTTCTAGTAAGCCCCAACCTCAGCATTTCTGCAATATGTAACCAACAT   | 660  |
|    |      |   |      |
| Qy | 2227 | GTCACAAACAAGCAGCATGTAACAGACTGGCACATGTGCCAGCTGAATTTAAAAATATAAT   | 2286 |
|    |      |   |      |
| Db | 661  | GTCACAAACAAGCAGCATGTAACAGACTGGCACATGTGCCAGCTGAATTTAAAAATATAAT   | 720  |
|    |      |   |      |
| Qy | 2287 | ACTTTTAAAAAGAAAATTATTACATCCTTTACATTGTTAAGATCAAACCTCACAAAGA      | 2346 |
|    |      |   |      |
| Db | 721  | ACTTTTAAAAAGAAAATTATTACATCCTTTACATTGTTAAGATCAAACCTCACAAAGA      | 780  |
|    |      |   |      |
| Qy | 2347 | GAAATAGAATGTTTGAAAGGCTATCCCAAAGACTTTTTTGAATCTGTCATTACATACC      | 2406 |
|    |      |   |      |
| Db | 781  | GAAATAGAATGTTTGAAAGGCTATCCCAAAGACTTTTTTGAATCTGTCATTACATACC      | 840  |
|    |      |   |      |
| Qy | 2407 | CTGTGAAGACAATACTATCTACAATTTTTTTCAGGATTATTAAAATCTTCTTTTTTCACTA   | 2466 |



|    |      |   |      |
|----|------|---|------|
| Db | 841  | CTGTGAAGACAATACTATCTACAATTTTTTCAGGATTATTAAAATCTTCTTTTTTCACTA  | 900  |
| Qy | 2467 | TCGTAGCTTAAACTCTGTTTGGTTTTGTCATCTGTAAATACTTACCTACATACACTGCAT  | 2526 |
| Db | 901  | TCGTAGCTTAAACTCTGTTTGGTTTTGTCATCTGTAAATACTTACCTACATACACTGCAT  | 960  |
| Qy | 2527 | GTAGATGATTAAATGAGGGCAGGCCCTGTGCTCATAGCTTTACGATGGAGAGATGCCAGT  | 2586 |
| Db | 961  | GTAGATGATTAAATGAGGGCAGGCCCTGTGCTCATAGCTTTACGATGGAGAGATGCCAGT  | 1020 |
| Qy | 2587 | GACCTCATAATAAAGACTGTGAACTGCCTGGTGCAGTGTCCACATGACAAAGGGGCAGGT  | 2646 |
| Db | 1021 | GACCTCATAATAAAGACTGTGAACTGCCTGGTGCAGTGTCCACATGACAAAGGGGCAGGT  | 1080 |
| Qy | 2647 | AGCACCCCTCTCTCACCCATGCTGTGGTTAAAATGGTTTCTAGCATATGTATAATGCTATA | 2706 |
| Db | 1081 | AGCACCCCTCTCTCACCCATGCTGTGGTTAAAATGGTTTCTAGCATATGTATAATGCTATA | 1140 |
| Qy | 2707 | GTTAAAATACTATTTTTCAAATCATAACAGATTAGTACATTTAACAGCTACCTGTAAAGC  | 2766 |
| Db | 1141 | GTTAAAATACTATTTTTCAAATCATAACAGATTAGTACATTTAACAGCTACCTGTAAAGC  | 1200 |
| Qy | 2767 | TTATTACTAATTTTTGTATTATTTTTGTAAATAGCCAATAGAAAAGTTTGCTTGACATGG  | 2826 |
| Db | 1201 | TTATTACTAATTTTTGTATTATTTTTGTAAATAGCCAATAGAAAAGTTTGCTTGACATGG  | 1260 |
| Qy | 2827 | TGCTTTTCTTTCATCTAGAGGCAAACTGCTTTTTGAGACCGTAAGAACCTCTTAGCTTT   | 2886 |
| Db | 1261 | TGCTTTTCTTTCATCTAGAGGCAAACTGCTTTTTGAGACCGTAAGAACCTCTTAGCTTT   | 1320 |
| Qy | 2887 | GTGCGTTCCTGCCTAATTTTTATATCTTCTAAGCAAAGTGCCTTAGGATAGCTTGGGATG  | 2946 |
| Db | 1321 | GTGCGTTCCTGCCTAATTTTTATATCTTCTAAGCAAAGTGCCTTAGGATAGCTTGGGATG  | 1380 |
| Qy | 2947 | AGATGTGTGTGAAAGTATGTACAAGAGAAAACGGAAGAGAGAGGAAATGAGGTGGGGTTG  | 3006 |
| Db | 1381 | AGATGTGTGTGAAAGTATGTACAAGAGAAAACGGAAGAGAGAGGAAATGAGGTGGGGTTG  | 1440 |
| Qy | 3007 | GAGGAAACCCATGGGGACAGATTCCCATTCTTAGCCTAACGTTTCGTATTGCCTCGTCAC  | 3066 |
| Db | 1441 | GAGGAAACCCATGGGGACAGATTCCCATTCTTAGCCTAACGTTTCGTATTGCCTCGTCAC  | 1500 |
| Qy | 3067 | ATCAATGCAAAAGGTCCTGATTTTGTTCAGCAAAACACAGTGCAATGTTCTCAGAGTGA   | 3126 |
| Db | 1501 | ATCAATGCAAAAGGTCCTGATTTTGTTCAGCAAAACACAGTGCAATGTTCTCAGAGTGA   | 1560 |
| Qy | 3127 | CTTTCGAAATAAATTGGGCCCCAAGAGCTTTAACTCGGTCTTAAAATATGCCCAAATTTTT | 3186 |
| Db | 1561 | CTTTCGAAATAAATTGGGCCCCAAGAGCTTTAACTCGGTCTTAAAATATGCCCAAATTTTT | 1620 |
| Qy | 3187 | ACTTTGTTTTTCTTTAATAGGCTGGGCCACATGTTGGAAATAAGCTAGTAATGTTGTTT   | 3246 |
| Db | 1621 | ACTTTGTTTTTCTTTAATAGGCTGGGCCACATGTTGGAAATAAGCTAGTAATGTTGTTT   | 1680 |
| Qy | 3247 | TCTGTCAATATTGAATGTGATGGTACAGTAAACCAAAACCAACAATGTGGCCAGAAAGA   | 3306 |

|    |      |  |      |
|----|------|--|------|
| Db | 1681 | TCTGTCAATATTGAATGTGATGGTACAGTAAACCAAAACCCAACAATGTGGCCAGAAAAGA  | 1740 |
| Qy | 3307 | AAGAGCAATAATAATTAATTACACACCATATGGATTCTATTTATAAATCACCCACAAAC    | 3366 |
| Db | 1741 | AAGAGCAATAATAATTAATTACACACCATATGGATTCTATTTATAAATCACCCACAAAC    | 1800 |
| Qy | 3367 | TTGTTCTTTAATTTTCATCCCAATCACTTTTTTCAGAGGCCTGTTATCATAGAAGTCATTTT | 3426 |
| Db | 1801 | TTGTTCTTTAATTTTCATCCCAATCACTTTTTTCAGAGGCCTGTTATCATAGAAGTCATTTT | 1860 |
| Qy | 3427 | AGACTCTCAATTTTAAATTAATTTTGAATCACTAATATTTTACAGTTTATTAATATATT    | 3486 |
| Db | 1861 | AGACTCTCAATTTTAAATTAATTTTGAATNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN    | 1920 |
| Qy | 3487 | TAATTTCTATTTAAATTTTAGATTATTTTTATTACCATGTACTGAATTTTACATCCTGA    | 3546 |
| Db | 1921 | NN         | 1980 |
| Qy | 3547 | TACCCTTTCCTTCTCCATGTCAGTATCATGTTCTCTAATTATCTTGCCAAATTTTGAAAC   | 3606 |
| Db | 1981 | TACCCTTTCCTTCTCCATGTCAGTATCATGTTCTCTAATTATCTTGCCAAATTTTGAAAC   | 2040 |
| Qy | 3607 | TACACACAAAAGCATACTTGCATTATTTATAATAAAATTGCATTCACTGGCTTTTTTAAA   | 3666 |
| Db | 2041 | TACACACAAAAGCATACTTGCATTATTTATAATAAAATTGCATTCACTGGCTTTTTTNNN   | 2100 |
| Qy | 3667 | AAAAATGTTTGATTCAAACCTTTAACATACTGATAAGTAAGAAACAATTATAATTTCTTT   | 3726 |
| Db | 2101 | NNNNNTGTTTGATTCAAACCTTTAACATACTGATAAGTAAGAAACAATTATAATTTCTTT   | 2160 |
| Qy | 3727 | ACATACTCAAACCAAGATAGAAAAGGTGCTATCGTTCAACTTCAAACATGTTTCCTA      | 3786 |
| Db | 2161 | ACATACTCAAACCAAGATAGAAAAGGTGCTATCGTTCAACTTCAAACATGTTTCCTA      | 2220 |
| Qy | 3787 | GTATTAAGGACTTTAATATAGCAACAGACAAAATTATTGTTAACATGGATGTTACAGCTC   | 3846 |
| Db | 2221 | GTATTAAGGACTTTAATATAGCAACAGACAAAATTATTGTTAACATGGATGTTACAGCTC   | 2280 |
| Qy | 3847 | AAAAGATTTATAAAAAGATTTTAACTATTTTCTCCCTTATTATCCACTGCTAATGTGGAT   | 3906 |
| Db | 2281 | AAAAGATTTATAAAAAGATTTTAACTATTTTCTCCCTTATTATCCACTGCTAATGTGGAT   | 2340 |
| Qy | 3907 | GTATGTTCAAACACCTTTTAGTATTGATAGCTTACATATGGCCAAAGGAATACAGTTTAT   | 3966 |
| Db | 2341 | GTATGTTCAAACACCTTTTAGTATTGATAGCTTACATATGGCCAAAGGAATACAGTTTAT   | 2400 |
| Qy | 3967 | AGCAAAACATGGGTATGCTGTAGCTAACTTTATAAAAGTGTAATATAACAATGTAAAAA    | 4026 |
| Db | 2401 | AGCAAAACATGGGTATGCTGTAGCTAACTTTATAAAAGTGTAATATAACAATGTAAAAA    | 2460 |
| Qy | 4027 | TTATATATCTGGGAGGATTTTTTGGTTGCCTAAAGTGGCTATAGTTACTGATTTTTTATT   | 4086 |
| Db | 2461 | TTATATATCTGGGAGGATTTTTTGGTTGCCTAAAGTGGCTATAGTTACTGATTTTTTATT   | 2520 |
| Qy | 4087 | ATGTAAGCAAAACCAATAAAAATTTAAGTTTTTTTAACTACCTTATTTTTTCACTGTA     | 4146 |
| Db | 2521 | ATGTAAGCAAAACCAATAAAAATTTAAGTTTTTTTAACTACCTTATTTTTTCACTGTA     | 2580 |

QY 4147 CAGACACTAATTCATTAAATACTAATTGATTGTTTAAAAGAAATATAAATGTGACAAGTG 4206  
 |||||  
 Db 2581 CAGACACTAATTCATTAAATACTAATTGATTGTTTAAAAGAAATATAAATGTGACAAGTG 2640  
 QY 4207 GACATTATTTATGTTAAATATACAATTATCAAGCAAGTATGAAGTTATTCAATTAAAAATG 4266  
 |||||  
 Db 2641 GACATTATTTATGTTAAATATACAATTATCAAGCAAGTATGAAGTTATTCAATTAAAAATG 2700  
 QY 4267 CCACATTTCTGGTCTCTGGG 4286  
 |||||  
 Db 2701 CCACATTTCTGGTCTCTGGG 2720

# RESULT 11

AC130785/c

LOCUS AC130785 169751 bp DNA linear HTG 29-AUG-2002

DEFINITION Papio anubis clone RP41-325P5, WORKING DRAFT SEQUENCE.

ACCESSION AC130785

VERSION AC130785.1 GI:22218455

KEYWORDS HTG; HTGS\_PHASE2; HTGS\_DRAFT.

SOURCE Papio anubis (olive baboon)

ORGANISM Papio anubis

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;  
 Cercopithecinae; Papio.

REFERENCE 1 (bases 1 to 169751)

AUTHORS Akhter, N., Antonellis, A., Ayele, K., Beckstrom-Sternberg, S.M.,  
 Benjamin, B., Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C.,  
 Brooks, S., Dietrich, N.L., Granite, S., Guan, X., Gupta, J.,  
 Haghighi, P., Han, J., Hansen, N., Ho, S.-L., Idol, J.R., Karlins, E.,  
 Laric, P., Lee-Lin, S.-Q., Legaspi, R., Maduro, Q.L., Maduro, V.B.,  
 Margulies, E.H., Masiello, C., Maskeri, B., Mastrian, S.D.,  
 McCloskey, J.C., McDowell, J., Paguirigan, C., Pearson, R.,  
 Portnoy, M.E., Prasad, A., Reddix-Dugue, N., Schueler, M.G., Sison, C.,  
 Stantripop, S., Thomas, J.W., Thomas, P.J., Touchman, J.W., Vogt, J.L.,  
 Wetherby, K.D., Wiggins, L., Young, A., Zhang, L.-H. and Green, E.D.

TITLE NISC Comparative Sequencing Initiative

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 169751)

AUTHORS Green, E.D.

TITLE Direct Submission

JOURNAL Submitted (14-AUG-2002) NIH Intramural Sequencing Center, 8717  
 Grovemont Circle, Gaithersburg, MD 20877, USA

REFERENCE 3 (bases 1 to 169751)

AUTHORS Green, E.D.

TITLE Direct Submission

JOURNAL Submitted (29-AUG-2002) NIH Intramural Sequencing Center, 8717  
 Grovemont Circle, Gaithersburg, MD 20877, USA

COMMENT

----- Genome Center  
 Center: NIH Intramural Sequencing Center  
 Center code: NISC  
 Web site: <http://www.nisc.nih.gov>  
 Contact: [nisc\\_zoo@nhgri.nih.gov](mailto:nisc_zoo@nhgri.nih.gov)  
 ----- Project Information  
 Center project name: deh  
 Center clone name: 325P05

The sequence data in this record represents an 'enhanced' version of a Phase 2 submission. Specifically, the indicated order and orientation of each sequence contig has been established using one or more of the following: read-pair data from individual subclones, overlaps with neighboring clones, alignment with available reference sequence (e.g., human), and/or confirmation by PCR testing. In addition, the sequence assembly is based on at least 8X average coverage in Q20 bases and has been reviewed to rule out gross misassemblies, the low-quality ends of sequence contigs have been trimmed away, and each base is associated with a Phrap-derived quality score.

----- Summary Statistics

Sequencing vector: plasmid; n/a; 100% of reads  
 Chemistry: Dye-terminator Big Dye; 100% of reads  
 Assembly program: Phrap; version 0.990319  
 Consensus quality: 169735 bases at least Q40  
 Consensus quality: 169747 bases at least Q30  
 Consensus quality: 169749 bases at least Q20  
 Insert size: 138000; agarose-fp  
 Insert size: 169751; sum-of-contigs  
 Quality coverage: 10.99x in Q20 bases; agarose-fp  
 Quality coverage: 8.94x in Q20 bases; sum-of-contigs

-----  
 \* NOTE: This is a 'working draft' sequence. It currently  
 \* consists of 1 contigs. Gaps between the contigs  
 \* are represented as runs of N. The order of the pieces  
 \* is believed to be correct as given, however the sizes  
 \* of the gaps between them are based on estimates that have  
 \* provided by the submittor.  
 \* This sequence will be replaced  
 \* by the finished sequence as soon as it is available and  
 \* the accession number will be preserved.

FEATURES

source

\* 1 169751: contig of 169751 bp in length.

Location/Qualifiers

1. .169751

/organism="Papio anubis"

/mol\_type="genomic DNA"

/sub\_species="anubis"

/db\_xref="taxon:9555"

/clone="RP41-325P5"

/clone\_lib="RP41"

misc\_feature

1. .169751

/note="assembly\_fragment"

clone\_end:T7

vector\_side:left

clone\_end:Sp6

vector\_side:right"

misc\_feature

1. .63149

/note="clone overlaps with GenBank Accession Number  
 AC129069 clone RP41-240D13 (center project name deg)"

ORIGIN

Query Match 59.3%; Score 2550; DB 2; Length 169751;  
 Best Local Similarity 94.8%; Pred. No. 0;  
 Matches 2717; Conservative 0; Mismatches 130; Indels 19; Gaps 7;

Qy 1430 AGTCATGCTTATGCTGCTGGTGCCAGTCATTTGAAGAAAAACAGTCCTTGGAGGAAAAGC 1489  
 |||  
 Db 29218 AGTCATGCTTATGCTGCTGGTGCCAGTCATTTGAAGAAAAACAGTCCTTGGAGGAAAAGC 29159

Qy 1490 AGTCGTGCTTAAAGTTCAAAGCTAATGATCACGGATATGACAACCTCCGTTCCAGTAATA 1549  
 |||  
 Db 29158 AGTCGTGCTTAAAGTTCAAAGCTAATGATCACGGATATGACAACCTCCGTTCCAGTAATA 29099

Qy 1550 AATACAGCTCATCTTGAAAGAAGAACTATTCACTGTATTTTCTTTATATTGGACC 1609  
 |||  
 Db 29098 AATACAGCTCATCTTGAAAGAAGAACTATTCACTGTATTTTCTTTATATTGGACC 29039

Qy 1610 GAAGTCATTAAAAACAAAATGAAACATTTGCCAAAACAAAACAAAAAATATGTATTTGCA 1669  
 |||  
 Db 29038 GAAGTCATTAAAAACAAAATGAAACATTTGTCAAAAACAAAACAAAAAATATGTATTTGCA 28979

Qy 1670 CAGCACACTATTAAAAATATTAAGTGTAATTATTTTAACTCACAGCTACATATGACATT 1729  
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 Db 28978 CAGCACACTATTAAAAATATTAAGTGTAATTATTTTAACTCATAGCTACATATGACATT 28919

Qy 1730 TTATGAGCTGTTTACGGCATGGAAAGAAAATCAGTGGGAATTAAGAAAGCCTCGTCGTGA 1789  
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 Db 28918 TTATGAGCTGTTTACAGCATGGAAAGAAAATCAGTGGGAATTAAGAAAGCCTCATTGTGA 28859

Qy 1790 AAGCACTTAATTTTTTACAGTTAGCACTTCAACATAGCTCTTAACAACCTCCAGGATATT 1849  
 |||  
 Db 28858 AAGCACTTACTTTTTTATGGTTAGCACTTCAACATAGCTCTTAATAACTTCCAGGATATT 28799

Qy 1850 CACACAACACTTAGGCTTAAAAATGAGCTCACTCAGAATTTCTATTCTTTCTAAAAAGAG 1909  
 |||  
 Db 28798 CACACAACCCTTAGGCTTAAAAATGAGCTCACTCGGAATTTCTATT-----TAAGAG 28747

Qy 1910 ATTTATTTTTTAAATCAATGGGACTCTGATATAAAGGAAGAATAAGTCACTGTAAACAGA 1969  
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 Db 28746 ATTTATTTTTTAAATCAATGTGAATCTGATACAAAGGAAGAGTAAGTCACTGTAAACAGA 28687

Qy 1970 ACTTTTAAATGAAGCTTAAATTACTCAATTTAAAATTTTAAAATCCTTTAAAACAACCTT 2029  
 |||  
 Db 28686 ACTTTTAAATGAAGCTTAAATTACCCAATTTGAAATTTTAAAATCCTTTAAAAGAACCTT 28627

Qy 2030 TCAATTAATATTATCACACT-ATTATCAGATTGTAATTAGATGCAAATGAGAGAGCAGTT 2088  
 |  
 Db 28626 TTAATTAATATTTTTCACACTGCTGATCAGACTGTAATTAGATGCAAATGAGAGAGTAGTT 28567

Qy 2089 TAGTTGTTGCATTTTTTCGGACACTGGAAACATTTAAATGATCAGGAGGGAGTAACAGAAA 2148  
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 Db 28566 TAGTTGCTGTATTTTTTGGACACTAGAAACATTTAAATGATCAGGAGGGAGTAACAGAAA 28507

Qy 2149 GAGCAAGGCTGTTTTTGAAAATCATTACA---CTTTCCTAGTAAGCCCAAACCTCAGCAT 2205  
 ||  
 Db 28506 GAACAAGGCTGTTTTTGAAAATCATTACACTCCTTTCCTAGTAAGCCCAAACCTCAGCAT 28447

Qy 2206 TCTGCAATATGTAACCAACATGTCACAAACAAGCAGCATGTAACAGACTGGCACATGTGC 2265  
 |||  
 Db 28446 TCTGCAATATGTAACCAACATGTTACAAACAAGCAGCATGTAACAAACTGGCACATGTGT 28387

Qy 2266 CAGCTGAATTTAAAATATAATACTTTTAAAAAGAAAATTATTACATCCTTTACATTTCAGT 2325  
 |||| ||| |||||||||||||||||||||||||||||||||||||||  
 Db 28386 CAGCCAAATCTAAAATATAATACTTTTAAAAAGAAAATTATTACACCCTTTACATTTCAGA 28327  
 Qy 2326 TAAGATCAAACCTCACAAAGAGAAATAGAATGTTTGAAAGGCTATCCCAAAGACTTTTT 2385  
 ||||||||||||||||||||||||||||||||||||||| |||||  
 Db 28326 TAAGATCAAACCTCACAAAGAGAAATAGAATGTTTGAAAGGCTGCCCAAAGACTTCTT 28267  
 Qy 2386 TGAATCTGTCATTACATACCCTGTGAAGACAATACTATCTACAATTTTTTCAGGATTAT 2445  
 ||||||| ||||||| | ||||||| ||||||| ||||||| |||||||  
 Db 28266 TGAATCTGCCATTACACAGCCTGTGAAGAAAATACTATCTACAAATTTTTTCAGGATTAT 28207  
 Qy 2446 TAAATCTTCTTTTTTCACTATCGTAGCTTAACTCTGTTTGGTTTTGTCATCTGTAAAT 2505  
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 Db 28206 TAAATCTTCTTCTTTCACTATTGTAGCTTAACTCTGTTTGGTTTTGTCATCCGTAAAT 28147  
 Qy 2506 ACTTACCTACATACACTGCATGTAGATGATTAAATGAGGGCAGGCCCTGTGCTCATAGCT 2565  
 ||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||  
 Db 28146 ACTTAGCTACATACACTGCATGTAGACGATTAAACGAGGGCGGGCCCTGTGTTTCATAGTT 28087  
 Qy 2566 TTACGATGGAGAGATGCCAGTGACCTCATAATAAGACTGTGAAGTGCCTGGTGCAGTGT 2625  
 ||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||  
 Db 28086 TTACAATGGAGAGATGCCAGTGACCTCATAATAGAGACTGTGAAGTGCCTGGTGCAGTGT 28027  
 Qy 2626 CCACATGACAAAGGGGCAGGTAGCACCCCTCTCTACCCCATGCTGTGGTTAAATGGTTTC 2685  
 ||||||||||| ||||||| ||||||| ||||||| ||||||| |||||||  
 Db 28026 CCACATGACAAAGGGGCAGGTAGCACCCCTCTCTACCCCATGCTGTAGTTAAATGGTTTC 27967  
 Qy 2686 TAGCATATGTATAATGCTATAGTTAAATACTATTTTTCAAATCATACAGATTAGTACA 2745  
 ||||||||||| ||||||| ||||| ||||| ||||||| |||||||  
 Db 27966 TAGCATATGTATAATGCTGTAGTTAAACACTGTTTTGCAAATCATACAGATTAGTACA 27907  
 Qy 2746 TTTAACAGCTACCTGTAAAGCTTATTACTAATTTTTGTATTATTTTTGTAAATAGCCAAT 2805  
 ||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||  
 Db 27906 TTTAATGGCTACCTGTAAAGCTTATTACTAGTTTTGTATTATTTTTGTAAATAGCCAAT 27847  
 Qy 2806 AGAAAAGTTTGCTTGACATGGTGCTTTTCTTTTCATCTAGAGGCAAACCTGCTTTTTGAGA 2865  
 ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||  
 Db 27846 AGAAAAGTGTGCTTGACGTGGTGCTTTTCTTTCACTTAGAGGCAAACCTGCTTTTTGAGA 27787  
 Qy 2866 CCGTAAGAACCTCTTAGCTTTGTGCGTTCCTGCCTAATTTTTATATCTTCTAAGCAAAGT 2925  
 | ||||||| ||||||| ||||||| ||||||| ||||||| |||||||  
 Db 27786 CTGTAAGAACCTCTTAGCTTTGTGCGTTCCTGCCTAATTTTAAATCTTCTAAGCAAAGT 27727  
 Qy 2926 GCCTTAGGATAGCTTGGGATGAGATGTGTGTGAAAGTATGTACAAGAGAAAACGGAAGAG 2985  
 ||||||| ||||||| ||||||| ||||||| ||||||| |||||||  
 Db 27726 GCCTTAGAATAGCTTGGGATGAGATGTGTGTGAAAGTATGTACAAGAGAAAACGGAAGAG 27667  
 Qy 2986 AGAGGAAATGAGGTGGGGTTGGAGGAAACCCATGGGGACAGATTCCCATTCTTAGCCTAA 3045  
 ||||||| ||||||| ||||||| ||||||| ||||||| |||||||  
 Db 27666 AGAGGAAATGAGGTGGGGTTGGAGGAAACTCATGGGGACAGATTCCCATTCTTAGCCTAA 27607  
 Qy 3046 CGTTCGTCATTGCCTCGTCACATCAATGCAAAGGTCCTGATTTTGTTCAGCAAACAC 3105  
 ||||||| ||||||| ||||||| ||||||| ||||||| |||||||  
 Db 27606 CGTTCGTCATTGCCTCGTCACATCAATGCAAAGGTCCTGATTTTGTTCAGCAAACAC 27547  
 Qy 3106 AGTGCAATGTTCTCAGAGTGACTTTCGAAATAAATTGGGCCCCAAGAGCTTTAACTCGGTC 3165

|    |       |  |       |
|----|-------|--|-------|
| Db | 27546 | AGTGCAATGTTCTCAGAGTGACTTTAGAAATAAATTGGGCCCAAGAGCTTTAACTCGGTC   | 27487 |
| Qy | 3166  | TTAAAATATGCCCAAATTTTTACTTTGTTTTCTTTTAAATAGGCTGGGCCACATGTTGGA   | 3225  |
| Db | 27486 | TTAAAATATGCCCAAATTTTTACTTTTTTTTCTTTTAGTAAACTGGGCCACATGTTGGA    | 27427 |
| Qy | 3226  | AATAAGCTAGTAATGTTGTTTTCTGTCAATATTGAATGTGATGGTACAGTAAACCAAAAC   | 3285  |
| Db | 27426 | AATAAGCTAGTAATGTTGTTTTCTGTCAATATCGAATGTGATGGTGCAGTAAACCAAAAC   | 27367 |
| Qy | 3286  | CCAACAATGTGGCCAGAAAGAAAGAGCAATAATAATTAATTCACACACCATATGGATTCT   | 3345  |
| Db | 27366 | CCAACAATGTGGCCAGAAAGAAAGAGCAATAATGATTAATTCACATGCCATGTGGATTCT   | 27307 |
| Qy | 3346  | ATTTATAAATCACCCACAAACTTGTTCTTTAATTTTCATCCCAATCACTTTTTTCAGAGGCC | 3405  |
| Db | 27306 | ATTTATAAATCACCCACAAACTTGTTTTTTAATTTTCATCCCAATCATTTTTTCAGAGGCC  | 27247 |
| Qy | 3406  | TGTTATCATAGAAGTCATTTTAGACTCTCAATTTTAAATTAATTTGAATCACTAATATT    | 3465  |
| Db | 27246 | TGTTATCATAGAAGACATTTTAGACTTGCAATTTTAAATTAACCTTGAATCACTAATATT   | 27187 |
| Qy | 3466  | TTCACAGTTTATTAATATA-TTTAATTTCTATTTAAATTTTAGATTATTTTTATTACCAT   | 3524  |
| Db | 27186 | TTCACAGTTTATTAATATATTTTTATTCTATTTAAATTTTAGATTATTTTTATTACCAT    | 27127 |
| Qy | 3525  | GTAAGTGAATTTTACATCCTGATACCCTTTCCTTCTCCATGTCAGTATCATGTTCTCTAA   | 3584  |
| Db | 27126 | GTAAGTGAATTTTATATCCTGATACCCTTTCCTTCTCCATGTCAGTATCATGTTCTGTAA   | 27067 |
| Qy | 3585  | TTATCTTGCCAAATTTTGAACTACACACAAAAAGCATACTTGCATTATTTATAATAAAA    | 3644  |
| Db | 27066 | TTATCTTACCAAATTTTGAACTGCACACAAAAAGCATACTTGCATTATTTATAATAAAA    | 27007 |
| Qy | 3645  | TTGCATTTCAGTGGCTTTTTTAAAAAAATGTTTGATTCAAACTTTAACATACTGATAAGT   | 3704  |
| Db | 27006 | TTGCATTTCAGTGGCTTTTT-AAAAAATGTTTGATTCAAAATTTAACATACTGATAAGT    | 26948 |
| Qy | 3705  | AAGAAACAATTATAATTTCTTTACATACTCAAACCAAGATAGAAAAAGGTGCTATCGTT    | 3764  |
| Db | 26947 | AAGAAACAATAATAATTTCTTTACATACTCAAACCAAGATAGAAAAAGGTGCTATTATT    | 26888 |
| Qy | 3765  | CAACTTCAAACATGTTTCCTAGTATTAAGGACTTTAATATAGCAACAGACAAAATTATT    | 3824  |
| Db | 26887 | TAACCTCAAACATGTTTCCTAGTATTAAGAACTTTAATATAGCAACAGACAAAATTATT    | 26828 |
| Qy | 3825  | GTTAACATGGATGTTACAGCTCAAAGATTTATAAAAGATTTTAACCTATTTTCTCCCTT    | 3884  |
| Db | 26827 | GTTAACATGAATGTTACAGCTCAGAAGATTTATAAAAGATTTTAACCTATTTTCTCCCTT   | 26768 |
| Qy | 3885  | ATTATCCACTGCTAATGTGGATGTATGTTCAAACACCTTTTAGTATTGATAGCTTACATA   | 3944  |
| Db | 26767 | ATTATCCACTGCTAATGTGGATATATGTTCAAACACCTTTTAGTATTGATAGCTTACATA   | 26708 |
| Qy | 3945  | TGGCCAAAAGGAATACAGTTTATAGCAAACATGGGTATGCTGTAGCTAACTTTATAAAAG   | 4004  |

|    |       |  |       |
|----|-------|--|-------|
| Db | 26707 | TGGCCAAAGGAATACAGTTTATAGTGAAACATGGGTATACTGTAGCTAACTTTATAAAAC   | 26648 |
| Qy | 4005  | TGTAATATAACAATGTAAAAAATTATATATCTGGGAGGATTTTTTGGTTGCCTAAAGTGG   | 4064  |
| Db | 26647 | TGTAATATAACAATGTAAAAAATTATATACCTGGGGGGATTTTTTGGTTGCTTAAAGTGG   | 26588 |
| Qy | 4065  | CTATAGTTACTGA-TTTTTTATTATGTAAGCAAAACCAATAAA----AATTTAAGTTTTT   | 4119  |
| Db | 26587 | CTATAGTCACTGATTTTTTTTATTATGTAAGCAAAACCAATAAACTTTAGGTTGTGTTTTT  | 26528 |
| Qy | 4120  | TTAACAACCTACCTTATTTTTTCACTGTACAGACACTAATTCATTAAATACTAATTGATTGT | 4179  |
| Db | 26527 | TTAACAACCTAGCTTATTTTTTCATTGTACAGGCACTAATTCATTAAATACTAATTGACTGT | 26468 |
| Qy | 4180  | TTAAAAGAAATATAAATGTGACAAGTGGACATTATTTATGTTAAATATACAATTATCAAG   | 4239  |
| Db | 26467 | TTAAAGGAAATATAAATGTGACAAGTGGACACTATTTATGTTAAATATACAATCATCAAG   | 26408 |
| Qy | 4240  | CAAGTATGAAGTTATTCAATTAAAAATGCCACATTCTGGTCTCTGG                 | 4285  |
| Db | 26407 | GAAGTATGAAGTTATTCAATTAAAAATGCCACATTCTGGTCTCTGG                 | 26362 |



JOURNAL Submitted (19-SEP-2002) NIH Intramural Sequencing Center, 8717  
Grovemont Circle, Gaithersburg, MD 20877, USA  
COMMENT On Sep 19, 2002 this sequence version replaced gi:21955004.

----- Genome Center  
Center: NIH Intramural Sequencing Center  
Center code: NISC  
Web site: <http://www.nisc.nih.gov>  
Contact: [nisc\\_zoo@nhgri.nih.gov](mailto:nisc_zoo@nhgri.nih.gov)

----- Project Information  
Center project name: deg  
Center clone name: 240D13

The sequence data in this record represents an 'enhanced' version of a Phase 2 submission. Specifically, the indicated order and orientation of each sequence contig has been established using one or more of the following: read-pair data from individual subclones, overlaps with neighboring clones, alignment with available reference sequence (e.g., human), and/or confirmation by PCR testing. In addition, the sequence assembly is based on at least 8X average coverage in Q20 bases and has been reviewed to rule out gross misassemblies, the low-quality ends of sequence contigs have been trimmed away, and each base is associated with a Phrap-derived quality score.

----- Summary Statistics  
Sequencing vector: plasmid; n/a; 100% of reads  
Chemistry: Dye-terminator Big Dye; 100% of reads  
Assembly program: Phrap; version 0.990319  
Consensus quality: 184076 bases at least Q40  
Consensus quality: 185363 bases at least Q30  
Consensus quality: 185733 bases at least Q20  
Insert size: 152000; agarose-fp  
Insert size: 185870; sum-of-contigs  
Quality coverage: 7.20x in Q20 bases; agarose-fp  
Quality coverage: 5.89x in Q20 bases; sum-of-contigs

-----  
\* NOTE: This is a 'working draft' sequence. It currently  
\* consists of 1 contigs. Gaps between the contigs  
\* are represented as runs of N. The order of the pieces  
\* is believed to be correct as given, however the sizes  
\* of the gaps between them are based on estimates that have  
\* provided by the submitter.  
\* This sequence will be replaced  
\* by the finished sequence as soon as it is available and  
\* the accession number will be preserved.  
\* 1 185870: contig of 185870 bp in length.

FEATURES  
source Location/Qualifiers  
1. .185870  
/organism="Papio anubis"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9555"  
/clone="RP41-240D13"  
/clone\_lib="RP41"  
misc\_feature 1. .185870  
/note="assembly\_fragment  
clone\_end:T7  
vector\_side:left

missing approximately 55 bases, including Sp6 clone end,  
on 3' end of insert"  
misc\_feature 121812. .185870  
/note="clone overlaps with GenBank Accession Number  
AC130785 clone RP41-325P5 (center project name deh)"

ORIGIN

Query Match 59.3%; Score 2550; DB 2; Length 185870;  
Best Local Similarity 94.8%; Pred. No. 0;  
Matches 2717; Conservative 0; Mismatches 130; Indels 19; Gaps 7;

Qy 1430 AGTCATGCTTATGCTGCTGGTGCCAGTCATTTGAAGAAAAACAGTCCTTGGAGGAAAAGC 1489  
|||||  
Db 151685 AGTCATGCTTATGCTGCTGGTGCCAGTCATTTGAAGAAAAACAGTCCTTGGAGGAAAAGC  
151626

Qy 1490 AGTCGTGCTTAAAGTTCAAAGCTAATGATCACGGATATGACAACTTCCGTTCCAGTAATA 1549  
|||||  
Db 151625 AGTCGTGCTTAAAGTTCAAAGCTAATGATCACGGATATGACAACTTCCGTTCCAGTAATA  
151566

Qy 1550 AATACAGCTCATCTTGAAAGAAGAACTATTCAGTGTATTTCAATTTCTTTATATTGGACC 1609  
|||||  
Db 151565 AATACAGCTCATCTTGAAAGAAGAACTATTCAGTGTATTTCAATTTCTTTATATTGGACC  
151506

Qy 1610 GAAGTCATTAAAACAAAATGAAACATTTGCCAAAACAAAACAAAAACTATGTATTTGCA 1669  
|||||  
Db 151505 GAAGTCATTAAAACAAAATGAAACATTTGTCAAACAAAACAAAAACTATGTATTTGCA  
151446

Qy 1670 CAGCACACTATTAATAATTAAGTGTAAATTATTTAACACTCACAGCTACATATGACATT 1729  
|||||  
Db 151445 CAGCACACTATTAATAATTAAGTGTAAATTATTTAACACTCATAGCTACATATGACATT  
151386

Qy 1730 TTATGAGCTGTTTACGGCATGGAAAGAAAATCAGTGGAATTAAGAAAGCCTCGTCGTGA 1789  
|||||  
Db 151385 TTATGAGCTGTTTACAGCATGGAAAGAAAATCAGTGGAATTAAGAAAGCCTCATTGTGA  
151326

Qy 1790 AAGCACTTAATTTTTTACAGTTAGCACTTCAACATAGCTCTTAACAACTTCCAGGATATT 1849  
|||||  
Db 151325 AAGCACTTACTTTTTTATGGTTAGCACTTCAACATAGCTCTTAATAACTTCCAGGATATT  
151266

Qy 1850 CACACAACACTTAGGCTTAAAAATGAGCTCACTCAGAATTTCTATTCTTTCTAAAAAGAG 1909  
|||||  
Db 151265 CACACAACCCTTAGGCTTAAAAATGAGCTCACTCGGAATTTCTATT-----TAAGAG  
151214

Qy 1910 ATTTATTTTAAATCAATGGGACTCTGATATAAAGGAAGAATAAGTCACTGTAAACAGA 1969  
|||||  
Db 151213 ATTTATTTTAAATCAATGTGAATCTGATACAAAGGAAGAGTAAGTCACTGTAAACAGA  
151154

Qy 1970 ACTTTTAAATGAAGCTTAAATTACTCAATTTAAATTTTAAATCCTTTAAACAACTTT 2029

|        |        |   |      |
|--------|--------|---|------|
| Db     | 151153 | ACTTTTAAATGAAGCTTAAATTACCCAATTTGAAATTTTAAAATCCTTTAAAAGAACTTT  |      |
| 151094 |        |   |      |
| Qy     | 2030   | TCAATTAATATTATCACACT-ATTATCAGATTGTAATTAGATGCAAATGAGAGAGCAGTT  | 2088 |
| Db     | 151093 | TTAATTAATATTTTCACACTGCTGATCAGACTGTAATTAGATGCAAATGAGAGAGTAGTT  |      |
| 151034 |        |   |      |
| Qy     | 2089   | TAGTTGTTGCATTTTTTCGGACACTGGAAACATTTAAATGATCAGGAGGGAGTAACAGAAA | 2148 |
| Db     | 151033 | TAGTTGCTGTATTTTTTGGACACTAGAAACATTTAAATGATCAGGAGGGAGTAACTGAAA  |      |
| 150974 |        |   |      |
| Qy     | 2149   | GAGCAAGGCTGTTTTTGAAAATCATTACA---CTTTCACTAGAAGCCCAAACCTCAGCAT  | 2205 |
| Db     | 150973 | GAACAAGGCTGTTTTTGAAAATCATTACACTCCTTTCACTAGAAGCCCAAACCTCAGCAT  |      |
| 150914 |        |   |      |
| Qy     | 2206   | TCTGCAATATGTAACCAACATGTCACAAACAAGCAGCATGTAACAGACTGGCACATGTGC  | 2265 |
| Db     | 150913 | TCTGCAATATGTAACCAACATGTTACAAACAAGCAGCATGTAACAACTGGCACATGTGT   |      |
| 150854 |        |   |      |
| Qy     | 2266   | CAGCTGAATTTAAATATAATACTTTTAAAAAGAAAATTATTACATCCTTTACATTCACT   | 2325 |
| Db     | 150853 | CAGCCAAATCTAAATATAATACTTTTAAAAAGAAAATTATTACACCCTTTACATTGAGA   |      |
| 150794 |        |   |      |
| Qy     | 2326   | TAAGATCAAACCTCACAAAGAGAAATAGAATGTTTGAAAGGCTATCCCAAAGACTTTTT   | 2385 |
| Db     | 150793 | TAAGATCAAACCTCACAAAGAGAAATAGAATGTTTGAAAGGCTGCCCAAAGACTTCTT    |      |
| 150734 |        |   |      |
| Qy     | 2386   | TGAATCTGTCATTACATACCCTGTGAAGACAATACTATCTACAATTTTTTCAGGATTAT   | 2445 |
| Db     | 150733 | TGAATCTGCCATTACACAGCCTGTGAAGAAAATACTATCTACAAATTTTTTCAGGATTAT  |      |
| 150674 |        |   |      |
| Qy     | 2446   | TAAATCTTCTTTTTTCACTATCGTAGCTTAAACTCTGTTTGGTTTTGTCATCTGTAAAT   | 2505 |
| Db     | 150673 | TAAATCTTCTTCTTTCACTATTGTAGCTTAAACTCTGTTTGGTTTTGTCATCCGTAAAT   |      |
| 150614 |        |   |      |
| Qy     | 2506   | ACTTACCTACATACACTGCATGTAGATGATTAAATGAGGGCAGGCCCTGTGCTCATAGCT  | 2565 |
| Db     | 150613 | ACTTAGCTACATACACTGCATGTAGACGATTAAACGAGGGCGGGCCCTGTGTTTCATAGTT |      |
| 150554 |        |   |      |
| Qy     | 2566   | TTACGATGGAGAGATGCCAGTGACCTCATAATAAGACTGTGAACTGCCTGGTGCAGTGT   | 2625 |
| Db     | 150553 | TTACAATGGAGAGATGCCAGTGACCTCATAATAGAGACTGTGAACTGCCTGGTGCGATGT  |      |
| 150494 |        |   |      |
| Qy     | 2626   | CCACATGACAAAGGGGCAGGTAGCACCCCTCTCTACCCATGCTGTGGTTAAATGGTTTC   | 2685 |
|        |        |   |      |

Db 150493 CCACATGACAAGGGGGCAGGTAGCACCCCTCTCTCACCCATGCTGTAGTTAAATGGTTTC  
 150434

Qy 2686 TAGCATATGTATAATGCTATAGTTAAAATACTATTTTTCAAATCATACAGATTAGTACA 2745  
 |||

Db 150433 TAGCATATGTATAATGCTGTAGTTAAAACACTGTTTGC AAAATCATACAGATTAGTACA  
 150374

Qy 2746 TTTAACAGCTACCTGTAAAGCTTATTACTAATTTTTGTATTATTTTTGTAAATAGCCAAT 2805  
 |||

Db 150373 TTTAATGGCTACCTGTAAAGCTTATTACTAGTTTTGTATTATTTTTGTAAATAGCCAAT  
 150314

Qy 2806 AGAAAAGTTTGCTTGACATGGTGCTTTTCTTTCATCTAGAGGCAAACTGCTTTTTGAGA 2865  
 |||

Db 150313 AGAAAAGTTTGCTTGACGTGGTGCTTTTCTTTCACCTAGAGGCAAACTGCTTTTTGAGA  
 150254

Qy 2866 CCGTAAGAACCTCTTAGCTTTGTGCGTTCCTGCCTAATTTTTATATCTTCTAAGCAAAGT 2925  
 |

Db 150253 CTGTAAGAACCTCTTAGCTTTGTGCGTTCCTGCCTAATTTTTAAATCTTCTAAGCAAAGT  
 150194

Qy 2926 GCCTTAGGATAGCTTGGGATGAGATGTGTGTGAAAGTATGTACAAGAGAAAACGGAAGAG 2985  
 |||

Db 150193 GCCTTAGAATAGCTTGGGATGAGATGTGTGTGAAAGTATGTACAAGAGAAAACGGAAGAG  
 150134

Qy 2986 AGAGGAAATGAGGTGGGGTTGGAGGAAACCCATGGGGACAGATCCCATTCTTAGCCTAA 3045  
 |||

Db 150133 AGAGGAAATGAGGTGGGGTGAGAGGAAACTCATGGGGACAGATCCCATTCTTAGCCTAA  
 150074

Qy 3046 CGTTCGTCATTGCCTCGTCACATCAATGCAAAGGTCCTGATTTTGTTCAGCAAACAC 3105  
 |||

Db 150073 CGTTCGTCATTGCCTCGTCACATCAATGCAAAGGTCCTGATTTTGTTCAGCAAACAC  
 150014

Qy 3106 AGTGCAATGTTCTCAGAGTGACTTTCGAAATAAATTGGGCCCAAGAGCTTTAACTCGGTC 3165  
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Db 150013 AGTGCAATGTTCTCAGAGTGACTTTAGAAATAAATTGGGCCCAAGAGCTTTAACTCGGTC  
 149954

Qy 3166 TTAAATATGCCCAAATTTTTACTTTGTTTTCTTTTAAATAGGCTGGGCCACATGTTGGA 3225  
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Db 149953 TTAAATATGCCCAAATTTTTACTTTTTTTCTTTTAGTAAACTGGGCCACATGTTGGA  
 149894

Qy 3226 AATAAGCTAGTAATGTTGTTTTCTGTCAATATTGAATGTGATGGTACAGTAAACCAAAC 3285  
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Db 149893 AATAAGCTAGTAATGTTGTTTTCTGTCAATATCGAATGTGATGGTGCAGTAAACCAAAC  
 149834

Qy 3286 CCAACAATGTGGCCAGAAAGAAAGAGCAATAATAATTAATTCACACACCATATGGATTCT 3345  
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Db 149833 CCAACAATGTGGCCAGAAAGAAAGAGCAATAATGATTAATTCACATGCCATGTGGATTCT  
 149774

Qy 3346 ATTTATAAATCACCCACAACTTGTTCCTTTAATTTTCATCCCAATCACTTTTTTCAGAGGCC 3405  
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 Db 149773 ATTTATAAATCACCCACAACTTGTTCCTTTAATTTTCATCCCAATCACTTTTTTCAGAGGCC  
 149714

Qy 3406 TGTTATCATAGAAGTCATTTTAGACTCTCAATTTTAAATTAATTTTGAATCACTAATATT 3465  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 149713 TGTTATCATAGAAGACATTTTAGACTTGCAATTTTAAATTAATTTTGAATCACTAATATT  
 149654

Qy 3466 TTCACAGTTTATTAATATA-TTTAATTTCTATTTAAATTTTAGATTATTTTATTACCAT 3524  
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 Db 149653 TTCACAGTTTATTAATATATTTTATTTCTATTTAAATTTTAGATTATTTTATTACCAT  
 149594

Qy 3525 GTACTGAATTTTTACATCCTGATACCCCTTTCCTTCTCCATGTCAGTATCATGTTCTCTAA 3584  
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 Db 149593 GTACTGAATTTTTATATCCTGATACCCCTTTCCTTCTCCATGTCAGTATCATGTTCTGTAA  
 149534

Qy 3585 TTATCTTGCCAAATTTTGAACTACACACAAAAAGCATACTTGCATTATTTATAATAAAAA 3644  
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 Db 149533 TTATCTTACCAAATTTTGAACTGCACACAAAAAGCATACTTGCATTATTTATAATAAAAA  
 149474

Qy 3645 TTGCATTCACTGGCTTTTTTAAAAAATGTTTGATTCAAACTTTAACATACTGATAAGT 3704  
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 Db 149473 TTGCATTCACTGGCTTTTT-AAAAAATGTTTGATTCAAACTTTAACATACTGATAAGT  
 149415

Qy 3705 AAGAAACAATTATAATTTCTTTACATACTCAAACCAAGATAGAAAAAGGTGCTATCGTT 3764  
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 Db 149414 AAGAAACAATAATAATTTCTTTACATACTCAAACCAAGATAGAAAAAGGTGCTATTATT  
 149355

Qy 3765 CAACTTCAAACATGTTTCCTAGTATTAAGGACTTTAATATAGCAACAGACAAAATTATT 3824  
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 Db 149354 TAACTTCAAACATGTTTCCTAGTATTAAGAATTTAATATAGCAACAGACAAAATTATT  
 149295

Qy 3825 GTTAACATGGATGTTACAGCTCAAAGATTTATAAAAGATTTTAACTATTTTCTCCCTT 3884  
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 Db 149294 GTTAACATGAATGTTACAGCTCAGAAGATTTATAAAAGATTTTAACTATTTTCTCCCTT  
 149235

Qy 3885 ATTATCCACTGCTAATGTGGATGTATGTTCAAACACCTTTTAGTATTGATAGCTTACATA 3944  
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 Db 149234 ATTATCCACTGCTAATGTGGATATATGTTCAAACACCTTTTAGTATTGATAGCTTACATA  
 149175

Qy 3945 TGGCCAAAGGAATACAGTTTATAGCAAAACATGGGTATGCTGTAGCTAACTTTATAAAAG 4004  
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 Db 149174 TGGCCAAAGGAATACAGTTTATAGTGAAACATGGGTATACTGTAGCTAACTTTATAAAAC  
 149115

Qy 4005 TGTAATATAACAATGTAAAAAATTATATATCTGGGAGGATTTTTTGGTTGCCTAAAGTGG 4064

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|||||
Db 149114 TGTAATATAACAATGTAAAAAATTATATACCTGGGGGGATTTTTTGGTTGCTTAAAGTGG
149055

Qy 4065 CTATAGTTACTGA-TTTTTTATTATGTAAGCAAAACCAATAAA----AATTTAAGTTTTT 4119
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Db 149054 CTATAGTCACTGATTTTTTTATTATGTAAGCAAAACCAATAAACTTTAGGTTGTGTTTTT
148995

Qy 4120 TTAACAACCTACCTTATTTTTTCACTGTACAGACACTAATTCATTAAATACTAATTGATTGT 4179
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Db 148994 TTAACAACCTAGCTTATTTTTTCATTGTACAGGCACTAATTCATTAAATACTAATTGACTGT
148935

Qy 4180 TTAAGGAAATATAAAATGTGACAAGTGGACATTATTTATGTTAAATATACAATTATCAAG 4239
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Db 148934 TTAAGGAAATATAAAATGTGACAAGTGGACACTATTTATGTTAAATATACAATCATCAAG
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Qy 4240 CAAGTATGAAGTTATTCAATTAAAATGCCACATTTCTGGTCTCTGG 4285
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Db 148874 GAAGTATGAAGTTATTCAATTAAAATGCCACATTTCTGGTCTCTGG 148829

```

# RESULT 13

AR165435

LOCUS AR165435 1873 bp DNA linear PAT 17-OCT-2001

DEFINITION Sequence 13 from patent US 6280931.

ACCESSION AR165435

VERSION AR165435.1 GI:16240327

KEYWORDS .

SOURCE Unknown.

ORGANISM Unknown.

Unclassified.

REFERENCE 1 (bases 1 to 1873)

AUTHORS Sakamoto,A. and Hanaoka,F.

TITLE Method for specifically amplifying a dystroglycan,  
.alpha.-sarcoglycan, or endothelin Breceptor cDNA of an extremely  
small

JOURNAL Patent: US 6280931-A 13 28-AUG-2001;

FEATURES Location/Qualifiers

source 1. .1873

/organism="unknown"

/mol\_type="unassigned DNA"

## ORIGIN

Query Match 39.3%; Score 1691.8; DB 6; Length 1873;  
Best Local Similarity 99.6%; Pred. No. 5.5e-293;  
Matches 1696; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

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Qy 178 TGAAACTTGGCTCTGAAACTGCGGAGCGGCCACCGGACGCCTTCTGGAGCAGGTAGCAGC 237
||

Db 171 TGTCTCTAGGCTCTGAAACTGCGGAGCGGCCACCGGACGCCTTCTGGAGCAGGTAGCAGC 230

Qy 238 ATGCAGCCGCCTCCAAGTCTGTGCGGACGCGCCCTGGTTGCGCTGGTTCTTGCCTGCGGC 297
|||||

Db 231 ATGCAGCCGCCTCCAAGTCTGTGCGGACGCGCCCTGGTTGCGCTGGTTCTTGCCTGCGGC 290

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|    |      |  |      |
|----|------|--|------|
| Qy | 298  | CTGTGCGGGATCTGGGGAGAGGAGAGAGGCTTCCCGCCTGACAGGGCCACTCCGCTTTTG   | 357  |
|    |      |  |      |
| Db | 291  | CTGTGCGGGATCTGGGGAGAGGAGAGAGGCTTCCCGCCTGACAGGGCCACTCCGCTTTTG   | 350  |
| Qy | 358  | CAAACCGCAGAGATAATGACGCCACCCACTAAGACCTTATGGCCCAAGGGTTCCAACGCC   | 417  |
|    |      |  |      |
| Db | 351  | CAAACCGCAGAGATAATGACGCCACCCACTAAGACCTTATGGCCCAAGGGTTCCAACGCC   | 410  |
| Qy | 418  | AGTCTGGCGCGGTTCGTTGGCACCTGCGGAGGTGCCTAAAGGAGACAGGACGGCAGGATCT  | 477  |
|    |      |  |      |
| Db | 411  | AGTCTGGCGCGGTTCGTTGGCACCTGCGGAGGTGCCTAAAGGAGACAGGACGGCAGGATCT  | 470  |
| Qy | 478  | CCGCCACGCACCATCTCCCCTCCCCGTGCCAAGGACCCATCGAGATCAAGGAGACTTTC    | 537  |
|    |      |  |      |
| Db | 471  | CCGCCACGCACCATCTCCCCTCCCCGTGCCAAGGACCCATCGAGATCAAGGAGACTTTC    | 530  |
| Qy | 538  | AAATACATCAACACGGTTGTGTCCTGCCTTGTGTTCTGTGCTGGGGATCATCGGGAACCTCC | 597  |
|    |      |  |      |
| Db | 531  | AAATACATCAACACGGTTGTGTCCTGCCTTGTGTTCTGTGCTGGGGATCATCGGGAACCTCC | 590  |
| Qy | 598  | ACACTTCTGAGAATTATCTACAAGAACAAGTGCATGCGAAACGGTCCCAATATCTTGATC   | 657  |
|    |      |  |      |
| Db | 591  | ACACTTCTGAGAATTATCTACAAGAACAAGTGCATGCGAAACGGTCCCAATATCTTGATC   | 650  |
| Qy | 658  | GCCAGCTTGGCTCTGGGAGACCTGCTGCACATCGTCATTGACATCCCTATCAATGTCTAC   | 717  |
|    |      |  |      |
| Db | 651  | GCCAGCTTGGCTCTGGGAGACCTGCTGCACATCGTCATTGACATCCCTATCAATGTCTAC   | 710  |
| Qy | 718  | AAGCTGCTGGCAGAGGACTGGCCATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTTCATA  | 777  |
|    |      |  |      |
| Db | 711  | AAGCTGCTGGCAGAGGACTGGCCATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTTCATA  | 770  |
| Qy | 778  | CAGAAAGCCTCCGTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATAT   | 837  |
|    |      |  |      |
| Db | 771  | CAGAAAGCCTCCGTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATAT   | 830  |
| Qy | 838  | CGAGCTGTTGCTTCTTGGAGTAGAATTAAAGGAATTGGGGTTCCAAAATGGACAGCAGTA   | 897  |
|    |      |  |      |
| Db | 831  | CGAGCTGTTGCTTCTTGGAGTAGAATTAAAGGAATTGGGGTTCCAAAATGGACAGCAGTA   | 890  |
| Qy | 898  | GAAATTGTTTTGATTTGGGTGGTCTCTGTGGTTCTGGCTGTCCCTGAAGCCATAGGTTTT   | 957  |
|    |      |  |      |
| Db | 891  | GAAATTGTTTTGATTTGGGTGGTCTCTGTGGTTCTGGCTGTCCCTGAAGCCATAGGTTTT   | 950  |
| Qy | 958  | GATATAATTACGATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTT   | 1017 |
|    |      |  |      |
| Db | 951  | GATATAATTACGATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTT   | 1010 |
| Qy | 1018 | CAGAAGACAGCTTTCATGCAGTTTTACAAGACAGCAAAAGATTGGTGGCTGTTTCAGTTTC  | 1077 |
|    |      |  |      |
| Db | 1011 | CAGAAGACAGCTTTCATGCAGTTTTACAAGACAGCAAAAGATTGGTGGCTATTTCAGTTTC  | 1070 |
| Qy | 1078 | TATTTCTGCTTGCCATTGGCCATCACTGCATTTTTTTTATACATAATGACCTGTGAAATG   | 1137 |
|    |      |  |      |
| Db | 1071 | TATTTCTGCTTGCCATTGGCCATCACTGCATTTTTTTTATACATAATGACCTGTGAAATG   | 1130 |

Qy 1138 TTGAGAAAGAAAAGTGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAA 1197  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 1131 TTGAGAAAGAAAAGTGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAA 1190  
 Qy 1198 GTGGCCAAAACCGTCTTTTGCCTGGTCCTTGTCTTTGCCCTCTGCTGGCTTCCCCTTCAC 1257  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 1191 GTGGCCAAAACCGTCTTTTGCCTGGTCCTTGTCTTTGCCCTCTGCTGGCTTCCCCTTCAC 1250  
 Qy 1258 CTCAGCAGGATTCTGAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGAACTT 1317  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 1251 CTCAGCAGGATTCTGAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGAACTT 1310  
 Qy 1318 TTGAGCTTTCTGTTGGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCCTGC 1377  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 1311 TTGAGCTTTCTGTTGGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCCTGC 1370  
 Qy 1378 ATTAACCCAATTGCTCTGTATTTGGTGAGCAAAAGATTCAAAAAGCTTTAAGTCATGC 1437  
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 Db 1371 ATTAACCCAATTGCTCTGTATTTGGTGAGCAAAAGATTCAAAAAGCTTTAAGTCATGC 1430  
 Qy 1438 TTATGCTGCTGGTGCCAGTCATTTGAAGAAAAACAGTCCTTGGAGGAAAAGCAGTCGTGC 1497  
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 Db 1431 TTATGCTGCTGGTGCCAGTCATTTGAAGAAAAACAGTCCTTGGAGGAAAAGCAGTCGTGC 1490  
 Qy 1498 TTAAAGTTCAAAGCTAATGATCACGGATATGACAACTTCCGTTCCAGTAATAAAATACAGC 1557  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 1491 TTAAAGTTCAAAGCTAATGATCACGGATATGACAACTTCCGTTCCAGTAATAAAATACAGC 1550  
 Qy 1558 TCATCTTGAAAGAAGAACTATTCACTGTATTTCAATTTCTTTATATTGGACCGAAGTCAT 1617  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 1551 TCATCTTGAAAGAAGAACTATTCACTGTATTTCAATTTCTTTATATTGGACCGAAGTCAT 1610  
 Qy 1618 TAAAACAAAATGAAACATTTGCCAAAACAAAACAAAAAACTATGTATTTGCACAGCACAC 1677  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 1611 TAAAACAAAATGAAACATTTGCCAAAACAAAACAAAAAACTATGTATTTGCACAGCACAC 1670  
 Qy 1678 TATTAAATATTAAGTGAATTATTTTAACACTCACAGCTACATATGACATTTTATGAGC 1737  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 1671 TATTAAATATTAAGTGAATTATTTTAACACTCACAGCTACATATGACATTTTATGAGC 1730  
 Qy 1738 TGTTTACGGCATGGAAAGAAAATCAGTGGGAATTAAGAAAGCCTCGTCGTGAAAGCACTT 1797  
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 Db 1731 TGTTTACGGCATGGAAAGAAAATCAGTGGGAATTAAGAAAGCCTCGTCGTGAAAGCACTT 1790  
 Qy 1798 AATTTTTTTACAGTTAGCACTTCAACATAGCTCTTAACAACTTCCAGGATATTCACACAAC 1857  
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 Db 1791 AATTTTTTTACAGTTAGCACTTCAACATAGCTCTTAACAACTTCCAGGATATTCACACAAC 1850  
 Qy 1858 ACTTAGGCTTAAAAATGAGCTCA 1880  
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 Db 1851 ACTTAGGCTTAAAAATGAGCTCA 1873

RESULT 14

E15242

LOCUS E15242 1873 bp DNA linear PAT 28-JUL-1999  
 DEFINITION Human mRNA for endothelin B receptor, complete cds.





|    |      |  |      |
|----|------|--|------|
| Qy | 478  | CCGCCACGCACCATCTCCCCTCCCCCGTGCCAAGGACCCATCGAGATCAAGGAGACTTTC   | 537  |
|    |      |  |      |
| Db | 471  | CCGCCACGCACCATCTCCCCTCCCCCGTGCCAAGGACCCATCGAGATCAAGGAGACTTTC   | 530  |
| Qy | 538  | AAATACATCAACACGGTTGTGTCCTGCCTTGTGTTTCGTGCTGGGGATCATCGGGAACCTCC | 597  |
|    |      |  |      |
| Db | 531  | AAATACATCAACACGGTTGTGTCCTGCCTTGTGTTTCGTGCTGGGGATCATCGGGAACCTCC | 590  |
| Qy | 598  | ACACTTCTGAGAATTATCTACAAGAACAAGTGCATGCGAAACGGTCCCAATATCTTGATC   | 657  |
|    |      |  |      |
| Db | 591  | ACACTTCTGAGAATTATCTACAAGAACAAGTGCATGCGAAACGGTCCCAATATCTTGATC   | 650  |
| Qy | 658  | GCCAGCTTGGCTCTGGGAGACCTGCTGCACATCGTCATTGACATCCCTATCAATGTCTAC   | 717  |
|    |      |  |      |
| Db | 651  | GCCAGCTTGGCTCTGGGAGACCTGCTGCACATCGTCATTGACATCCCTATCAATGTCTAC   | 710  |
| Qy | 718  | AAGCTGCTGGCAGAGGACTGGCCATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTCATA   | 777  |
|    |      |  |      |
| Db | 711  | AAGCTGCTGGCAGAGGACTGGCCATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTCATA   | 770  |
| Qy | 778  | CAGAAAGCCTCCGTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATAT   | 837  |
|    |      |  |      |
| Db | 771  | CAGAAAGCCTCCGTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATAT   | 830  |
| Qy | 838  | CGAGCTGTTGCTTCTTGGAGTAGAATTAAAGGAATTGGGGTTCCAAAATGGACAGCAGTA   | 897  |
|    |      |  |      |
| Db | 831  | CGAGCTGTTGCTTCTTGGAGTAGAATTAAAGGAATTGGGGTTCCAAAATGGACAGCAGTA   | 890  |
| Qy | 898  | GAAATTGTTTTGATTTGGGTGGTCTCTGTGGTTCTGGCTGTCCCTGAAGCCATAGGTTTT   | 957  |
|    |      |  |      |
| Db | 891  | GAAATTGTTTTGATTTGGGTGGTCTCTGTGGTTCTGGCTGTCCCTGAAGCCATAGGTTTT   | 950  |
| Qy | 958  | GATATAATTACGATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTT   | 1017 |
|    |      |  |      |
| Db | 951  | GATATAATTACGATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTT   | 1010 |
| Qy | 1018 | CAGAAGACAGCTTTTCATGCAGTTTTACAAGACAGCAAAGATTGGTGGCTGTTTCAGTTTC  | 1077 |
|    |      |  |      |
| Db | 1011 | CAGAAGACAGCTTTTCATGCAGTTTTACAAGACAGCAAAGATTGGTGGCTATTTCAGTTTC  | 1070 |
| Qy | 1078 | TATTTCTGCTTGCCATTGGCCATCACTGCATTTTTTTATACACTAATGACCTGTGAAATG   | 1137 |
|    |      |  |      |
| Db | 1071 | TATTTCTGCTTGCCATTGGCCATCACTGCATTTTTTTATACACTAATGACCTGTGAAATG   | 1130 |
| Qy | 1138 | TTGAGAAAGAAAAGTGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAA   | 1197 |
|    |      |  |      |
| Db | 1131 | TTGAGAAAGAAAAGTGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAA   | 1190 |
| Qy | 1198 | GTGGCCAAAACCGTCTTTTGCCCTGGTCCTTGTCTTTGCCCTCTGCTGGCTTCCCCTTCAC  | 1257 |
|    |      |  |      |
| Db | 1191 | GTGGCCAAAACCGTCTTTTGCCCTGGTCCTTGTCTTTGCCCTCTGCTGGCTTCCCCTTCAC  | 1250 |
| Qy | 1258 | CTCAGCAGGATTCTGAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGAACTT   | 1317 |
|    |      |  |      |
| Db | 1251 | CTCAGCAGGATTCTGAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGAACTT   | 1310 |

QY 1318 TTGAGCTTTCTGTTGGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCCTGC 1377  
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 Db 1311 TTGAGCTTTCTGTTGGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCCTGC 1370  
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 QY 1378 ATTAACCCAATTGCTCTGTATTTGGTGAGCAAAAGATTCAAAAAGCTGCTTTAAGTCATGC 1437  
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 QY 1498 TTAAAGTTCAAAGCTAATGATCACGGATATGACAACTTCCGTTCCAGTAATAAATACAGC 1557  
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 Db 1491 TTAAAGTTCAAAGCTAATGATCACGGATATGACAACTTCCGTTCCAGTAATAAATACAGC 1550  
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 QY 1558 TCATCTTGAAAGAAGAACTATTCAGTGTATTTTCATTTTCTTTATATTGGACCGAAGTCAT 1617  
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 Db 1551 TCATCTTGAAAGAAGAACTATTCAGTGTATTTTCATTTTCTTTATATTGGACCGAAGTCAT 1610  
 |||  
 QY 1618 TAAACAAAAATGAAACATTTGCCAAAAACAAAAAACTATGTATTTGCACAGCACAC 1677  
 |||  
 Db 1611 TAAACAAAAATGAAACATTTGCCAAAAACAAAAAACTATGTATTTGCACAGCACAC 1670  
 |||  
 QY 1678 TATTAAATATTAAGTGTAATTATTTTAACACTCACAGCTACATATGACATTTTATGAGC 1737  
 |||  
 Db 1671 TATTAAATATTAAGTGTAATTATTTTAACACTCACAGCTACATATGACATTTTATGAGC 1730  
 |||  
 QY 1738 TGTTTACGGCATGGAAAGAAAATCAGTGGGAATTAAGAAAGCCTCGTCGTGAAAGCACTT 1797  
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 Db 1731 TGTTTACGGCATGGAAAGAAAATCAGTGGGAATTAAGAAAGCCTCGTCGTGAAAGCACTT 1790  
 |||  
 QY 1798 AATTTTTTACAGTTAGCACTTCAACATAGCTCTTAACAACCTCCAGGATATTCACACAAC 1857  
 |||  
 Db 1791 AATTTTTTACAGTTAGCACTTCAACATAGCTCTTAACAACCTCCAGGATATTCACACAAC 1850  
 |||  
 QY 1858 ACTTAGGCTTAAAAATGAGCTCA 1880  
 |||  
 Db 1851 ACTTAGGCTTAAAAATGAGCTCA 1873

RESULT 15

S44866

LOCUS S44866 1872 bp mRNA linear PRI 07-MAY-1993

DEFINITION ETB endothelin receptor [human, mRNA, 1872 nt].

ACCESSION S44866

VERSION S44866.1 GI:233233

KEYWORDS .

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 1872)

AUTHORS Sakamoto,A., Yanagisawa,M., Sakurai,T., Takuwa,Y., Yanagisawa,H.  
 and Masaki,T.

TITLE Cloning and functional expression of human cDNA for the ETB  
 endothelin receptor



|    |      |  |      |
|----|------|--|------|
| Qy | 538  | AAATACATCAACACGGTTGTGTCCTGCCTTGTGTTTCGTGCTGGGGATCATCGGGAACCTCC | 597  |
|    |      |  |      |
| Db | 531  | AAATACATCAACACGGTTGTGTCCTGCCTTGTGTTTCGTGCTGGGGATCATCGGGAACCTCC | 590  |
| Qy | 598  | AACTTCTGAGAATTATCTACAAGAACAAGTGCATGCGAAACGGTCCCAATATCTTGATC    | 657  |
|    |      |  |      |
| Db | 591  | AACTTCTGAGAATTATCTACAAGAACAAGTGCATGCGAAACGGTCCCAATATCTTGATC    | 650  |
| Qy | 658  | GCCAGCTTGGCTCTGGGAGACCTGCTGCACATCGTCATTGACATCCCTATCAATGTCTAC   | 717  |
|    |      |  |      |
| Db | 651  | GCCAGCTTGGCTCTGGGAGACCTGCTGCACATCGTCATTGACATCCCTATCAATGTCTAC   | 710  |
| Qy | 718  | AAGCTGCTGGCAGAGGACTGGCCATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTCATA   | 777  |
|    |      |  |      |
| Db | 711  | AAGCTGCTGGCAGAGGACTGGCCATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTCATA   | 770  |
| Qy | 778  | CAGAAAGCCTCCGTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATAT   | 837  |
|    |      |  |      |
| Db | 771  | CAGAAAGCCTCCGTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATAT   | 830  |
| Qy | 838  | CGAGCTGTTGCTTCTTGGAGTAGAATTAAGGAATTGGGGTTCCAAAATGGACAGCAGTA    | 897  |
|    |      |  |      |
| Db | 831  | CGAGCTGTTGCTTCTTGGAGTAGAATTAAGGAATTGGGGTTCCAAAATGGACAGCAGTA    | 890  |
| Qy | 898  | GAAATTGTTTTGATTTGGGTGGTCTCTGTGGTTCTGGCTGTCCCTGAAGCCATAGGTTTT   | 957  |
|    |      |  |      |
| Db | 891  | GAAATTGTTTTGATTTGGGTGGTCTCTGTGGTTCTGGCTGTCCCTGAAGCCATAGGTTTT   | 950  |
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| Db | 951  | GATATAATTACGATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTT   | 1010 |
| Qy | 1018 | CAGAAGACAGCTTTCATGCAGTTTTACAAGACAGCAAAGATTGGTGGCTGTTTCAGTTTC   | 1077 |
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| Qy | 1078 | TATTTCTGCTTGCCATTGGCCATCACTGCATTTTTTTTATACACTAATGACCTGTGAAATG  | 1137 |
|    |      |  |      |
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| Qy | 1138 | TTGAGAAAGAAAAGTGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAA   | 1197 |
|    |      |  |      |
| Db | 1131 | TTGAGAAAGAAAAGTGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAA   | 1190 |
| Qy | 1198 | GTGGCCAAAACCGTCTTTTGCCTGGTCTTGTCTTTGCCCTCTGCTGGCTTCCCCTTCAC    | 1257 |
|    |      |  |      |
| Db | 1191 | GTGGCCAAAACCGTCTTTTGCCTGGTCTTGTCTTTGCCCTCTGCTGGCTTCCCCTTCAC    | 1250 |
| Qy | 1258 | CTCAGCAGGATTCTGAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGAACTT   | 1317 |
|    |      |  |      |
| Db | 1251 | CTCAGCAGGATTCTGAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGAACTT   | 1310 |
| Qy | 1318 | TTGAGCTTTCTGTTGGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCCTGC   | 1377 |
|    |      |  |      |
| Db | 1311 | TTGAGCTTTCTGTTGGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCCTGC   | 1370 |

|    |      |   |      |
|----|------|---|------|
| Qy | 1378 | ATTAACCCAATTGCTCTGTATTTGGTGAGCAAAAGATTCAAAAAGCTGCTTTAAGTCATGC | 1437 |
|    |      |   |      |
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| Qy | 1438 | TTATGCTGCTGGTGCCAGTCATTTGAAGAAAAACAGTCCTTGAGGAAAAGCAGTCGTGC   | 1497 |
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| Db | 1431 | TTATGCTGCTGGTGCCAGTCATTTGAAGAAAAACAGTCCTTGAGGAAAAGCAGTCGTGC   | 1490 |
| Qy | 1498 | TTAAAGTTCAAAGCTAATGATCACGGATATGACAACTTCCGTTCCAGTAATAAAATACAGC | 1557 |
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| Db | 1551 | TCATCTTGAAAGAAGAACTATTCACGTGATTTTCAATTTCTTTATATTGGACCGAAGTCAT | 1610 |
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|    |      |   |      |
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| Qy | 1678 | TATTAATAATTAAGTGTAATTATTTTAACACTCACAGCTACATATGACATTTTATGAGC   | 1737 |
|    |      |   |      |
| Db | 1671 | TATTAATAATTAAGTGTAATTATTTTAACACTCACAGCTACATATGACATTTTATGAGC   | 1730 |
| Qy | 1738 | TGTTTACGGCATGGAAAGAAAATCAGTGGAATTAAGAAAGCCTCGTCGTGAAAGCACTT   | 1797 |
|    |      |   |      |
| Db | 1731 | TGTTTACGGCATGGAAAGAAAATCAGTGGAATTAAGAAAGCCTCGTCGTGAAAGCACTT   | 1790 |
| Qy | 1798 | AATTTTTTACAGTTAGCACTTCAACATAGCTCTTAACAACTTCCAGGATATTCACACAAC  | 1857 |
|    |      |   |      |
| Db | 1791 | AATTTTTTACAGTTAGCACTTCAACATAGCTCTTAACAACTTCCAGGATATTCACACAAC  | 1850 |
| Qy | 1858 | ACTTAGGCTTAAAAATGAGCTC  | 1879 |
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| Db | 1851 | ACTTAGGCTTAAAAATGAGCTC  | 1872 |

Search completed: May 14, 2004, 10:14:31  
 Job time : 16263.7 secs

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: May 13, 2004, 23:15:48 ; Search time 1503.76 Seconds  
(without alignments)  
12150.511 Million cell updates/sec

Title: US-09-931-157-2  
Perfect score: 4301  
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Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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1: geneseqn1980s:\*  
2: geneseqn1990s:\*  
3: geneseqn2000s:\*  
4: geneseqn2001as:\*  
5: geneseqn2001bs:\*  
6: geneseqn2002s:\*  
7: geneseqn2003as:\*  
8: geneseqn2003bs:\*  
9: geneseqn2003cs:\*  
10: geneseqn2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score  | Query Match | Length | DB | ID       | Description        |
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| 2          | 4284.4 | 99.6        | 4286   | 3  | AAA35162 | Aaa35162 Human ade |
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| 4          | 4284.4 | 99.6        | 4286   | 6  | ABV94186 | Abv94186 Breast ca |
| 5          | 4284.4 | 99.6        | 4286   | 7  | ABZ96978 | Abz96978 Human nuc |
| 6          | 4284.4 | 99.6        | 4286   | 7  | ACC72646 | Acc72646 Human end |
| 7          | 4284.4 | 99.6        | 4286   | 7  | ABZ42661 | Abz42661 Human end |

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|   | 13 | 4202.4 | 97.7 | 4305   | 8 | ACH03911 |
|   | 14 | 2857   | 66.4 | 2972   | 6 | ABK94410 |
| c | 15 | 2841.8 | 66.1 | 183337 | 7 | ABQ77402 |
|   | 16 | 1691.8 | 39.3 | 1873   | 2 | AAV17875 |
|   | 17 | 1690.8 | 39.3 | 1872   | 3 | AAA35161 |
|   | 18 | 1690.8 | 39.3 | 1872   | 3 | AAF21283 |
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|   | 45 | 395.8  | 9.2  | 1868   | 3 | AAF20915 |

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| Add18443 | Human pro |
| Aaf21288 | Human low |
| Abz96982 | Human nuc |
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| Abk94410 | DNA encod |
| Abq77402 | Human EDN |
| Aav17875 | Homo sapi |
| Aaa35161 | Human ade |
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| Aaf21285 | Human low |
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| Aad24966 | Human G-p |
| Abi97988 | Non-endog |
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| Adb52872 | Primary r |
| Abi99321 | Mouse isc |
| Aaq25892 | Sequence  |
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| Abs51841 | Novel hum |
| Abk94409 | DNA encod |
| Abl63647 | Breast ca |
| Abl64653 | Stomach c |
| Abn95562 | Gene #206 |
| Ach20099 | Human adu |
| Aaq63209 | Human end |
| Aaa34793 | Human ade |
| Aaa34781 | Human ade |
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# ALIGNMENTS

## RESULT 1

AAQ34584

ID AAQ34584 standard; DNA; 4301 BP.

XX

AC AAQ34584;

XX

DT 25-MAR-2003 (revised)

DT 11-MAY-1993 (first entry)

XX

DE ETb receptor gene.

XX

KW Human; ETa; ETb; endothelin; receptor; transmembrane domain; N tail;

KW extracellular; cytoplasmic; C tail; post translational; bovine;

KW modification; ET-1 receptor; antagonist; circulatory system; ss.



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 PD 13-JAN-1993.  
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 PF 10-JUL-1992; 92EP-00306347.  
 XX  
 PR 12-JUL-1991; 91JP-00172828.  
 XX  
 PA (SHIO ) SHIONOGI SEIYAKU KK.  
 XX  
 PI Imura H, Nakao K, Nakanishi S;  
 XX  
 DR WPI; 1993-010677/02.  
 DR P-PSDB; AAR30886.  
 XX  
 PT Human ETa and ETb endothelin receptors - for measuring endothelin and  
 PT screening for endothelin antagonists.  
 XX  
 PS Claim 12; Fig 2; 39pp; English.  
 XX  
 CC The sequences given in AAQ34583-84 encode the human ETa and ETb  
 CC endothelin receptors respectively. ETa is a 427 amino acid protein with a  
 CC molecular weight of 48,726. ETb comprises 442 amino acids and has a  
 CC molecular weight of 49,629. ETa has a higher affinity for endothelin (ET)  
 CC -1 and ET-2, whereas ETb has no selectivity for ET-1, ET-2 or ET-3. The  
 CC receptors each contain seven transmembrane domains and have an  
 CC extracellular N tail and a cytoplasmic C tail. There are several  
 CC potential sites for post translational modification, these sites are  
 CC identical to those of bovine ET-1 receptor. ETa cDNA is 91.2% homologous  
 CC to bovine ET-1 receptor cDNA and ETb cDNA is 61.1% homologous to that of  
 CC bovine ETa-receptor. The receptor proteins are useful as reagents for  
 CC measuring the amount of ET or screening for antagonists of the ET  
 CC receptor when studying the circulatory system. (Updated on 25-MAR-2003 to  
 CC correct PN field.)  
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 SQ Sequence 4301 BP; 1342 A; 830 C; 815 G; 1314 T; 0 U; 0 Other;  
  
 Query Match 99.9%; Score 4297.8; DB 2; Length 4301;  
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 Qy 61 AGGTAGGCATTTGCCCCGGTGGGACGCCTTGCCAGAGCAGTGTGTGGCAGGCCCCCGTGG 120  
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 Db 61 AGGTAGGCATTTGCCCCGGTGGGACGCCTTGCCAGAGCAGTGTGTGGCAGGCCCCCGTGG 120  
  
 Qy 121 AGGATCAACACAGTGGCTGAACACTGGGAAGGAACTGGTACTTGGAGTCTGGACATCTGA 180  
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 Db 121 AGGATCAACACAGTGGCTGAACACTGGGAAGGAACTGGTACTTGGAGTCTGGACATCTGA 180  
  
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|----|------|---|------|
| Qy | 241  | CAGCCGCCTCCAAGTCTGTGCGGACGCGCCCTGGTTGCGCTGGTTCTTGCCCTGCGGCCTG | 300  |
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| Db | 241  | CAGCCGCCTCCAAGTCTGTGCGGACGCGCCCTGGTTGCGCTGGTTCTTGCCCTGCGGCCTG | 300  |
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| Db | 301  | TCGCGGATCTGGGGAGAGGAGAGAGGCTTCCCGCCTGACAGGGCCACTCCGCTTTTGCAA  | 360  |
| Qy | 361  | ACCGCAGAGATAATGACGCCACCCACTAAGACCTTATGGCCCAAGGGTTCCAACGCCAGT  | 420  |
|    |      |   |      |
| Db | 361  | ACCGCAGAGATAATGACGCCACCCACTAAGACCTTATGGCCCAAGGGTTCCAACGCCAGT  | 420  |
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| Db | 421  | CTGGCGCGGTTCGTTGGCACCTGCGGAGGTGCCTAAAGGAGACAGGACGGCAGGATCTCCG | 480  |
| Qy | 481  | CCACGCACCATCTCCCCCTCCCCCGTGCCAAGGACCCATCGAGATCAAGGAGACTTTCAA  | 540  |
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| Db | 481  | CCACGCACCATCTCCCCCTCCCCCGTGCCAAGGACCCATCGAGATCAAGGAGACTTTCAA  | 540  |
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|    |      |   |      |
| Db | 541  | TACATCAACACGGTTGTGTCTGCCTTGTGTTTCGTGCTGGGGATCATCGGGAACCTCCACA | 600  |
| Qy | 601  | CTTCTGAGAATTATCTACAAGAACAAGTGCATGCGAAACGGTCCCAATATCTTGATCGCC  | 660  |
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| Db | 601  | CTTCTGAGAATTATCTACAAGAACAAGTGCATGCGAAACGGTCCCAATATCTTGATCGCC  | 660  |
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|    |      |   |      |
| Db | 841  | GCTGTTGCTTCTTGGAGTAGAATTAAAGGAATTGGGGTTCCAAAATGGACAGCAGTAGAA  | 900  |
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|    |      |   |      |
| Db | 901  | ATTGTTTTGATTTGGGTGGTCTCTGTGGTTCTGGCTGTCCCTGAAGCCATAGGTTTTGAT  | 960  |
| Qy | 961  | ATAATTACGATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTTCAG  | 1020 |
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| Db | 961  | ATAATTACGATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTTCAG  | 1020 |
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| Db | 1021 | AAGACAGCTTTCATGCAGTTTACAAAGACAGCAAAAGATTGGTGGCTGTTCAAGTTTCTAT | 1080 |
| Qy | 1081 | TTCTGCTTGCCATTGGCCATCACTGCATTTTTTTTATACACTAATGACCTGTGAAATGTTG | 1140 |

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|----|------|---|------|
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| Qy | 1261 | AGCAGGATTCTGAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGAACTTTTG      | 1320 |
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| Qy | 1321 | AGCTTCTGTGTTGGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCCTGCATT     | 1380 |
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| Qy | 1381 | AACCCAATTGCTCTGTATTTGGTGAGCAAAAGATTCAAAAAGTCTTTAAGTCATGCTTA       | 1440 |
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| Qy | 1561 | TCTTGAAAGAAGAACTATTCAGTGTATTTTCTTTTATATTGGACCGAAGTCATTAA          | 1620 |
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| Db | 1681 | <br>TAAAATATTAAGTGTAATTATTTTAACACTCACAGCTACATATGACATTTTATGAGCTGT  | 1740 |
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| Db | 1801 | <br>TTTTTACAGTTAGCACTTCAACATAGCTCTTAACAACCTCCAGGATATTCACACAACACT  | 1860 |
| Qy | 1861 | TAGGCTTAAAAATGAGCTCACTCAGAATTTCTATTCTTTCTAAAAAGAGATTTATTTT        | 1920 |
| Db | 1861 | <br>TAGGCTTAAAAATGAGCTCACTCAGAATTTCTATTCTTTCTAAAAAGAGATTTATTTT    | 1920 |
| Qy | 1921 | AATCAATGGGACTCTGATATAAAGGAAGAATAAGTCACTGTAAAACAGAACTTTTAAATG      | 1980 |
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|    |      |   |      |
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| Qy | 1981 | AAGCTTAAATTACTCAATTTAAATTTTAAATCCTTTAAACAACCTTTTCAATTAATAT    | 2040 |
| Db | 1981 | AAGCTTAAATTACTCAATTTAAATTTTAAATCCTTTAAACAACCTTTTCAATTAATAT    | 2040 |
| Qy | 2041 | TATCACACTATTATCAGATTGTAATTAGATGCAAATGAGAGAGCAGTTTAGTTGTTGCAT  | 2100 |
| Db | 2041 | TATCACACTATTATCAGATTGTAATTAGATGCAAATGAGAGAGCAGTTTAGTTGTTGCAT  | 2100 |
| Qy | 2101 | TTTTCGGACACTGGAAACATTTAAATGATCAGGAGGGAGTAACAGAAAGAGCAAGGCTGT  | 2160 |
| Db | 2101 | TTTTCGGACACTGGAAACATTTAAATGATCAGGAGGGAGTAACAGAAAGAGCAAGGCTGT  | 2160 |
| Qy | 2161 | TTTTGAAAATCATTACACTTTCTACTAGAAGCCCAAACCTCAGCATTCTGCAATATGTAAC | 2220 |
| Db | 2161 | TTTTGAAAATCATTACACTTTCTACTAGAAGCCCAAACCTCAGCATTCTGCAATATGTAAC | 2220 |
| Qy | 2221 | CAACATGTCACAAACAAGCAGCATGTAACAGACTGGCACATGTGCCAGCTGAATTTAAAA  | 2280 |
| Db | 2221 | CAACATGTCACAAACAAGCAGCATGTAACAGACTGGCACATGTGCCAGCTGAATTTAAAA  | 2280 |
| Qy | 2281 | TATAATACTTTTAAAAAGAAAATTATTACATCCTTTACATTAGTTAAGATCAAACCTCA   | 2340 |
| Db | 2281 | TATAATACTTTTAAAAAGAAAATTATTACATCCTTTACATTAGTTAAGATCAAACCTCA   | 2340 |
| Qy | 2341 | CAAAGAGAAATAGAATGTTTGAAAGGCTATCCCAAAGACTTTTTTTGAATCTGTCATTCA  | 2400 |
| Db | 2341 | CAAAGAGAAATAGAATGTTTGAAAGGCTATCCCAAAGACTTTTTTTGAATCTGTCATTCA  | 2400 |
| Qy | 2401 | CATACCCTGTGAAGACAATACTATCTACAATTTTTTCAGGATTATTAAATCTTCTTTTT   | 2460 |
| Db | 2401 | CATACCCTGTGAAGACAATACTATCTACAATTTTTTCAGGATTATTAAATCTTCTTTTT   | 2460 |
| Qy | 2461 | TCACTATCGTAGCTTAAACTCTGTTTGGTTTTGTCATCTGTAAATACTTACCTACATACA  | 2520 |
| Db | 2461 | TCACTATCGTAGCTTAAACTCTGTTTGGTTTTGTCATCTGTAAATACTTACCTACATACA  | 2520 |
| Qy | 2521 | CTGCATGTAGATGATTAAATGAGGGCAGGCCCTGTGCTCATAGCTTTACGATGGAGAGAT  | 2580 |
| Db | 2521 | CTGCATGTAGATGATTAAATGAGGGCAGGCCCTGTGCTCATAGCTTTACGATGGAGAGAT  | 2580 |
| Qy | 2581 | GCCAGTGACCTCATAATAAAGACTGTGAACTGCCTGGTGCAGTGTCCACATGACAAAGGG  | 2640 |
| Db | 2581 | GCCAGTGACCTCATAATAAAGACTGTGAACTGCCTGGTGCAGTGTCCACATGACAAAGGG  | 2640 |
| Qy | 2641 | GCAGGTAGCACCTCTCTCACCCATGCTGTGGTTAAATGGTTTCTAGCATATGTATAAT    | 2700 |
| Db | 2641 | GCAGGTAGCACCTCTCTCACCCATGCTGTGGTTAAATGGTTTCTAGCATATGTATAAT    | 2700 |
| Qy | 2701 | GCTATAGTTAAAATACTATTTTTCAAATCATACAGATTAGTACATTTAACAGCTACCTG   | 2760 |
| Db | 2701 | GCTATAGTTAAAATACTATTTTTCAAATCATACAGATTAGTACATTTAACAGCTACCTG   | 2760 |
| Qy | 2761 | TAAAGCTTATTACTAATTTTTGTATTATTTTTGTAAATAGCCAATAGAAAAGTTTGCTTG  | 2820 |
| Db | 2761 | TAAAGCTTATTACTAATTTTTGTATTATTTTTGTAAATAGCCAATAGAAAAGTTTGCTTG  | 2820 |

|    |      |   |      |
|----|------|---|------|
| Qy | 2821 | ACATGGTGCTTTTCTTTTCATCTAGAGGCAAACTGCTTTTTGAGACCGTAAGAACCTCTT  | 2880 |
|    |      |   |      |
| Db | 2821 | ACATGGTGCTTTTCTTTTCATCTAGAGGCAAACTGCTTTTTGAGACCGTAAGAACCTCTT  | 2880 |
| Qy | 2881 | AGCTTTGTGCGTTCCTGCCTAATTTTATATCTTCTAAGCAAAGTGCCTTAGGATAGCTT   | 2940 |
|    |      |   |      |
| Db | 2881 | AGCTTTGTGCGTTCCTGCCTAATTTTATATCTTCTAAGCAAAGTGCCTTAGGATAGCTT   | 2940 |
| Qy | 2941 | GGGATGAGATGTGTGTGAAAGTATGTACAAGAGAAAACGGAAGAGAGAGGAAATGAGGTG  | 3000 |
|    |      |   |      |
| Db | 2941 | GGGATGAGATGTGTGTGAAAGTATGTACAAGAGAAAACGGAAGAGAGAGGAAATGAGGTG  | 3000 |
| Qy | 3001 | GGGTTGGAGGAAACCCATGGGGACAGATTCCCATTCTTAGCCTAACGTTTCGTCATTGCCT | 3060 |
|    |      |   |      |
| Db | 3001 | GGGTTGGAGGAAACCCATGGGGACAGATTCCCATTCTTAGCCTAACGTTTCGTCATTGCCT | 3060 |
| Qy | 3061 | CGTCACATCAATGCAAAAGGTCCTGATTTTGTTCAGCAAAACACAGTGCAATGTTCTCA   | 3120 |
|    |      |   |      |
| Db | 3061 | CGTCACATCAATGCAAAAGGTCCTGATTTTGTTCAGCAAAACACAGTGCAATGTTCTCA   | 3120 |
| Qy | 3121 | GAGTGACTTTTCAAATAAATTGGGCCCAAGAGCTTTAACTCGGTCTTAAAATATGCCCAA  | 3180 |
|    |      |   |      |
| Db | 3121 | GAGTGACTTTTCAAATAAATTGGGCCCAAGAGCTTTAACTCGGTCTTAAAATATGCCCAA  | 3180 |
| Qy | 3181 | ATTTTTACTTTGTTTTCTTTTAATAGGCTGGGCCACATGTTGGAAATAAGCTAGTAATG   | 3240 |
|    |      |   |      |
| Db | 3181 | ATTTTTACTTTGTTTTCTTTTAATAGGCTGGGCCACATGTTGGAAATAAGCTAGTAATG   | 3240 |
| Qy | 3241 | TTGTTTTCTGTCAATATTGAATGTGATGGTACAGTAAACCAAACCCAACAATGTGGCCA   | 3300 |
|    |      |   |      |
| Db | 3241 | TTGTTTTCTGTCAATATTGAATGTGATGGTACAGTAAACCAAACCCAACAATGTGGCCA   | 3300 |
| Qy | 3301 | GAAAGAAAGAGCAATAATAATTAATTCACACACCATATGGATTCTATTTATAAATCACCC  | 3360 |
|    |      |   |      |
| Db | 3301 | GAAAGAAAGAGCAATAATAATTAATTCACACACCATATGGATTCTATTTATAAATCACCC  | 3360 |
| Qy | 3361 | ACAACTTGTTCTTTAATTTTCATCCCAATCACTTTTTTCAGAGGCCTGTTATCATAGAAGT | 3420 |
|    |      |   |      |
| Db | 3361 | ACAACTTGTTCTTTAATTTTCATCCCAATCACTTTTTTCAGAGGCCTGTTATCATAGAAGT | 3420 |
| Qy | 3421 | CATTTTAGACTCTCAATTTTAAATTAATTTGAATCACTAATATTTTCACAGTTTATTAA   | 3480 |
|    |      |   |      |
| Db | 3421 | CATTTTAGACTCTCAATTTTAAATTAATTTGAATCACTAATATTTTCACAGTTTATTAA   | 3480 |
| Qy | 3481 | TATATTTAATTTCTATTTAAATTTTAGATTATTTTATTACCATGTACTGAATTTTACA    | 3540 |
|    |      |   |      |
| Db | 3481 | TATATTTAATTTCTATTTAAATTTTAGATTATTTTATTACCATGTACTGAATTTTACA    | 3540 |
| Qy | 3541 | TCCTGATACCCTTTCTTCTCCATGTCAGTATCATGTTCTCTAATTATCTTGCCAAATTT   | 3600 |
|    |      |   |      |
| Db | 3541 | TCCTGATACCCTTTCTTCTCCATGTCAGTATCATGTTCTCTAATTATCTTGCCAAATTT   | 3600 |
| Qy | 3601 | TGAACTACACACAAAAAGCATACTTGCAATTATTATAATAAAATTGCATTTCAGTGGCTT  | 3660 |
|    |      |   |      |
| Db | 3601 | TGAACTACACACAAAAAGCATACTTGCAATTATTATAATAAAATTGCATTTCAGTGGCTT  | 3660 |

|    |      |  |      |
|----|------|--|------|
| Qy | 3661 | TTTAAAAAAATGTTTGATTCAAAACTTTAACATACTGATAAGTAAGAAACAATTATAAT  | 3720 |
| Db | 3661 | TTTAAAAAAATGTTTGATTCAAAACTTTAACATACTGATAAGTAAGAAACAATTATAAT  | 3720 |
| Qy | 3721 | TTCTTTACATACTCAAACCAAGATAGAAAAAGGTGCTATCGTTCAACTTCAAAACATGT  | 3780 |
| Db | 3721 | TTCTTTACATACTCAAACCAAGATAGAAAAAGGTGCTATCGTTCAACTTCAAAACATGT  | 3780 |
| Qy | 3781 | TTCCTAGTATTAAGGACTTTAATATAGCAACAGACAAAATTATTGTTAACATGGATGTTA | 3840 |
| Db | 3781 | TTCCTAGTATTAAGGACTTTAATATAGCAACAGACAAAATTATTGTTAACATGGATGTTA | 3840 |
| Qy | 3841 | CAGCTCAAAGATTTATAAAAGATTTTAACCTATTTTCTCCCTTATTATCCACTGCTAAT  | 3900 |
| Db | 3841 | CAGCTCAAAGATTTATAAAAGATTTTAACCTATTTTCTCCCTTATTATCCACTGCTAAT  | 3900 |
| Qy | 3901 | GTGGATGTATGTTCAAACACCTTTTAGTATTGATAGCTTACATATGGCCAAAGGAATACA | 3960 |
| Db | 3901 | GTGGATGTATGTTCAAACACCTTTTAGTATTGATAGCTTACATATGGCCAAAGGAATACA | 3960 |
| Qy | 3961 | GTTTATAGCAAACATGGGTATGCTGTAGCTAACTTTATAAAAGTGTAATATAACAATGT  | 4020 |
| Db | 3961 | GTTTATAGCAAACATGGGTATGCTGTAGCTAACTTTATAAAAGTGTAATATAACAATGT  | 4020 |
| Qy | 4021 | AAAAAATTATATATCTGGGAGGATTTTTTGGTTGCCTAAAGTGGCTATAGTTACTGATTT | 4080 |
| Db | 4021 | AAAAAATTATATATCTGGGAGGATTTTTTGGTTGCCTAAAGTGGCTATAGTTACTGATTT | 4080 |
| Qy | 4081 | TTTATTATGTAAGCAAACCAATAAAAATTTAAGTTTTTTTAACAACCTACCTTATTTTTC | 4140 |
| Db | 4081 | TTTATTATGTAAGCAAACCAATAAAAATTTAAGTTTTTTTAACAACCTACCTTATTTTTC | 4140 |
| Qy | 4141 | ACTGTACAGACACTAATTCATTAAATACTAATTGATTGTTTAAAAGAAATATAAATGTGA | 4200 |
| Db | 4141 | ACTGTACAGACACTAATTCATTAAATACTAATTGATTGTTTAAAAGAAATATAAATGTGA | 4200 |
| Qy | 4201 | CAAGTGGACATTATTTATGTTAAATATACAATTATCAAGCAAGTATGAAGTTATTCAATT | 4260 |
| Db | 4201 | CAAGTGGACATTATTTATGTTAAATATACAATTATCAAGCAAGTATGAAGTTATTCAATT | 4260 |
| Qy | 4261 | AAAATGCCACATTTCTGGTCTCTGGGAAAAAAAAAAAAAAAAA                  | 4301 |
| Db | 4261 | AAAATGCCACATTTCTGGTCTCTGGGAAAAAAAAAAAAAAAAA                  | 4301 |

RESULT 2

AAA35162

ID AAA35162 standard; DNA; 4286 BP.

XX

AC AAA35162;

XX

DT 28-JUL-2000 (first entry)

XX

DE Human adenosine receptor related polynucleotide 2nd SEQ ID NO:36.

XX

KW Human; adenosine receptor; low adenosine antisense oligonucleotide;  
 KW phosphorothioate; impaired respiration; inflammation; allergy;

KW allergic disease; bronchoconstriction; inhibitor; antiinflammatory;  
 KW antiallergic; antiasthmatic; cytostatic; analgesic; impaired airway;  
 KW lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;  
 KW respiratory distress syndrome; pain; cystic fibrosis; emphysema;  
 KW pulmonary hypertension; chronic obstructive pulmonary disease; COPD;  
 KW cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200009525-A2.  
 XX  
 PD 24-FEB-2000.  
 XX  
 PF 03-AUG-1999; 99WO-US017712.  
 XX  
 PR 03-AUG-1998; 98US-0095212P.  
 XX  
 PA (UYEC-) UNIV EAST CAROLINA.  
 XX  
 PI Nyce JW;  
 XX  
 DR WPI; 2000-205971/18.  
 XX  
 PT New antisense oligonucleotides useful for treating e.g. pulmonary  
 PT vasoconstriction, inflammation, allergies, asthma, hypertension,  
 PT bronchitis, emphysema, respiratory distress syndrome, ischemia or  
 PT cancers.  
 XX  
 PS Disclosure; Page 1191-1192; 1343pp; English.  
 XX  
 CC The present invention describes a new composition comprising an antisense  
 CC oligonucleotide (ON) with low adenosine (up to 15%), which targets  
 CC nucleic acids involved in bronchoconstriction, allergies, and/or  
 CC inflammation. The ON can have antiinflammatory, antiallergic,  
 CC antiasthmatic, cytostatic and analgesic activities. The compositions are  
 CC useful for the treatment of diseases associated with inflammation,  
 CC impaired airways, including lung disease and diseases whose secondary  
 CC effects afflict the lungs of a subject. They can be used for treating  
 CC e.g. ischaemic conditions, pulmonary vasoconstriction, allergies, asthma,  
 CC impeded respiration, respiratory distress syndrome, pain, cystic  
 CC fibrosis, pulmonary hypertension, emphysema, chronic obstructive  
 CC pulmonary disease (COPD), and cancers such as leukaemias, lymphomas,  
 CC carcinomas, and cancers which may metastasise to the lungs, including  
 CC breast and prostate cancer. The reduction of the adenosine content of the  
 CC ONs reduces side effects. The A-containing ONs break down with the  
 CC release of deoxyadenosine which activates adenosine receptors causing  
 CC bronchoconstriction and inflammation. AAA32313 to AAA35312 represent the  
 CC nucleotide sequences given in the sequence listing from the present  
 CC invention, which correspond to SEQ ID NO:1 to 2815, and then the last 185  
 CC sequences are also called SEQ ID NO:1 to 185, but the sequences differ  
 CC from the previously named sequences. SEQ ID NO:11 to 1680 (AAA32323 to  
 CC AAA33992) are specifically claimed ONs from the present invention. N.B.  
 CC Sequences given in the disclosure of the present invention do not match  
 CC up with their corresponding SEQ ID NO: sequences given in the sequence  
 CC listing  
 XX  
 SQ Sequence 4286 BP; 1327 A; 829 C; 816 G; 1314 T; 0 U; 0 Other;



Query Match 99.6%; Score 4284.4; DB 3; Length 4286;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 4285; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

|    |     |   |     |
|----|-----|---|-----|
| Qy | 1   | GAGACATTCCGGTGGGGGACTCTGGCCAGCCCAGCAACGTGGATCCTGAGAGCACTCCC   | 60  |
|    |     |   |     |
| Db | 1   | GAGACATTCCGGTGGGGGACTCTGGCCAGCCCAGCAACGTGGATCCTGAGAGCACTCCC   | 60  |
| Qy | 61  | AGGTAGGCATTTGCCCCGGTGGGACGCCTTGCCAGAGCAGTGTGTGGCAGGCCCCCGTGG  | 120 |
|    |     |   |     |
| Db | 61  | AGGTAGGCATTTGCCCCGGTGGGACGCCTTGCCAGAGCAGTGTGTGGCAGGCCCCCGTGG  | 120 |
| Qy | 121 | AGGATCAACACAGTGGCTGAACACTGGGAAGGAAGTGGTACTTGGAGTCTGGACATCTGA  | 180 |
|    |     |   |     |
| Db | 121 | AGGATCAACACAGTGGCTGAACACTGGGAAGGAAGTGGTACTTGGAGTCTGGACATCTGA  | 180 |
| Qy | 181 | AACTTGGCTCTGAAACTGCGGAGCGGCCACCGACGCCTTCTGGAGCAGGTAGCAGCATG   | 240 |
|    |     |   |     |
| Db | 181 | AACTTGGCTCTGAAACTGCGCAGCGGCCACCGACGCCTTCTGGAGCAGGTAGCAGCATG   | 240 |
| Qy | 241 | CAGCCGCCTCCAAGTCTGTGCGGACGCGCCCTGGTTGCGCTGGTTCTTGCTGCGGCCTG   | 300 |
|    |     |   |     |
| Db | 241 | CAGCCGCCTCCAAGTCTGTGCGGACGCGCCCTGGTTGCGCTGGTTCTTGCTGCGGCCTG   | 300 |
| Qy | 301 | TCGCGGATCTGGGGAGAGGAGAGAGGCTTCCCGCCTGACAGGGCCACTCCGCTTTTGCAA  | 360 |
|    |     |   |     |
| Db | 301 | TCGCGGATCTGGGGAGAGGAGAGAGGCTTCCCGCCTGACAGGGCCACTCCGCTTTTGCAA  | 360 |
| Qy | 361 | ACCGCAGAGATAATGACGCCACCCACTAAGACCTTATGGCCCAAGGGTTCCAACGCCAGT  | 420 |
|    |     |   |     |
| Db | 361 | ACCGCAGAGATAATGACGCCACCCACTAAGACCTTATGGCCCAAGGGTTCCAACGCCAGT  | 420 |
| Qy | 421 | CTGGCGCGGTTCGTTGGCACCTGCGGAGGTGCCTAAAGGAGACAGGACGGCAGGATCTCCG | 480 |
|    |     |   |     |
| Db | 421 | CTGGCGCGGTTCGTTGGCACCTGCGGAGGTGCCTAAAGGAGACAGGACGGCAGGATCTCCG | 480 |
| Qy | 481 | CCACGCACCATCTCCCCTCCCCCGTGCCAAGGACCCATCGAGATCAAGGAGACTTTCAA   | 540 |
|    |     |   |     |
| Db | 481 | CCACGCACCATCTCCCCTCCCCCGTGCCAAGGACCCATCGAGATCAAGGAGACTTTCAA   | 540 |
| Qy | 541 | TACATCAACACGGTTGTGTCCTGCCTTGTGTTTCGTGCTGGGGATCATCGGGAACCCACA  | 600 |
|    |     |   |     |
| Db | 541 | TACATCAACACGGTTGTGTCCTGCCTTGTGTTTCGTGCTGGGGATCATCGGGAACCCACA  | 600 |
| Qy | 601 | CTTCTGAGAATTATCTACAAGAACAAGTGCATGCGAAACGGTCCCAATATCTTGATCGCC  | 660 |
|    |     |   |     |
| Db | 601 | CTTCTGAGAATTATCTACAAGAACAAGTGCATGCGAAACGGTCCCAATATCTTGATCGCC  | 660 |
| Qy | 661 | AGCTTGGCTCTGGGAGACCTGCTGCACATCGTCATTGACATCCCTATCAATGTCTACAAG  | 720 |
|    |     |   |     |
| Db | 661 | AGCTTGGCTCTGGGAGACCTGCTGCACATCGTCATTGACATCCCTATCAATGTCTACAAG  | 720 |
| Qy | 721 | CTGCTGGCAGAGGACTGGCCATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTCATACAG  | 780 |
|    |     |   |     |
| Db | 721 | CTGCTGGCAGAGGACTGGCCATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTCATACAG  | 780 |

|    |      |   |      |
|----|------|---|------|
| Qy | 781  | AAAGCCTCCGTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATATCGA  | 840  |
|    |      |   |      |
| Db | 781  | AAAGCCTCCGTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATATCGA  | 840  |
| Qy | 841  | GCTGTTGCTTCTTGGAGTAGAATTAAAGGAATTGGGGTCCAAAATGGACAGCAGTAGAA   | 900  |
|    |      |   |      |
| Db | 841  | GCTGTTGCTTCTTGGAGTAGAATTAAAGGAATTGGGGTCCAAAATGGACAGCAGTAGAA   | 900  |
| Qy | 901  | ATTGTTTTGATTTGGGTGGTCTCTGTGGTTCTGGCTGTCCCTGAAGCCATAGGTTTTGAT  | 960  |
|    |      |   |      |
| Db | 901  | ATTGTTTTGATTTGGGTGGTCTCTGTGGTTCTGGCTGTCCCTGAAGCCATAGGTTTTGAT  | 960  |
| Qy | 961  | ATAATTACGATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTTCAG  | 1020 |
|    |      |   |      |
| Db | 961  | ATAATTACGATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTTCAG  | 1020 |
| Qy | 1021 | AAGACAGCTTTCATGCAGTTTTTACAAGACAGCAAAAGATTGGTGGCTGTTCACTTTCTAT | 1080 |
|    |      |   |      |
| Db | 1021 | AAGACAGCTTTCATGCAGTTTTTACAAGACAGCAAAAGATTGGTGGCTGTTCACTTTCTAT | 1080 |
| Qy | 1081 | TTCTGCTTGCCATTGGCCATCACTGCATTTTTTTATACACTAATGACCTGTGAAATGTTG  | 1140 |
|    |      |   |      |
| Db | 1081 | TTCTGCTTGCCATTGGCCATCACTGCATTTTTTTATACACTAATGACCTGTGAAATGTTG  | 1140 |
| Qy | 1141 | AGAAAGAAAAGTGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAAGTG  | 1200 |
|    |      |   |      |
| Db | 1141 | AGAAAGAAAAGTGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAAGTG  | 1200 |
| Qy | 1201 | GCCAAAACCGTCTTTTGCCTGGTCCTTGCTTTGCCCTCTGCTGGCTTCCCTTCACCTC    | 1260 |
|    |      |   |      |
| Db | 1201 | GCCAAAACCGTCTTTTGCCTGGTCCTTGCTTTGCCCTCTGCTGGCTTCCCTTCACCTC    | 1260 |
| Qy | 1261 | AGCAGGATTCTGAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGAACCTTTG  | 1320 |
|    |      |   |      |
| Db | 1261 | AGCAGGATTCTGAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGAACCTTTG  | 1320 |
| Qy | 1321 | AGCTTTCTGTTGGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCCTGCATT  | 1380 |
|    |      |   |      |
| Db | 1321 | AGCTTTCTGTTGGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCCTGCATT  | 1380 |
| Qy | 1381 | AACCCAATTGCTCTGTATTTGGTGAGCAAAAGATTCAAAAAGCTTTAAGTCATGCTTA    | 1440 |
|    |      |   |      |
| Db | 1381 | AACCCAATTGCTCTGTATTTGGTGAGCAAAAGATTCAAAAAGCTTTAAGTCATGCTTA    | 1440 |
| Qy | 1441 | TGCTGCTGGTGCCAGTCATTTGAAGAAAAACAGTCCTTGAGAGAAAAGCAGTCGTGCTTA  | 1500 |
|    |      |   |      |
| Db | 1441 | TGCTGCTGGTGCCAGTCATTTGAAGAAAAACAGTCCTTGAGAGAAAAGCAGTCGTGCTTA  | 1500 |
| Qy | 1501 | AAGTTCAAAGCTAATGATCACGGATATGACAACCTCCGTTCCAGTAATAAATACAGCTCA  | 1560 |
|    |      |   |      |
| Db | 1501 | AAGTTCAAAGCTAATGATCACGGATATGACAACCTCCGTTCCAGTAATAAATACAGCTCA  | 1560 |
| Qy | 1561 | TCTTGAAAGAAGAACTATTCACTGTATTTTCTTTTATATTGGACCGAAGTCATTAA      | 1620 |
|    |      |   |      |
| Db | 1561 | TCTTGAAAGAAGAACTATTCACTGTATTTTCTTTTATATTGGACCGAAGTCATTAA      | 1620 |
| Qy | 1621 | AACAAAATGAAACATTTGCCAAAACAAAACAAAACATATGTATTTGCACAGCACACTAT   | 1680 |

|    |      |   |      |
|----|------|---|------|
| Db | 1621 | <br>AACAAAATGAAACATTTGCCAAAACAAAACAAAAACTATGTATTTGCACAGCACACTAT   | 1680 |
| Qy | 1681 | TAAAAATATTAAGTGTAATTATTTTAACTACAGCTACATATGACATTTTATGAGCTGT        | 1740 |
| Db | 1681 | <br>TAAAAATATTAAGTGTAATTATTTTAACTACAGCTACATATGACATTTTATGAGCTGT    | 1740 |
| Qy | 1741 | TTACGGCATGGAAAGAAAATCAGTGGGAATTAAGAAAGCCTCGTCGTGAAAGCACTTAAT      | 1800 |
| Db | 1741 | <br>TTACGGCATGGAAAGAAAATCAGTGGGAATTAAGAAAGCCTCGTCGTGAAAGCACTTAAT  | 1800 |
| Qy | 1801 | TTTTTACAGTTAGCACTTCAACATAGCTCTTAACAACTTCCAGGATATTCACACAACACT      | 1860 |
| Db | 1801 | <br>TTTTTACAGTTAGCACTTCAACATAGCTCTTAACAACTTCCAGGATATTCACACAACACT  | 1860 |
| Qy | 1861 | TAGGCTTAAAAATGAGCTCACTCAGAATTTCTATTCTTTCTAAAAAGAGATTTATTTTTTA     | 1920 |
| Db | 1861 | <br>TAGGCTTAAAAATGAGCTCACTCAGAATTTCTATTCTTTCTAAAAAGAGATTTATTTTTTA | 1920 |
| Qy | 1921 | AATCAATGGGACTCTGATATAAAGGAAGAATAAGTCACTGTAAACAGAACTTTTAAATG       | 1980 |
| Db | 1921 | <br>AATCAATGGGACTCTGATATAAAGGAAGAATAAGTCACTGTAAACAGAACTTTTAAATG   | 1980 |
| Qy | 1981 | AAGCTTAAATTACTCAATTTAAAAATTTTAAATCCTTTAAACAACTTTTCAATTAATAT       | 2040 |
| Db | 1981 | <br>AAGCTTAAATTACTCAATTTAAAAATTTTAAATCCTTTAAACAACTTTTCAATTAATAT   | 2040 |
| Qy | 2041 | TATCACACTATTATCAGATTGTAATTAGATGCAAATGAGAGAGCAGTTTAGTTGTTGCAT      | 2100 |
| Db | 2041 | <br>TATCACACTATTATCAGATTGTAATTAGATGCAAATGAGAGAGCAGTTTAGTTGTTGCAT  | 2100 |
| Qy | 2101 | TTTTCGGACACTGGAAACATTTAAATGATCAGGAGGGAGTAACAGAAAGAGCAAGGCTGT      | 2160 |
| Db | 2101 | <br>TTTTCGGACACTGGAAACATTTAAATGATCAGGAGGGAGTAACAGAAAGAGCAAGGCTGT  | 2160 |
| Qy | 2161 | TTTTGAAAATCATTACACTTTCACTAGAAGCCCAAACCTCAGCATTCTGCAATATGTAAC      | 2220 |
| Db | 2161 | <br>TTTTGAAAATCATTACACTTTCACTAGAAGCCCAAACCTCAGCATTCTGCAATATGTAAC  | 2220 |
| Qy | 2221 | CAACATGTCACAAACAAGCAGCATGTAACAGACTGGCACATGTGCCAGCTGAATTTAAAA      | 2280 |
| Db | 2221 | <br>CAACATGTCACAAACAAGCAGCATGTAACAGACTGGCACATGTGCCAGCTGAATTTAAAA  | 2280 |
| Qy | 2281 | TATAATACTTTTAAAAAGAAAATTTATACATCCTTTACATTCAAGTAAAGATCAAACCTCA     | 2340 |
| Db | 2281 | <br>TATAATACTTTTAAAAAGAAAATTTATACATCCTTTACATTCAAGTAAAGATCAAACCTCA | 2340 |
| Qy | 2341 | CAAAGAGAAATAGAATGTTTGAAAGGCTATCCCAAAGACTTTTTTGAATCTGTCATTCA       | 2400 |
| Db | 2341 | <br>CAAAGAGAAATAGAATGTTTGAAAGGCTATCCCAAAGACTTTTTTGAATCTGTCATTCA   | 2400 |
| Qy | 2401 | CATACCCTGTGAAGACAATACTATCTACAATTTTTTTCAGGATTATTAAAATCTTCTTTTT     | 2460 |
| Db | 2401 | <br>CATACCCTGTGAAGACAATACTATCTACAATTTTTTTCAGGATTATTAAAATCTTCTTTTT | 2460 |
| Qy | 2461 | TCACTATCGTAGCTTAAACTCTGTTTGGTTTTGTCATCTGTAAATACTTACCTACATACA      | 2520 |
|    |      |   |      |

Db 2461 TCACTATCGTAGCTTAAACTCTGTTTGGTTTTGTCATCTGTAAATACTTACCTACATACA 2520  
 QY 2521 CTGCATGTAGATGATTAAATGAGGGCAGGCCCTGTGCTCATAGCTTTACGATGGAGAGAT 2580  
 Db 2521 CTGCATGTAGATGATTAAATGAGGGCAGGCCCTGTGCTCATAGCTTTACGATGGAGAGAT 2580  
 QY 2581 GCCAGTGACCTCATAATAAAGACTGTGAACCTGCCTGGTGCAGTGTCCACATGACAAAGGG 2640  
 Db 2581 GCCAGTGACCTCATAATAAAGACTGTGAACCTGCCTGGTGCAGTGTCCACATGACAAAGGG 2640  
 QY 2641 GCAGGTAGCACCTCTCTCACCCATGCTGTGGTTAAAATGGTTTCTAGCATATGTATAAT 2700  
 Db 2641 GCAGGTAGCACCTCTCTCACCCATGCTGTGGTTAAAATGGTTTCTAGCATATGTATAAT 2700  
 QY 2701 GCTATAGTTAAAATACTATTTTTCAAATCATACAGATTAGTACATTTAACAGCTACCTG 2760  
 Db 2701 GCTATAGTTAAAATACTATTTTTCAAATCATACAGATTAGTACATTTAACAGCTACCTG 2760  
 QY 2761 TAAAGCTTATTACTAATTTTTGTATTATTTTTGTAAATAGCCAATAGAAAAGTTTGCTTG 2820  
 Db 2761 TAAAGCTTATTACTAATTTTTGTATTATTTTTGTAAATAGCCAATAGAAAAGTTTGCTTG 2820  
 QY 2821 ACATGGTGCTTTTCTTTTCATCTAGAGGCAAACTGCTTTTGTAGACCGTAAGAACCTCTT 2880  
 Db 2821 ACATGGTGCTTTTCTTTTCATCTAGAGGCAAACTGCTTTTGTAGACCGTAAGAACCTCTT 2880  
 QY 2881 AGCTTTGTGCGTTCCTGCCTAATTTTTATATCTTCTAAGCAAAGTGCCTTAGGATAGCTT 2940  
 Db 2881 AGCTTTGTGCGTTCCTGCCTAATTTTTATATCTTCTAAGCAAAGTGCCTTAGGATAGCTT 2940  
 QY 2941 GGGATGAGATGTGTGTGAAAGTATGTACAAGAGAAAACGGAAGAGAGAGGAAATGAGGTG 3000  
 Db 2941 GGGATGAGATGTGTGTGAAAGTATGTACAAGAGAAAACGGAAGAGAGAGGAAATGAGGTG 3000  
 QY 3001 GGGTTGGAGGAAACCCATGGGGACAGATTCCCATTCTTAGCCTAACGTTTCGTCATTGCCT 3060  
 Db 3001 GGGTTGGAGGAAACCCATGGGGACAGATTCCCATTCTTAGCCTAACGTTTCGTCATTGCCT 3060  
 QY 3061 CGTCACATCAATGCAAAAGGTCCTGATTTTGTTCAGCAAAACACAGTGCAATGTTCTCA 3120  
 Db 3061 CGTCACATCAATGCAAAAGGTCCTGATTTTGTTCAGCAAAACACAGTGCAATGTTCTCA 3120  
 QY 3121 GAGTGACTTTCGAAATAAATTGGGCCCAAGAGCTTTAACTCGGTCTTAAATATGCCCAA 3180  
 Db 3121 GAGTGACTTTCGAAATAAATTGGGCCCAAGAGCTTTAACTCGGTCTTAAATATGCCCAA 3180  
 QY 3181 ATTTTTACTTTGTTTTCTTTAATAGGCTGGGCCACATGTTGGAAATAAGCTAGTAATG 3240  
 Db 3181 ATTTTTACTTTGTTTTCTTTAATAGGCTGGGCCACATGTTGGAAATAAGCTAGTAATG 3240  
 QY 3241 TTGTTTTCTGTCAATATTGAATGTGATGGTACAGTAAACCAAACCAATGTGGCCA 3300  
 Db 3241 TTGTTTTCTGTCAATATTGAATGTGATGGTACAGTAAACCAAACCAATGTGGCCA 3300  
 QY 3301 GAAAGAAAGAGCAATAATAATTAATTCACACACCATATGGATTCTATTTATAAATCACCC 3360  
 Db 3301 GAAAGAAAGAGCAATAATAATTAATTCACACACCATATGGATTCTATTTATAAATCACCC 3360

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|----|------|--|------|
| Qy | 3361 | ACAACTTGTCTTTAATTTTCATCCCAATCACTTTTTCAGAGGCCTGTTATCATAGAAGT  | 3420 |
| Db | 3361 | ACAACTTGTCTTTAATTTTCATCCCAATCACTTTTTCAGAGGCCTGTTATCATAGAAGT  | 3420 |
| Qy | 3421 | CATTTTAGACTCTCAATTTTAAATTAATTTTGAATCACTAATATTTTCACAGTTTATTAA | 3480 |
| Db | 3421 | CATTTTAGACTCTCAATTTTAAATTAATTTTGAATCACTAATATTTTCACAGTTTATTAA | 3480 |
| Qy | 3481 | TATATTTAATTTCTATTTAAATTTTAGATTATTTTATTACCATGTAATTTTACA       | 3540 |
| Db | 3481 | TATATTTAATTTCTATTTAAATTTTAGATTATTTTATTACCATGTAATTTTACA       | 3540 |
| Qy | 3541 | TCCTGATACCTTTCTTCTCCATGTCAGTATCATGTTCTCTAATTATCTTGCCAAATTT   | 3600 |
| Db | 3541 | TCCTGATACCTTTCTTCTCCATGTCAGTATCATGTTCTCTAATTATCTTGCCAAATTT   | 3600 |
| Qy | 3601 | TGAACTACACACAAAAAGCATACTTGCATTATTTATAATAAAATTGCATTTCAGTGGCTT | 3660 |
| Db | 3601 | TGAACTACACACAAAAAGCATACTTGCATTATTTATAATAAAATTGCATTTCAGTGGCTT | 3660 |
| Qy | 3661 | TTTAAAAAAATGTTTGATTCAAACTTTAACATACTGATAAGTAAGAAACAATTATAAT   | 3720 |
| Db | 3661 | TTTAAAAAAATGTTTGATTCAAACTTTAACATACTGATAAGTAAGAAACAATTATAAT   | 3720 |
| Qy | 3721 | TTCTTTACATACTCAAACCAAGATAGAAAAAGGTGCTATCGTTCAACTTCAAACATGT   | 3780 |
| Db | 3721 | TTCTTTACATACTCAAACCAAGATAGAAAAAGGTGCTATCGTTCAACTTCAAACATGT   | 3780 |
| Qy | 3781 | TTCCTAGTATTAAGGACTTTAATATAGCAACAGACAAAATTATTGTTAACATGGATGTTA | 3840 |
| Db | 3781 | TTCCTAGTATTAAGGACTTTAATATAGCAACAGACAAAATTATTGTTAACATGGATGTTA | 3840 |
| Qy | 3841 | CAGCTCAAAAGATTTATAAAAGATTTTAACCTATTTTCTCCCTTATTATCCACTGCTAAT | 3900 |
| Db | 3841 | CAGCTCAAAAGATTTATAAAAGATTTTAACCTATTTTCTCCCTTATTATCCACTGCTAAT | 3900 |
| Qy | 3901 | GTGGATGTATGTTCAAACACCTTTTAGTATTGATAGCTTACATATGGCCAAAGGAATACA | 3960 |
| Db | 3901 | GTGGATGTATGTTCAAACACCTTTTAGTATTGATAGCTTACATATGGCCAAAGGAATACA | 3960 |
| Qy | 3961 | GTTTATAGCAAAACATGGGTATGCTGTAGCTAACTTTATAAAAGTGTAATATAACAATGT | 4020 |
| Db | 3961 | GTTTATAGCAAAACATGGGTATGCTGTAGCTAACTTTATAAAAGTGTAATATAACAATGT | 4020 |
| Qy | 4021 | AAAAAATTATATATCTGGGAGGATTTTTTGGTTGCCTAAAGTGGCTATAGTTACTGATTT | 4080 |
| Db | 4021 | AAAAAATTATATATCTGGGAGGATTTTTTGGTTGCCTAAAGTGGCTATAGTTACTGATTT | 4080 |
| Qy | 4081 | TTTATTATGTAAGCAAAACCAATAAAAATTTAAGTTTTTTTAACTACCTTATTTTC     | 4140 |
| Db | 4081 | TTTATTATGTAAGCAAAACCAATAAAAATTTAAGTTTTTTTAACTACCTTATTTTC     | 4140 |
| Qy | 4141 | ACTGTACAGACACTAATTCATTAAATACTAATTGATTGTTTAAAGAAATATAAATGTGA  | 4200 |
| Db | 4141 | ACTGTACAGACACTAATTCATTAAATACTAATTGATTGTTTAAAGAAATATAAATGTGA  | 4200 |

QY 4201 CAAGTGGACATTATTTATGTTAAATATACAATTATCAAGCAAGTATGAAGTTATTCAATT 4260  
 |||||  
 Db 4201 CAAGTGGACATTATTTATGTTAAATATACAATTATCAAGCAAGTATGAAGTTATTCAATT 4260  
 QY 4261 AAAATGCCACATTTCTGGTCTCTGGG 4286  
 |||||  
 Db 4261 AAAATGCCACATTTCTGGTCTCTGGG 4286

RESULT 3

AAF21284

ID AAF21284 standard; DNA; 4286 BP.

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AC AAF21284;

XX

DT 14-MAR-2001 (first entry)

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DE Human low adenosine antisense oligonucleotide related sequence #2851.

XX

KW Low adenosine antisense oligonucleotide; phosphorothioate; allergy;  
 KW human; airway disorder; bronchoconstriction; lung inflammation;  
 KW surfactant depletion; respiratory; bronchodilator; antiinflammatory;  
 KW immunosuppressive; antiasthmatic; analgesic; hypotensive; cytostatic;  
 KW respiratory obstruction; pulmonary obstruction; impeded respiration;  
 KW surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;  
 KW respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;  
 KW pulmonary hypertension; emphysema; pulmonary transplantation rejection;  
 KW chronic obstructive pulmonary disease; pulmonary infection; bronchitis;  
 KW cancer; ss.

XX

OS Homo sapiens.

XX

PN WO200062736-A2.

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PD 26-OCT-2000.

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PF 24-MAR-2000; 2000WO-US008020.

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PR 06-APR-1999; 99US-0127958P.

XX

PA (UYEC-) UNIV EAST CAROLINA.

PA (NYCE/) NYCE J W.

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PI Nyce JW;

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DR WPI; 2000-679539/66.

XX

PT Low adenosine (A) content antisense oligonucleotides which do not trigger  
 PT adenosine receptors during metabolism, useful e.g. for treating cancers  
 PT and respiratory obstructions.

XX

PS Disclosure; Page 1273-1274; 1592pp; English.

XX

CC The present invention describes low adenosine (A) content antisense  
 CC oligonucleotides and compositions (I) comprising them. In the antisense  
 CC oligonucleotides the A is replaced by a 'Universal' or alternative base.  
 CC (I) can have respiratory, bronchodilator, antiinflammatory, analgesic,

CC immunosuppressive, antiasthmatic, hypotensive and cytostatic activities.  
 CC The antisense oligonucleotides and (I) can be used to down-regulate the  
 CC expression and or activity of target polypeptides associated with  
 CC lung/respiratory disorders and malignancies, such as stimulating and  
 CC activating peptide factors and transmitters, transcription factors,  
 CC immunoglobulins and antibodies, antibody receptors, cytokines and  
 CC chemokines, endogenously produced specific and non-specific enzymes,  
 CC binding proteins, adhesion molecules and their receptors, cytokine and  
 CC chemokine receptors, adenosine receptors, bradykinin receptors, central  
 CC nervous system (CNS) and peripheral nervous and non-nervous system  
 CC receptors, CNS and peripheral nervous and non-nervous system peptide  
 CC transmitters, defensins, growth factors, vasoactive peptides and  
 CC receptors, binding proteins and malignancy associated proteins. The  
 CC antisense oligonucleotides may be used in this way to treat disorders  
 CC including respiratory obstruction (especially pulmonary obstruction  
 CC and/or bronchoconstriction) and/or lung inflammation, allergy(ies) and/or  
 CC surfactant hypoproduction which are associated with a disease or  
 CC condition selected from pulmonary vasoconstriction, inflammation,  
 CC allergies, asthma, impeded respiration, respiratory distress syndrome  
 CC (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary  
 CC hypertension, emphysema, chronic obstructive pulmonary disease (COPD),  
 CC pulmonary transplantation rejection, pulmonary infections, bronchitis,  
 CC and/or cancer. AAF18434 to AAF21543 represent human polynucleotide  
 CC fragments and antisense oligonucleotides used in the exemplification of  
 CC the present invention

XX

SQ Sequence 4286 BP; 1327 A; 829 C; 816 G; 1314 T; 0 U; 0 Other;

Query Match 99.6%; Score 4284.4; DB 3; Length 4286;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 4285; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

|    |     |   |     |
|----|-----|---|-----|
| Qy | 1   | GAGACATTCCGGTGGGGGACTCTGGCCAGCCCCGAGCAACGTGGATCCTGAGAGCACTCCC | 60  |
|    |     |   |     |
| Db | 1   | GAGACATTCCGGTGGGGGACTCTGGCCAGCCCCGAGCAACGTGGATCCTGAGAGCACTCCC | 60  |
| Qy | 61  | AGGTAGGCATTTGCCCCGGTGGGACGCCTTGCCAGAGCAGTGTGTGGCAGGCCCCCGTGG  | 120 |
|    |     |   |     |
| Db | 61  | AGGTAGGCATTTGCCCCGGTGGGACGCCTTGCCAGAGCAGTGTGTGGCAGGCCCCCGTGG  | 120 |
| Qy | 121 | AGGATCAACACAGTGGCTGAACACTGGGAAGGAACTGGTACTTGGAGTCTGGACATCTGA  | 180 |
|    |     |   |     |
| Db | 121 | AGGATCAACACAGTGGCTGAACACTGGGAAGGAACTGGTACTTGGAGTCTGGACATCTGA  | 180 |
| Qy | 181 | AACTTGGCTCTGAAACTGCGGAGCGGCCACCGACGCCTTCTGGAGCAGGTAGCAGCATG   | 240 |
|    |     |   |     |
| Db | 181 | AACTTGGCTCTGAAACTGCGGAGCGGCCACCGACGCCTTCTGGAGCAGGTAGCAGCATG   | 240 |
| Qy | 241 | CAGCCGCCTCCAAGTCTGTGCGGACGCGCCCTGGTTGCGCTGGTTCTGCCTGCGGCCTG   | 300 |
|    |     |   |     |
| Db | 241 | CAGCCGCCTCCAAGTCTGTGCGGACGCGCCCTGGTTGCGCTGGTTCTGCCTGCGGCCTG   | 300 |
| Qy | 301 | TCGCGGATCTGGGGAGAGGAGAGAGGCTTCCCGCTGACAGGGCCACTCCGCTTTTGCAA   | 360 |
|    |     |   |     |
| Db | 301 | TCGCGGATCTGGGGAGAGGAGAGAGGCTTCCCGCTGACAGGGCCACTCCGCTTTTGCAA   | 360 |
| Qy | 361 | ACCGCAGAGATAATGACGCCACCCACTAAGACCTTATGGCCCAAGGGTTCCAACGCCAGT  | 420 |

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|    |  |      |
| Db | 361 ACCGCAGAGATAATGACGCCACCCACTAAGACCTTATGGCCCAAGGGTTCCAACGCCAGT   | 420  |
| Qy | 421 CTGGCGCGGTCGTTGGCACCTGCGGAGGTGCCTAAAGGAGACAGGACGGCAGGATCTCCG   | 480  |
| Db | 421 CTGGCGCGGTCGTTGGCACCTGCGGAGGTGCCTAAAGGAGACAGGACGGCAGGATCTCCG   | 480  |
| Qy | 481 CCACGCACCATCTCCCCTCCCCCGTGCCAAGGACCCATCGAGATCAAGGAGACTTTCAA    | 540  |
| Db | 481 CCACGCACCATCTCCCCTCCCCCGTGCCAAGGACCCATCGAGATCAAGGAGACTTTCAA    | 540  |
| Qy | 541 TACATCAACACGGTTGTGTCTGCCTTGTGTTTCGTGCTGGGGATCATCGGGAACCTCACA   | 600  |
| Db | 541 TACATCAACACGGTTGTGTCTGCCTTGTGTTTCGTGCTGGGGATCATCGGGAACCTCACA   | 600  |
| Qy | 601 CTTCTGAGAATTATCTACAAGAACAAGTGCATGCGAAACGGTCCCAATATCTTGATCGCC   | 660  |
| Db | 601 CTTCTGAGAATTATCTACAAGAACAAGTGCATGCGAAACGGTCCCAATATCTTGATCGCC   | 660  |
| Qy | 661 AGCTTGGCTCTGGGAGACCTGCTGCACATCGTCATTGACATCCCTATCAATGTCTACAAG   | 720  |
| Db | 661 AGCTTGGCTCTGGGAGACCTGCTGCACATCGTCATTGACATCCCTATCAATGTCTACAAG   | 720  |
| Qy | 721 CTGCTGGCAGAGGACTGGCCATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTCATACAG   | 780  |
| Db | 721 CTGCTGGCAGAGGACTGGCCATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTCATACAG   | 780  |
| Qy | 781 AAAGCCTCCGTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATATCGA   | 840  |
| Db | 781 AAAGCCTCCGTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATATCGA   | 840  |
| Qy | 841 GCTGTTGCTTCTTGGAGTAGAATTAAAGGAATTGGGGTTCCAAAATGGACAGCAGTAGAA   | 900  |
| Db | 841 GCTGTTGCTTCTTGGAGTAGAATTAAAGGAATTGGGGTTCCAAAATGGACAGCAGTAGAA   | 900  |
| Qy | 901 ATTGTTTTGATTTGGGTGGTCTCTGTGGTTCTGGCTGTCCCTGAAGCCATAGGTTTTGAT   | 960  |
| Db | 901 ATTGTTTTGATTTGGGTGGTCTCTGTGGTTCTGGCTGTCCCTGAAGCCATAGGTTTTGAT   | 960  |
| Qy | 961 ATAATTACGATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTTTCAG  | 1020 |
| Db | 961 ATAATTACGATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTTTCAG  | 1020 |
| Qy | 1021 AAGACAGCTTTCATGCAGTTTTACAAGACAGCAAAAGATTGGTGGCTGTTTCAGTTTCTAT | 1080 |
| Db | 1021 AAGACAGCTTTCATGCAGTTTTACAAGACAGCAAAAGATTGGTGGCTGTTTCAGTTTCTAT | 1080 |
| Qy | 1081 TTCTGCTTGCCATTGGCCATCACTGCATTTTTTTATACACTAATGACCTGTGAAATGTTG  | 1140 |
| Db | 1081 TTCTGCTTGCCATTGGCCATCACTGCATTTTTTTATACACTAATGACCTGTGAAATGTTG  | 1140 |
| Qy | 1141 AGAAAGAAAAGTGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAAGTG  | 1200 |
| Db | 1141 AGAAAGAAAAGTGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAAGTG  | 1200 |
| Qy | 1201 GCCAAAACCGTCTTTTGCCTGGTCTTGTCTTTGCCCTCTGCTGGCTTCCCCTTCACCTC   | 1260 |



Db 1201 GCCAAAACCGTCTTTTGCCTGGTCCTTGTCTTTGCCCTCTGCTGGCTTCCCCTTCACCTC 1260  
 Qy 1261 AGCAGGATTCTGAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGAACCTTTTG 1320  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 1261 AGCAGGATTCTGAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGAACCTTTTG 1320  
 Qy 1321 AGCTTTCTGTTGGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCCTGCATT 1380  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 1321 AGCTTTCTGTTGGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCCTGCATT 1380  
 Qy 1381 AACCCAATTGCTCTGTATTTGGTGAGCAAAAGATTCAAAAACCTGCTTTAAGTCATGCTTA 1440  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 1381 AACCCAATTGCTCTGTATTTGGTGAGCAAAAGATTCAAAAACCTGCTTTAAGTCATGCTTA 1440  
 Qy 1441 TGCTGCTGGTGCCAGTCATTTGAAGAAAAACAGTCCTTGGAGGAAAAGCAGTCGTGCTTA 1500  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 1441 TGCTGCTGGTGCCAGTCATTTGAAGAAAAACAGTCCTTGGAGGAAAAGCAGTCGTGCTTA 1500  
 Qy 1501 AAGTTCAAAGCTAATGATCACGGATATGACAACTTCCGTTCCAGTAATAAATACAGCTCA 1560  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 1501 AAGTTCAAAGCTAATGATCACGGATATGACAACTTCCGTTCCAGTAATAAATACAGCTCA 1560  
 Qy 1561 TCTTGAAAGAAGAACTATTCACTGTATTTCAATTTTCTTTATATTGGACCGAAGTCATTAA 1620  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 1561 TCTTGAAAGAAGAACTATTCACTGTATTTCAATTTTCTTTATATTGGACCGAAGTCATTAA 1620  
 Qy 1621 AACAAAATGAAACATTTGCCAAAACAAAACAAAAAACTATGTATTTGCACAGCACACTAT 1680  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 1621 AACAAAATGAAACATTTGCCAAAACAAAACAAAAAACTATGTATTTGCACAGCACACTAT 1680  
 Qy 1681 TAAAATATTAAGTGTAATTATTTTAACACTCACAGCTACATATGACATTTTATGAGCTGT 1740  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 1681 TAAAATATTAAGTGTAATTATTTTAACACTCACAGCTACATATGACATTTTATGAGCTGT 1740  
 Qy 1741 TTACGGCATGGAAGAAAATCAGTGGGAATTAAGAAAGCCTCGTCGTGAAAGCACTTAAT 1800  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 1741 TTACGGCATGGAAGAAAATCAGTGGGAATTAAGAAAGCCTCGTCGTGAAAGCACTTAAT 1800  
 Qy 1801 TTTTACAGTTAGCACTTCAACATAGCTCTTAACAACCTCCAGGATATTCACACAACACT 1860  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 1801 TTTTACAGTTAGCACTTCAACATAGCTCTTAACAACCTCCAGGATATTCACACAACACT 1860  
 Qy 1861 TAGGCTTAAAAATGAGCTCACTCAGAATTTCTATTCTTTCTAAAAAGAGATTTATTTT 1920  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 1861 TAGGCTTAAAAATGAGCTCACTCAGAATTTCTATTCTTTCTAAAAAGAGATTTATTTT 1920  
 Qy 1921 AATCAATGGGACTCTGATATAAAGGAAGAATAAGTCACTGTAAAACAGAACCTTTTAAATG 1980  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 1921 AATCAATGGGACTCTGATATAAAGGAAGAATAAGTCACTGTAAAACAGAACCTTTTAAATG 1980  
 Qy 1981 AAGCTTAAATTACTCAATTTAAAAATTTTAAAAATCCTTTAAAAACAACCTTTTCAATTAATAT 2040  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 1981 AAGCTTAAATTACTCAATTTAAAAATTTTAAAAATCCTTTAAAAACAACCTTTTCAATTAATAT 2040  
 Qy 2041 TATCACACTATTATCAGATTGTAATTAGATGCAAATGAGAGAGCAGTTTAGTTGTTGCAT 2100  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 2041 TATCACACTATTATCAGATTGTAATTAGATGCAAATGAGAGAGCAGTTTAGTTGTTGCAT 2100

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|----|------|--|------|
| QY | 2101 | TTTTCGGACACTGGAAACATTTAAATGATCAGGAGGGAGTAACAGAAAGAGCAAGGCTGT   | 2160 |
|    |      |  |      |
| Db | 2101 | TTTTCGGACACTGGAAACATTTAAATGATCAGGAGGGAGTAACAGAAAGAGCAAGGCTGT   | 2160 |
| QY | 2161 | TTTTGAAAATCATTACACTTTTCTACTAGAAGCCCAAACCTCAGCATTCTGCAATATGTAAC | 2220 |
|    |      |  |      |
| Db | 2161 | TTTTGAAAATCATTACACTTTTCTACTAGAAGCCCAAACCTCAGCATTCTGCAATATGTAAC | 2220 |
| QY | 2221 | CAACATGTCACAAACAAGCAGCATGTAACAGACTGGCACATGTGCCAGCTGAATTTAAAA   | 2280 |
|    |      |  |      |
| Db | 2221 | CAACATGTCACAAACAAGCAGCATGTAACAGACTGGCACATGTGCCAGCTGAATTTAAAA   | 2280 |
| QY | 2281 | TATAATACTTTTAAAAAGAAAATTATTACATCCTTTACATTTCAGTTAAGATCAAACCTCA  | 2340 |
|    |      |  |      |
| Db | 2281 | TATAATACTTTTAAAAAGAAAATTATTACATCCTTTACATTTCAGTTAAGATCAAACCTCA  | 2340 |
| QY | 2341 | CAAAGAGAAATAGAATGTTTGAAAGGCTATCCCAAAGACTTTTTTGAATCTGTCATTCA    | 2400 |
|    |      |  |      |
| Db | 2341 | CAAAGAGAAATAGAATGTTTGAAAGGCTATCCCAAAGACTTTTTTGAATCTGTCATTCA    | 2400 |
| QY | 2401 | CATACCCTGTGAAGACAATACTATCTACAATTTTTTCAGGATTATTTAAATCTTCTTTTT   | 2460 |
|    |      |  |      |
| Db | 2401 | CATACCCTGTGAAGACAATACTATCTACAATTTTTTCAGGATTATTTAAATCTTCTTTTT   | 2460 |
| QY | 2461 | TCATCTATCGTAGCTTAAACTCTGTTTGGTTTTGTCTATCTGTAAATACTTACCTACATACA | 2520 |
|    |      |  |      |
| Db | 2461 | TCATCTATCGTAGCTTAAACTCTGTTTGGTTTTGTCTATCTGTAAATACTTACCTACATACA | 2520 |
| QY | 2521 | CTGCATGTAGATGATTAAATGAGGGCAGGCCCTGTGCTCATAGCTTTACGATGGAGAGAT   | 2580 |
|    |      |  |      |
| Db | 2521 | CTGCATGTAGATGATTAAATGAGGGCAGGCCCTGTGCTCATAGCTTTACGATGGAGAGAT   | 2580 |
| QY | 2581 | GCCAGTGACCTCATAATAAAGACTGTGAACTGCCTGGTGCAGTGTCCACATGACAAAGGG   | 2640 |
|    |      |  |      |
| Db | 2581 | GCCAGTGACCTCATAATAAAGACTGTGAACTGCCTGGTGCAGTGTCCACATGACAAAGGG   | 2640 |
| QY | 2641 | GCAGGTAGCACCCCTCTCTCACCCATGCTGTGGTTAAATGGTTTCTAGCATATGTATAAT   | 2700 |
|    |      |  |      |
| Db | 2641 | GCAGGTAGCACCCCTCTCTCACCCATGCTGTGGTTAAATGGTTTCTAGCATATGTATAAT   | 2700 |
| QY | 2701 | GCTATAGTTAAAATACTATTTTTTCAAAATCATAACAGATTAGTACATTTAACAGCTACCTG | 2760 |
|    |      |  |      |
| Db | 2701 | GCTATAGTTAAAATACTATTTTTTCAAAATCATAACAGATTAGTACATTTAACAGCTACCTG | 2760 |
| QY | 2761 | TAAAGCTTATTACTAATTTTTTGTATTATTTTTGTAAATAGCCAATAGAAAAGTTTGCTTG  | 2820 |
|    |      |  |      |
| Db | 2761 | TAAAGCTTATTACTAATTTTTTGTATTATTTTTGTAAATAGCCAATAGAAAAGTTTGCTTG  | 2820 |
| QY | 2821 | ACATGGTGCTTTTCTTTTCATCTAGAGGCAAACCTGCTTTTTTGAGACCGTAAGAACCTCTT | 2880 |
|    |      |  |      |
| Db | 2821 | ACATGGTGCTTTTCTTTTCATCTAGAGGCAAACCTGCTTTTTTGAGACCGTAAGAACCTCTT | 2880 |
| QY | 2881 | AGCTTTGTGCGTTCCTGCCTAATTTTTTATATCTTCTAAGCAAAGTGCCTTAGGATAGCTT  | 2940 |
|    |      |  |      |
| Db | 2881 | AGCTTTGTGCGTTCCTGCCTAATTTTTTATATCTTCTAAGCAAAGTGCCTTAGGATAGCTT  | 2940 |

Qy 2941 GGGATGAGATGTGTGTGAAAGTATGTACAAGAGAAAACGGAAGAGAGAGGAAATGAGGTG 3000  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 2941 GGGATGAGATGTGTGTGAAAGTATGTACAAGAGAAAACGGAAGAGAGAGGAAATGAGGTG 3000  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Qy 3001 GGGTTGGAGGAAACCCATGGGGACAGATTCCCATTCTTAGCCTAACGTTTCGTCATTGCCT 3060  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 3001 GGGTTGGAGGAAACCCATGGGGACAGATTCCCATTCTTAGCCTAACGTTTCGTCATTGCCT 3060  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Qy 3061 CGTCACATCAATGCAAAAGGTCCTGATTTTGTTCAGCAAAACACAGTGCAATGTTCTCA 3120  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 3061 CGTCACATCAATGCAAAAGGTCCTGATTTTGTTCAGCAAAACACAGTGCAATGTTCTCA 3120  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Qy 3121 GAGTGACTTTCGAAATAAATTGGGCCCAAGAGCTTTAACTCGGTCTTAAATATGCCCAA 3180  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 3121 GAGTGACTTTCGAAATAAATTGGGCCCAAGAGCTTTAACTCGGTCTTAAATATGCCCAA 3180  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Qy 3181 ATTTTACTTTGTTTTCTTTTAAATAGGCTGGGCCACATGTTGGAAATAAGCTAGTAATG 3240  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 3181 ATTTTACTTTGTTTTCTTTTAAATAGGCTGGGCCACATGTTGGAAATAAGCTAGTAATG 3240  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Qy 3241 TTGTTTTCTGTCAATATTGAATGTGATGGTACAGTAAACCAAAACCAACAATGTGGCCA 3300  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 3241 TTGTTTTCTGTCAATATTGAATGTGATGGTACAGTAAACCAAAACCAACAATGTGGCCA 3300  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Qy 3301 GAAAGAAAGAGCAATAATAATTAATTCACACACCATATGGATTCTATTTATAAATCACCC 3360  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 3301 GAAAGAAAGAGCAATAATAATTAATTCACACACCATATGGATTCTATTTATAAATCACCC 3360  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Qy 3361 ACAAACTTGTTCTTTAATTTTCATCCCAATCACTTTTTTCAGAGGCCTGTTATCATAGAAGT 3420  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 3361 ACAAACTTGTTCTTTAATTTTCATCCCAATCACTTTTTTCAGAGGCCTGTTATCATAGAAGT 3420  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Qy 3421 CATTTTAGACTCTCAATTTTAAATTAATTTTGAATCACTAATATTTTCACAGTTTATTAA 3480  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 3421 CATTTTAGACTCTCAATTTTAAATTAATTTTGAATCACTAATATTTTCACAGTTTATTAA 3480  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Qy 3481 TATATTTAATTTCTATTTAAATTTTAGATTATTTTATTACCATGTACTGAATTTTACA 3540  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 3481 TATATTTAATTTCTATTTAAATTTTAGATTATTTTATTACCATGTACTGAATTTTACA 3540  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Qy 3541 TCCTGATACCCTTTCCTTCTCCATGTCAGTATCATGTTCTCTAATTATCTTGCCAAATTT 3600  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 3541 TCCTGATACCCTTTCCTTCTCCATGTCAGTATCATGTTCTCTAATTATCTTGCCAAATTT 3600  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Qy 3601 TGAAACTACACACAAAAAGCATACTTGCATTATTTATAATAAAATTGCATTTCAGTGGCTT 3660  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 3601 TGAAACTACACACAAAAAGCATACTTGCATTATTTATAATAAAATTGCATTTCAGTGGCTT 3660  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Qy 3661 TTTAAAAAAATGTTTGATTCAAACTTTAACATACTGATAAGTAAGAAACAATTATAAT 3720  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 3661 TTTAAAAAAATGTTTGATTCAAACTTTAACATACTGATAAGTAAGAAACAATTATAAT 3720  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Qy 3721 TTCTTTACATACTCAAACCAAGATAGAAAAAGGTGCTATCGTTCAACTTCAAACATGT 3780  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 3721 TTCTTTACATACTCAAACCAAGATAGAAAAAGGTGCTATCGTTCAACTTCAAACATGT 3780  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Qy 3781 TTCCTAGTATTAAGGACTTTAATATAGCAACAGACAAAATTATTGTTAACATGGATGTTA 3840

|    |      |  |  |      |
|----|------|--|--|------|
| Db | 3781 |  | TTCCTAGTATTAAGGACTTTAATATAGCAACAGACAAAATTATTGTTAACATGGATGTTA | 3840 |
| Qy | 3841 |  | CAGCTCAAAGATTATATAAGATTTTAACCTATTTCTCCCTTATTATCCACTGCTAAT    | 3900 |
| Db | 3841 |  | CAGCTCAAAGATTATATAAGATTTTAACCTATTTCTCCCTTATTATCCACTGCTAAT    | 3900 |
| Qy | 3901 |  | GTGGATGTATGTTCAAACACCTTTTAGTATTGATAGCTTACATATGGCCAAAGGAATACA | 3960 |
| Db | 3901 |  | GTGGATGTATGTTCAAACACCTTTTAGTATTGATAGCTTACATATGGCCAAAGGAATACA | 3960 |
| Qy | 3961 |  | GTTTATAGCAAAACATGGGTATGCTGTAGCTAACTTTATAAAAGTGTAATATAACAATGT | 4020 |
| Db | 3961 |  | GTTTATAGCAAAACATGGGTATGCTGTAGCTAACTTTATAAAAGTGTAATATAACAATGT | 4020 |
| Qy | 4021 |  | AAAAAATTATATATCTGGGAGGATTTTTTGGTTGCCTAAAGTGGCTATAGTTACTGATTT | 4080 |
| Db | 4021 |  | AAAAAATTATATATCTGGGAGGATTTTTTGGTTGCCTAAAGTGGCTATAGTTACTGATTT | 4080 |
| Qy | 4081 |  | TTTATTATGTAAGCAAACCAATAAAAAATTTAAGTTTTTTTAACTACCTTATTTTTC    | 4140 |
| Db | 4081 |  | TTTATTATGTAAGCAAACCAATAAAAAATTTAAGTTTTTTTAACTACCTTATTTTTC    | 4140 |
| Qy | 4141 |  | ACTGTACAGACACTAATTCATTAAATACTAATTGATTGTTTAAAGAAATATAAATGTGA  | 4200 |
| Db | 4141 |  | ACTGTACAGACACTAATTCATTAAATACTAATTGATTGTTTAAAGAAATATAAATGTGA  | 4200 |
| Qy | 4201 |  | CAAGTGGACATTATTTATGTTAAATATACAATTATCAAGCAAGTATGAAGTTATTCAATT | 4260 |
| Db | 4201 |  | CAAGTGGACATTATTTATGTTAAATATACAATTATCAAGCAAGTATGAAGTTATTCAATT | 4260 |
| Qy | 4261 |  | AAAATGCCACATTTCTGGTCTCTGGG                                   | 4286 |
| Db | 4261 |  | AAAATGCCACATTTCTGGTCTCTGGG                                   | 4286 |

RESULT 4

ABV94186

ID ABV94186 standard; cDNA; 4286 BP.

XX

AC ABV94186;

XX

DT 08-JAN-2003 (first entry)

XX

DE Breast carcinoma related nucleotide sequence SEQ ID NO:177.

XX

KW Human; breast carcinoma; cancer; tumour; cytostatic; anti-tumour; gene;  
KW ss.

XX

OS Homo sapiens.

XX

PN WO200246467-A2.

XX

PD 13-JUN-2002.

XX

PF 07-DEC-2001; 2001WO-IB002811.

XX

|    |     |  |     |
|----|-----|--|-----|
| Qy | 1   | GAGACATTCCGGTGGGGGACTCTGGCCAGCCCAGCAACGTGGATCCTGAGAGCACTCCC  | 60  |
|    |     |  |     |
| Db | 1   | GAGACATTCCGGTGGGGGACTCTGGCCAGCCCAGCAACGTGGATCCTGAGAGCACTCCC  | 60  |
| Qy | 61  | AGGTAGGCATTTGCCCCGGTGGGACGCCTTGCCAGAGCAGTGTGTGGCAGGCCCCCGTGG | 120 |
|    |     |  |     |
| Db | 61  | AGGTAGGCATTTGCCCCGGTGGGACGCCTTGCCAGAGCAGTGTGTGGCAGGCCCCCGTGG | 120 |
| Qy | 121 | AGGATCAACACAGTGGCTGAACACTGGGAAGGAACTGGTACTTGAGTCTGGACATCTGA  | 180 |
|    |     |  |     |

Db 121 AGGATCAACACAGTGGCTGAACACTGGGAAGGAAGTGGTACTTGGAGTCTGGACATCTGA 180  
 Qy 181 AACTTGGCTCTGAAACTGCGGAGCGGCCACCGGACGCCTTCTGGAGCAGGTAGCAGCATG 240  
 ||||||||||||||||||| ||||||||||||||||||| |||||||||||||||||||  
 Db 181 AACTTGGCTCTGAAACTGCGCAGCGGCCACCGGACGCCTTCTGGAGCAGGTAGCAGCATG 240  
 Qy 241 CAGCCGCCTCCAAGTCTGTGCGGACGCGCCCTGGTTGCGCTGGTTCTTGCCTGCGGCCTG 300  
 ||||||||||||||||||| ||||||||||||||||||| |||||||||||||||||||  
 Db 241 CAGCCGCCTCCAAGTCTGTGCGGACGCGCCCTGGTTGCGCTGGTTCTTGCCTGCGGCCTG 300  
 Qy 301 TCGCGGATCTGGGGAGAGGAGAGAGGCTTCCCGCCTGACAGGGCCACTCCGCTTTTGCAA 360  
 ||||||||||||||||||| ||||||||||||||||||| |||||||||||||||||||  
 Db 301 TCGCGGATCTGGGGAGAGGAGAGAGGCTTCCCGCCTGACAGGGCCACTCCGCTTTTGCAA 360  
 Qy 361 ACCGCAGAGATAATGACGCCACCCACTAAGACCTTATGGCCCAAGGGTTCCAACGCCAGT 420  
 ||||||||||||||||||| ||||||||||||||||||| |||||||||||||||||||  
 Db 361 ACCGCAGAGATAATGACGCCACCCACTAAGACCTTATGGCCCAAGGGTTCCAACGCCAGT 420  
 Qy 421 CTGGCGCGGTTCGTTGGCACCTGCGGAGGTGCCTAAAGGAGACAGGACGGCAGGATCTCCG 480  
 ||||||||||||||||||| ||||||||||||||||||| |||||||||||||||||||  
 Db 421 CTGGCGCGGTTCGTTGGCACCTGCGGAGGTGCCTAAAGGAGACAGGACGGCAGGATCTCCG 480  
 Qy 481 CCACGCACCATCTCCCCTCCCCCGTGCCAAGGACCCATCGAGATCAAGGAGACTTTTCAA 540  
 ||||||||||||||||||| ||||||||||||||||||| |||||||||||||||||||  
 Db 481 CCACGCACCATCTCCCCTCCCCCGTGCCAAGGACCCATCGAGATCAAGGAGACTTTTCAA 540  
 Qy 541 TACATCAACACGGTTGTGTCTGCCTTGTGTTTCGTGCTGGGGATCATCGGGAAGTCCACA 600  
 ||||||||||||||||||| ||||||||||||||||||| |||||||||||||||||||  
 Db 541 TACATCAACACGGTTGTGTCTGCCTTGTGTTTCGTGCTGGGGATCATCGGGAAGTCCACA 600  
 Qy 601 CTTCTGAGAATTATCTACAAGAACAAGTGCATGCGAAACGGTCCCAATATCTTGATCGCC 660  
 ||||||||||||||||||| ||||||||||||||||||| |||||||||||||||||||  
 Db 601 CTTCTGAGAATTATCTACAAGAACAAGTGCATGCGAAACGGTCCCAATATCTTGATCGCC 660  
 Qy 661 AGCTTGGCTCTGGGAGACCTGCTGCACATCGTCATTGACATCCCTATCAATGTCTACAAG 720  
 ||||||||||||||||||| ||||||||||||||||||| |||||||||||||||||||  
 Db 661 AGCTTGGCTCTGGGAGACCTGCTGCACATCGTCATTGACATCCCTATCAATGTCTACAAG 720  
 Qy 721 CTGCTGGCAGAGGACTGGCCATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTCATACAG 780  
 ||||||||||||||||||| ||||||||||||||||||| |||||||||||||||||||  
 Db 721 CTGCTGGCAGAGGACTGGCCATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTCATACAG 780  
 Qy 781 AAAGCCTCCGTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATATCGA 840  
 ||||||||||||||||||| ||||||||||||||||||| |||||||||||||||||||  
 Db 781 AAAGCCTCCGTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATATCGA 840  
 Qy 841 GCTGTTGCTTCTTGGAGTAGAATTAAAGGAATTGGGGTTCCAAAATGGACAGCAGTAGAA 900  
 ||||||||||||||||||| ||||||||||||||||||| |||||||||||||||||||  
 Db 841 GCTGTTGCTTCTTGGAGTAGAATTAAAGGAATTGGGGTTCCAAAATGGACAGCAGTAGAA 900  
 Qy 901 ATTGTTTTGATTGGGTGGTCTCTGTGGTTCTGGCTGTCCCTGAAGCCATAGGTTTTGAT 960  
 ||||||||||||||||||| ||||||||||||||||||| |||||||||||||||||||  
 Db 901 ATTGTTTTGATTGGGTGGTCTCTGTGGTTCTGGCTGTCCCTGAAGCCATAGGTTTTGAT 960  
 Qy 961 ATAATTACGATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTTCAG 1020  
 ||||||||||||||||||| ||||||||||||||||||| |||||||||||||||||||  
 Db 961 ATAATTACGATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTTCAG 1020

|    |      |  |      |
|----|------|--|------|
| Qy | 1021 | AAGACAGCTTTTCATGCAGTTTTACAAGACAGCAAAAGATTGGTGGCTGTTTCAGTTTCTAT | 1080 |
|    |      |  |      |
| Db | 1021 | AAGACAGCTTTTCATGCAGTTTTACAAGACAGCAAAAGATTGGTGGCTGTTTCAGTTTCTAT | 1080 |
| Qy | 1081 | TTCTGCTTGCCATTGGCCATCACTGCATTTTTTTATACACTAATGACCTGTGAAATGTTG   | 1140 |
|    |      |  |      |
| Db | 1081 | TTCTGCTTGCCATTGGCCATCACTGCATTTTTTTATACACTAATGACCTGTGAAATGTTG   | 1140 |
| Qy | 1141 | AGAAAGAAAAGTGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAAGTG   | 1200 |
|    |      |  |      |
| Db | 1141 | AGAAAGAAAAGTGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAAGTG   | 1200 |
| Qy | 1201 | GCCAAAACCGTCTTTTGCTGGTCCTTGCTTTGCCCTCTGCTGGCTTCCCCTTCACCTC     | 1260 |
|    |      |  |      |
| Db | 1201 | GCCAAAACCGTCTTTTGCTGGTCCTTGCTTTGCCCTCTGCTGGCTTCCCCTTCACCTC     | 1260 |
| Qy | 1261 | AGCAGGATTCTGAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGAACCTTTG   | 1320 |
|    |      |  |      |
| Db | 1261 | AGCAGGATTCTGAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGAACCTTTG   | 1320 |
| Qy | 1321 | AGCTTTCTGTTGGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCCTGCATT   | 1380 |
|    |      |  |      |
| Db | 1321 | AGCTTTCTGTTGGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCCTGCATT   | 1380 |
| Qy | 1381 | AACCCAATTGCTCTGTATTTGGTGAGCAAAAGATTCAAAAAGCTTTAAGTCATGCTTA     | 1440 |
|    |      |  |      |
| Db | 1381 | AACCCAATTGCTCTGTATTTGGTGAGCAAAAGATTCAAAAAGCTTTAAGTCATGCTTA     | 1440 |
| Qy | 1441 | TGCTGCTGGTGCCAGTCATTTGAAGAAAACAGTCCTTGGAGGAAAAGCAGTCGTGCTTA    | 1500 |
|    |      |  |      |
| Db | 1441 | TGCTGCTGGTGCCAGTCATTTGAAGAAAACAGTCCTTGGAGGAAAAGCAGTCGTGCTTA    | 1500 |
| Qy | 1501 | AAGTTCAAAGCTAATGATCACGGATATGACAACTCCGTTCCAGTAATAAATACAGCTCA    | 1560 |
|    |      |  |      |
| Db | 1501 | AAGTTCAAAGCTAATGATCACGGATATGACAACTCCGTTCCAGTAATAAATACAGCTCA    | 1560 |
| Qy | 1561 | TCTTGAAAGAAGAACTATTCACTGTATTTTCTTTATATTGGACCGAAGTCATTAA        | 1620 |
|    |      |  |      |
| Db | 1561 | TCTTGAAAGAAGAACTATTCACTGTATTTTCTTTATATTGGACCGAAGTCATTAA        | 1620 |
| Qy | 1621 | AACAAAATGAAACATTTGCCAAAACAAAACAAAAAACTATGTATTTGCACAGCACACTAT   | 1680 |
|    |      |  |      |
| Db | 1621 | AACAAAATGAAACATTTGCCAAAACAAAACAAAAAACTATGTATTTGCACAGCACACTAT   | 1680 |
| Qy | 1681 | TAAAATATTAAGTGTAATTATTTTAACACTCACAGCTACATATGACATTTTATGAGCTGT   | 1740 |
|    |      |  |      |
| Db | 1681 | TAAAATATTAAGTGTAATTATTTTAACACTCACAGCTACATATGACATTTTATGAGCTGT   | 1740 |
| Qy | 1741 | TTACGGCATGGAAAGAAAATCAGTGGGAATTAAGAAAGCCTCGTCGTGAAAGCACTTAAT   | 1800 |
|    |      |  |      |
| Db | 1741 | TTACGGCATGGAAAGAAAATCAGTGGGAATTAAGAAAGCCTCGTCGTGAAAGCACTTAAT   | 1800 |
| Qy | 1801 | TTTTTACAGTTAGCACTTCAACATAGCTCTTAACAACTTCCAGGATATTCACACAACACT   | 1860 |
|    |      |  |      |
| Db | 1801 | TTTTTACAGTTAGCACTTCAACATAGCTCTTAACAACTTCCAGGATATTCACACAACACT   | 1860 |

|    |      |   |      |
|----|------|---|------|
| Qy | 1861 | TAGGCTTAAAAATGAGCTCACTCAGAATTTCTATTCTTTCTAAAAAGAGATTTATTTTTTA | 1920 |
| Db | 1861 | TAGGCTTAAAAATGAGCTCACTCAGAATTTCTATTCTTTCTAAAAAGAGATTTATTTTTTA | 1920 |
| Qy | 1921 | AATCAATGGGACTCTGATATAAAGGAAGAATAAGTCACTGTAAACAGAACTTTTAAATG   | 1980 |
| Db | 1921 | AATCAATGGGACTCTGATATAAAGGAAGAATAAGTCACTGTAAACAGAACTTTTAAATG   | 1980 |
| Qy | 1981 | AAGCTTAAATTACTCAATTTAAAATTTTAAAATCCTTTAAAACAACCTTTTCAATTAATAT | 2040 |
| Db | 1981 | AAGCTTAAATTACTCAATTTAAAATTTTAAAATCCTTTAAAACAACCTTTTCAATTAATAT | 2040 |
| Qy | 2041 | TATCACACTATTATCAGATTGTAATTAGATGCAAATGAGAGAGCAGTTTAGTTGTTGCAT  | 2100 |
| Db | 2041 | TATCACACTATTATCAGATTGTAATTAGATGCAAATGAGAGAGCAGTTTAGTTGTTGCAT  | 2100 |
| Qy | 2101 | TTTTCGGACACTGGAAACATTTAAATGATCAGGAGGGAGTAACAGAAAGAGCAAGGCTGT  | 2160 |
| Db | 2101 | TTTTCGGACACTGGAAACATTTAAATGATCAGGAGGGAGTAACAGAAAGAGCAAGGCTGT  | 2160 |
| Qy | 2161 | TTTTGAAAATCATTACACTTTTACTAGAAGCCCAAACCTCAGCATTCTGCAATATGTAAC  | 2220 |
| Db | 2161 | TTTTGAAAATCATTACACTTTTACTAGAAGCCCAAACCTCAGCATTCTGCAATATGTAAC  | 2220 |
| Qy | 2221 | CAACATGTCACAAACAAGCAGCATGTAACAGACTGGCACATGTGCCAGCTGAATTTAAAA  | 2280 |
| Db | 2221 | CAACATGTCACAAACAAGCAGCATGTAACAGACTGGCACATGTGCCAGCTGAATTTAAAA  | 2280 |
| Qy | 2281 | TATAATACTTTTAAAAAGAAAATTATTACATCCTTTACATTAGTTAAGATCAAACCTCA   | 2340 |
| Db | 2281 | TATAATACTTTTAAAAAGAAAATTATTACATCCTTTACATTAGTTAAGATCAAACCTCA   | 2340 |
| Qy | 2341 | CAAAGAGAAATAGAATGTTTGAAAGGCTATCCCAAAGACTTTTTTTGAATCTGTCATTCA  | 2400 |
| Db | 2341 | CAAAGAGAAATAGAATGTTTGAAAGGCTATCCCAAAGACTTTTTTTGAATCTGTCATTCA  | 2400 |
| Qy | 2401 | CATACCCTGTGAAGACAATACTATCTACAATTTTTTCAGGATTATTAAAATCTTCTTTTT  | 2460 |
| Db | 2401 | CATACCCTGTGAAGACAATACTATCTACAATTTTTTCAGGATTATTAAAATCTTCTTTTT  | 2460 |
| Qy | 2461 | TCACTATCGTAGCTTAAACTCTGTTTGGTTTTGTCATCTGTAAATACTTACCTACATACA  | 2520 |
| Db | 2461 | TCACTATCGTAGCTTAAACTCTGTTTGGTTTTGTCATCTGTAAATACTTACCTACATACA  | 2520 |
| Qy | 2521 | CTGCATGTAGATGATTAAATGAGGGCAGGCCCTGTGCTCATAGCTTTACGATGGAGAGAT  | 2580 |
| Db | 2521 | CTGCATGTAGATGATTAAATGAGGGCAGGCCCTGTGCTCATAGCTTTACGATGGAGAGAT  | 2580 |
| Qy | 2581 | GCCAGTGACCTCATAATAAAGACTGTGAACTGCCTGGTGCAGTGTCCACATGACAAAGGG  | 2640 |
| Db | 2581 | GCCAGTGACCTCATAATAAAGACTGTGAACTGCCTGGTGCAGTGTCCACATGACAAAGGG  | 2640 |
| Qy | 2641 | GCAGGTAGCACCTCTCTCACCCTGCTGTGGTTAAAATGGTTTCTAGCATATGTATAAT    | 2700 |
| Db | 2641 | GCAGGTAGCACCTCTCTCACCCTGCTGTGGTTAAAATGGTTTCTAGCATATGTATAAT    | 2700 |
| Qy | 2701 | GCTATAGTTAAAATACTATTTTTTCAAATCATACAGATTAGTACATTTAACAGCTACCTG  | 2760 |



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| Db | 2701 | <br>GCTATAGTTAAAATACTATTTTTCAAATCATACAGATTAGTACATTTAACAGCTACCTG    | 2760 |
| Qy | 2761 | TAAAGCTTATTACTAATTTTTGTATTATTTTTGTAAATAGCCAATAGAAAAGTTTGCTTG       | 2820 |
| Db | 2761 | <br>TAAAGCTTATTACTAATTTTTGTATTATTTTTGTAAATAGCCAATAGAAAAGTTTGCTTG   | 2820 |
| Qy | 2821 | ACATGGTGCTTTTCTTTTCATCTAGAGGCAAACTGCTTTTTGAGACCGTAAGAACCTCTT       | 2880 |
| Db | 2821 | <br>ACATGGTGCTTTTCTTTTCATCTAGAGGCAAACTGCTTTTTGAGACCGTAAGAACCTCTT   | 2880 |
| Qy | 2881 | AGCTTTGTGCGTTCCTGCCTAATTTTTATATCTTCTAAGCAAAGTGCCTTAGGATAGCTT       | 2940 |
| Db | 2881 | <br>AGCTTTGTGCGTTCCTGCCTAATTTTTATATCTTCTAAGCAAAGTGCCTTAGGATAGCTT   | 2940 |
| Qy | 2941 | GGGATGAGATGTGTGTGAAAGTATGTACAAGAGAAAACGGAAGAGAGAGGAAATGAGGTG       | 3000 |
| Db | 2941 | <br>GGGATGAGATGTGTGTGAAAGTATGTACAAGAGAAAACGGAAGAGAGAGGAAATGAGGTG   | 3000 |
| Qy | 3001 | GGGTTGGAGGAAACCCATGGGGACAGATTCCCATTCTTAGCCTAACGTTTCGTCAATTGCCT     | 3060 |
| Db | 3001 | <br>GGGTTGGAGGAAACCCATGGGGACAGATTCCCATTCTTAGCCTAACGTTTCGTCAATTGCCT | 3060 |
| Qy | 3061 | CGTCACATCAATGCAAAAGGTCCTGATTTTGTTCAGCAAAACACAGTGCAATGTTCTCA        | 3120 |
| Db | 3061 | <br>CGTCACATCAATGCAAAAGGTCCTGATTTTGTTCAGCAAAACACAGTGCAATGTTCTCA    | 3120 |
| Qy | 3121 | GAGTGACTTTCGAAATAAATTGGGCCCAAGAGCTTTAACTCGGTCTTAAATATGCCCAA        | 3180 |
| Db | 3121 | <br>GAGTGACTTTCGAAATAAATTGGGCCCAAGAGCTTTAACTCGGTCTTAAATATGCCCAA    | 3180 |
| Qy | 3181 | ATTTTTACTTTGTTTTTCTTTTAAATAGGCTGGGCCACATGTTGGAAATAAGCTAGTAATG      | 3240 |
| Db | 3181 | <br>ATTTTTACTTTGTTTTTCTTTTAAATAGGCTGGGCCACATGTTGGAAATAAGCTAGTAATG  | 3240 |
| Qy | 3241 | TTGTTTTCTGTCAATATTGAATGTGATGGTACAGTAAACCAAAACCCAACAATGTGGCCA       | 3300 |
| Db | 3241 | <br>TTGTTTTCTGTCAATATTGAATGTGATGGTACAGTAAACCAAAACCCAACAATGTGGCCA   | 3300 |
| Qy | 3301 | GAAAGAAAGAGCAATAATAATTAATTCACACACCATATGGATTCTATTTATAAATCACCC       | 3360 |
| Db | 3301 | <br>GAAAGAAAGAGCAATAATAATTAATTCACACACCATATGGATTCTATTTATAAATCACCC   | 3360 |
| Qy | 3361 | ACAAACTTGTTCTTTAATTTTCATCCCAATCACTTTTTTCAGAGGCCTGTTATCATAGAAGT     | 3420 |
| Db | 3361 | <br>ACAAACTTGTTCTTTAATTTTCATCCCAATCACTTTTTTCAGAGGCCTGTTATCATAGAAGT | 3420 |
| Qy | 3421 | CATTTTAGACTCTCAATTTTAAATTAATTTTGAATCACTAATATTTTCACAGTTTATTAA       | 3480 |
| Db | 3421 | <br>CATTTTAGACTCTCAATTTTAAATTAATTTTGAATCACTAATATTTTCACAGTTTATTAA   | 3480 |
| Qy | 3481 | TATATTTAATTTCTATTTAAATTTTAGATTATTTTTATTACCATGTACTGAATTTTACA        | 3540 |
| Db | 3481 | <br>TATATTTAATTTCTATTTAAATTTTAGATTATTTTTATTACCATGTACTGAATTTTACA    | 3540 |
| Qy | 3541 | TCCTGATACCCTTTTCCTTCTCCATGTCAAGTATCATGTTCTCTAATTATCTTGCCAAATTT     | 3600 |
|    |      |  |      |

|    |      |   |      |
|----|------|---|------|
| Db | 3541 | TCCTGATACCCCTTTCCTTCTCCATGTCAGTATCATGTTCTCTAATTATCTTGCCAAATTT | 3600 |
| Qy | 3601 | TGAAACTACACACAAAAAGCATACTTGCATTATTTATAATAAAATTGCATTTCAGTGGCTT | 3660 |
| Db | 3601 | TGAAACTACACACAAAAAGCATACTTGCATTATTTATAATAAAATTGCATTTCAGTGGCTT | 3660 |
| Qy | 3661 | TTTAAAAAAATGTTTGATTCAAAACTTTAACATACTGATAAGTAAGAAACAATTATAAT   | 3720 |
| Db | 3661 | TTTAAAAAAATGTTTGATTCAAAACTTTAACATACTGATAAGTAAGAAACAATTATAAT   | 3720 |
| Qy | 3721 | TTCTTTACATACTCAAACCAAGATAGAAAAAGGTGCTATCGTTCAACTTCAAACATGT    | 3780 |
| Db | 3721 | TTCTTTACATACTCAAACCAAGATAGAAAAAGGTGCTATCGTTCAACTTCAAACATGT    | 3780 |
| Qy | 3781 | TTCCTAGTATTAAGGACTTTAATATAGCAACAGACAAAATTATTGTTAACATGGATGTTA  | 3840 |
| Db | 3781 | TTCCTAGTATTAAGGACTTTAATATAGCAACAGACAAAATTATTGTTAACATGGATGTTA  | 3840 |
| Qy | 3841 | CAGCTCAAAAGATTTATAAAAGATTTTAACCTATTTTCTCCCTTATTATCCACTGCTAAT  | 3900 |
| Db | 3841 | CAGCTCAAAAGATTTATAAAAGATTTTAACCTATTTTCTCCCTTATTATCCACTGCTAAT  | 3900 |
| Qy | 3901 | GTGGATGTATGTTCAAACACCTTTTAGTATTGATAGCTTACATATGGCCAAAGGAATACA  | 3960 |
| Db | 3901 | GTGGATGTATGTTCAAACACCTTTTAGTATTGATAGCTTACATATGGCCAAAGGAATACA  | 3960 |
| Qy | 3961 | GTTTATAGCAAAACATGGGTATGCTGTAGCTAACTTTATAAAAGTGTAATATAACAATGT  | 4020 |
| Db | 3961 | GTTTATAGCAAAACATGGGTATGCTGTAGCTAACTTTATAAAAGTGTAATATAACAATGT  | 4020 |
| Qy | 4021 | AAAAAATTATATATCTGGGAGGATTTTTTGGTTGCCTAAAGTGGCTATAGTTACTGATTT  | 4080 |
| Db | 4021 | AAAAAATTATATATCTGGGAGGATTTTTTGGTTGCCTAAAGTGGCTATAGTTACTGATTT  | 4080 |
| Qy | 4081 | TTTATTATGTAAGCAAAACCAATAAAATTTAAGTTTTTTTAACTACCTTATTTTTT      | 4140 |
| Db | 4081 | TTTATTATGTAAGCAAAACCAATAAAATTTAAGTTTTTTTAACTACCTTATTTTTT      | 4140 |
| Qy | 4141 | ACTGTACAGACACTAATTCATTAAATACTAATTGATTGTTTAAAGAAATATAAATGTGA   | 4200 |
| Db | 4141 | ACTGTACAGACACTAATTCATTAAATACTAATTGATTGTTTAAAGAAATATAAATGTGA   | 4200 |
| Qy | 4201 | CAAGTGGACATTATTTATGTTAAATATACAATTATCAAGCAAGTATGAAGTTATTCAATT  | 4260 |
| Db | 4201 | CAAGTGGACATTATTTATGTTAAATATACAATTATCAAGCAAGTATGAAGTTATTCAATT  | 4260 |
| Qy | 4261 | AAAATGCCACATTTCTGGTCTCTGGG                                    | 4286 |
| Db | 4261 | AAAATGCCACATTTCTGGTCTCTGGG                                    | 4286 |

RESULT 5

ABZ96978

ID ABZ96978 standard; DNA; 4286 BP.

XX

AC ABZ96978;

XX

DT 17-OCT-2003 (first entry)  
 XX  
 DE Human nucleic acid sequence.  
 XX  
 KW Human; antisense; lung dysfunction; nasal airway dysfunction;  
 KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;  
 KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;  
 KW antisense gene therapy; respiratory; lung; adenosine sensitivity;  
 KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;  
 KW lung inflammation; respiratory disease; ds.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200285308-A2.  
 XX  
 PD 31-OCT-2002.  
 XX  
 PF 23-APR-2002; 2002WO-US013135.  
 XX  
 PR 24-APR-2001; 2001US-0286137P.  
 XX  
 PA (EPIG-) EPIGENESIS PHARM INC.  
 XX  
 PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;  
 PI Miller S, Tang L, Shahabuddin S;  
 XX  
 DR WPI; 2003-229219/22.  
 XX  
 PT Pharmaceutical composition for treating ailments associated with impaired  
 PT respiration, has oligo(s) antisense to specific gene(s) or its  
 PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or  
 PT ubiquinone.  
 XX  
 PS Disclosure; SEQ ID NO 12220; 872pp; English.  
 XX  
 CC The invention relates to a novel pharmaceutical composition, which has a  
 CC first active agent comprising an oligonucleotide antisense to the  
 CC initiation codon, coding region, 5' or 3' end genomic flanking regions,  
 CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of  
 CC junctions of genes encoding a polypeptide associated with lung and/or  
 CC nasal airway dysfunction and a second active agent comprising an  
 CC antiinflammatory steroid and ubiquinone. A composition of the invention  
 CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,  
 CC immunosuppressive, and cytostatic activity. The composition may have a  
 CC use in antisense gene therapy. The composition is useful for treating or  
 CC preventing a respiratory, lung or malignant disease or condition, also  
 CC for enhancing the prophylactic or therapeutic respiratory effect of an  
 CC antiinflammatory steroid in a subject, for reducing or depleting levels  
 CC of, or reducing sensitivity to adenosine, reducing levels of adenosine  
 CC receptor, producing bronchodilation, increasing levels of ubiquinone or  
 CC lung surfactant in a subject's tissue, or treating bronchoconstriction,  
 CC lung inflammation, lung allergies, or a respiratory disease or condition.  
 CC Note: The sequence data for this patent is not represented in the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 SQ Sequence 4286 BP; 1327 A; 829 C; 816 G; 1314 T; 0 U; 0 Other;

Query Match 99.6%; Score 4284.4; DB 7; Length 4286;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 4285; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
QY      1 GAGACATTCCGGTGGGGGACTCTGGCCAGCCCGAGCAACGTGGATCCTGAGAGCACTCCC 60
      |||
Db      1 GAGACATTCCGGTGGGGGACTCTGGCCAGCCCGAGCAACGTGGATCCTGAGAGCACTCCC 60

QY     61 AGGTAGGCATTTGCCCCGGTGGGACGCCTTGCCAGAGCAGTGTGTGGCAGGCCCCCGTGG 120
      |||
Db     61 AGGTAGGCATTTGCCCCGGTGGGACGCCTTGCCAGAGCAGTGTGTGGCAGGCCCCCGTGG 120

QY    121 AGGATCAACACAGTGGCTGAACACTGGGAAGGAACTGGTACTTGGAGTCTGGACATCTGA 180
      |||
Db    121 AGGATCAACACAGTGGCTGAACACTGGGAAGGAACTGGTACTTGGAGTCTGGACATCTGA 180

QY    181 AACTTGGCTCTGAAACTGCGGAGCGGCCACCGACGCCTTCTGGAGCAGGTAGCAGCATG 240
      |||
Db    181 AACTTGGCTCTGAAACTGCGCAGCGGCCACCGACGCCTTCTGGAGCAGGTAGCAGCATG 240

QY    241 CAGCCGCCTCCAAGTCTGTGCGGACGCGCCCTGGTTGCGCTGGTTCTTGCTGCGGCCTG 300
      |||
Db    241 CAGCCGCCTCCAAGTCTGTGCGGACGCGCCCTGGTTGCGCTGGTTCTTGCTGCGGCCTG 300

QY    301 TCGCGGATCTGGGGAGAGGAGAGAGGCTTCCCGCCTGACAGGGCCACTCCGCTTTTGCAA 360
      |||
Db    301 TCGCGGATCTGGGGAGAGGAGAGAGGCTTCCCGCCTGACAGGGCCACTCCGCTTTTGCAA 360

QY    361 ACCGCAGAGATAATGACGCCACCCACTAAGACCTTATGGCCCAAGGGTTCCAACGCCAGT 420
      |||
Db    361 ACCGCAGAGATAATGACGCCACCCACTAAGACCTTATGGCCCAAGGGTTCCAACGCCAGT 420

QY    421 CTGGCGCGGTTCGTTGGCACCTGCGGAGGTGCCTAAAGGAGACAGGACGGCAGGATCTCCG 480
      |||
Db    421 CTGGCGCGGTTCGTTGGCACCTGCGGAGGTGCCTAAAGGAGACAGGACGGCAGGATCTCCG 480

QY    481 CCACGCACCATCTCCCCTCCCCCGTGCCAAGGACCCATCGAGATCAAGGAGACTTTCAA 540
      |||
Db    481 CCACGCACCATCTCCCCTCCCCCGTGCCAAGGACCCATCGAGATCAAGGAGACTTTCAA 540

QY    541 TACATCAACACGGTTGTGTCCTGCCTTGTGTTTCGTGCTGGGGATCATCGGGAACCTCACA 600
      |||
Db    541 TACATCAACACGGTTGTGTCCTGCCTTGTGTTTCGTGCTGGGGATCATCGGGAACCTCACA 600

QY    601 CTTCTGAGAATTATCTACAAGAACAAGTGCATGCGAAACGGTCCCAATATCTTGATCGCC 660
      |||
Db    601 CTTCTGAGAATTATCTACAAGAACAAGTGCATGCGAAACGGTCCCAATATCTTGATCGCC 660

QY    661 AGCTTGGCTCTGGGAGACCTGCTGCACATCGTCATTGACATCCCTATCAATGTCTACAAG 720
      |||
Db    661 AGCTTGGCTCTGGGAGACCTGCTGCACATCGTCATTGACATCCCTATCAATGTCTACAAG 720

QY    721 CTGCTGGCAGAGGACTGGCCATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTCATACAG 780
      |||
Db    721 CTGCTGGCAGAGGACTGGCCATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTCATACAG 780
```

Qy 781 AAAGCCTCCGTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATATCGA 840  
 |||  
 Db 781 AAAGCCTCCGTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATATCGA 840

Qy 841 GCTGTTGCTTCTTGGAGTAGAATTAAAGGAATTGGGGTTCCAAAATGGACAGCAGTAGAA 900  
 |||  
 Db 841 GCTGTTGCTTCTTGGAGTAGAATTAAAGGAATTGGGGTTCCAAAATGGACAGCAGTAGAA 900

Qy 901 ATTGTTTTGATTTGGGTGGTCTCTGTGGTTCTGGCTGTCCCTGAAGCCATAGGTTTTGAT 960  
 |||  
 Db 901 ATTGTTTTGATTTGGGTGGTCTCTGTGGTTCTGGCTGTCCCTGAAGCCATAGGTTTTGAT 960

Qy 961 ATAATTACGATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTTCAG 1020  
 |||  
 Db 961 ATAATTACGATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTTCAG 1020

Qy 1021 AAGACAGCTTTTCATGCAGTTTTTACAAGACAGCAAAGATTGGTGGCTGTTTCAGTTTCTAT 1080  
 |||  
 Db 1021 AAGACAGCTTTTCATGCAGTTTTTACAAGACAGCAAAGATTGGTGGCTGTTTCAGTTTCTAT 1080

Qy 1081 TTCTGCTTGCCATTGGCCATCACTGCATTTTTTTATACACTAATGACCTGTGAAATGTTG 1140  
 |||  
 Db 1081 TTCTGCTTGCCATTGGCCATCACTGCATTTTTTTATACACTAATGACCTGTGAAATGTTG 1140

Qy 1141 AGAAAGAAAAGTGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAAGTG 1200  
 |||  
 Db 1141 AGAAAGAAAAGTGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAAGTG 1200

Qy 1201 GCCAAAACCGTCTTTTGCCTGGTCCTTGTCTTTGCCCTCTGCTGGCTTCCCCTTCACCTC 1260  
 |||  
 Db 1201 GCCAAAACCGTCTTTTGCCTGGTCCTTGTCTTTGCCCTCTGCTGGCTTCCCCTTCACCTC 1260

Qy 1261 AGCAGGATTCTGAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGAACTTTTG 1320  
 |||  
 Db 1261 AGCAGGATTCTGAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGAACTTTTG 1320

Qy 1321 AGCTTTCTGTTGGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCCTGCATT 1380  
 |||  
 Db 1321 AGCTTTCTGTTGGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCCTGCATT 1380

Qy 1381 AACCCAATTGCTCTGTATTTGGTGAGCAAAAGATTCAAAAAGTCTTTAAGTCATGCTTA 1440  
 |||  
 Db 1381 AACCCAATTGCTCTGTATTTGGTGAGCAAAAGATTCAAAAAGTCTTTAAGTCATGCTTA 1440

Qy 1441 TGCTGCTGGTGCCAGTCATTTGAAGAAAAACAGTCCTTGGAGGAAAAGCAGTCGTGCTTA 1500  
 |||  
 Db 1441 TGCTGCTGGTGCCAGTCATTTGAAGAAAAACAGTCCTTGGAGGAAAAGCAGTCGTGCTTA 1500

Qy 1501 AAGTTCAAAGCTAATGATCACGGATATGACAACTTCCGTTCCAGTAATAAATACAGCTCA 1560  
 |||  
 Db 1501 AAGTTCAAAGCTAATGATCACGGATATGACAACTTCCGTTCCAGTAATAAATACAGCTCA 1560

Qy 1561 TCTTGAAAGAAGAACTATTCACTGTATTTCAATTTCTTTATATTGGACCGAAGTCATTAA 1620  
 |||  
 Db 1561 TCTTGAAAGAAGAACTATTCACTGTATTTCAATTTCTTTATATTGGACCGAAGTCATTAA 1620

Qy 1621 AACAAAATGAAACATTTGCCAAAACAAAACAAAAAACTATGTATTTGCACAGCACACTAT 1680

|    |      |  |      |
|----|------|--|------|
| Db | 1621 | <br>AACAAAATGAAACATTTGCCAAAACAAAACAAAAAATATGTATTTGCACAGCACACTAT  | 1680 |
| Qy | 1681 | TAAATATTAAGTGTAAATTATTTTAACTCACAGCTACATATGACATTTTATGAGCTGT       | 1740 |
| Db | 1681 | <br>TAAATATTAAGTGTAAATTATTTTAACTCACAGCTACATATGACATTTTATGAGCTGT   | 1740 |
| Qy | 1741 | TTACGGCATGGAAAGAAAATCAGTGGGAATTAAGAAAGCCTCGTCGTGAAAGCACTTAAT     | 1800 |
| Db | 1741 | <br>TTACGGCATGGAAAGAAAATCAGTGGGAATTAAGAAAGCCTCGTCGTGAAAGCACTTAAT | 1800 |
| Qy | 1801 | TTTTTACAGTTAGCACTTCAACATAGCTCTTAACAACTTCCAGGATATTCACACAACACT     | 1860 |
| Db | 1801 | <br>TTTTTACAGTTAGCACTTCAACATAGCTCTTAACAACTTCCAGGATATTCACACAACACT | 1860 |
| Qy | 1861 | TAGGCTTAAAAATGAGCTCACTCAGAATTTCTATTCTTTCTAAAAAGAGATTTATTTT       | 1920 |
| Db | 1861 | <br>TAGGCTTAAAAATGAGCTCACTCAGAATTTCTATTCTTTCTAAAAAGAGATTTATTTT   | 1920 |
| Qy | 1921 | AATCAATGGGACTCTGATATAAAGGAAGAATAAGTCACTGTAAACAGAACTTTTAAATG      | 1980 |
| Db | 1921 | <br>AATCAATGGGACTCTGATATAAAGGAAGAATAAGTCACTGTAAACAGAACTTTTAAATG  | 1980 |
| Qy | 1981 | AAGCTTAAATTACTCAATTTAAATTTTAAATCCTTTAAACAACTTTTCAATTAATAT        | 2040 |
| Db | 1981 | <br>AAGCTTAAATTACTCAATTTAAATTTTAAATCCTTTAAACAACTTTTCAATTAATAT    | 2040 |
| Qy | 2041 | TATCAGCTATTATCAGATTGTAATTAGATGCAAATGAGAGAGCAGTTTAGTTGTTGCAT      | 2100 |
| Db | 2041 | <br>TATCAGCTATTATCAGATTGTAATTAGATGCAAATGAGAGAGCAGTTTAGTTGTTGCAT  | 2100 |
| Qy | 2101 | TTTTCGGACACTGGAAACATTTAAATGATCAGGAGGGAGTAACAGAAAGAGCAAGGCTGT     | 2160 |
| Db | 2101 | <br>TTTTCGGACACTGGAAACATTTAAATGATCAGGAGGGAGTAACAGAAAGAGCAAGGCTGT | 2160 |
| Qy | 2161 | TTTTGAAAATCATTACACTTTTACTAGAGCCCAACCTCAGCATTCTGCAATATGTAAC       | 2220 |
| Db | 2161 | <br>TTTTGAAAATCATTACACTTTTACTAGAGCCCAACCTCAGCATTCTGCAATATGTAAC   | 2220 |
| Qy | 2221 | CAACATGTCACAAACAAGCAGCATGTAACAGACTGGCACATGTGCCAGCTGAATTTAAAA     | 2280 |
| Db | 2221 | <br>CAACATGTCACAAACAAGCAGCATGTAACAGACTGGCACATGTGCCAGCTGAATTTAAAA | 2280 |
| Qy | 2281 | TATAATACTTTTAAAAAGAAAATTATTACATCCTTTACATTAGTTAAGATCAAACCTCA      | 2340 |
| Db | 2281 | <br>TATAATACTTTTAAAAAGAAAATTATTACATCCTTTACATTAGTTAAGATCAAACCTCA  | 2340 |
| Qy | 2341 | CAAAGAGAAATAGAATGTTTGAAAGGCTATCCCAAAGACTTTTTTGAATCTGTCATTCA      | 2400 |
| Db | 2341 | <br>CAAAGAGAAATAGAATGTTTGAAAGGCTATCCCAAAGACTTTTTTGAATCTGTCATTCA  | 2400 |
| Qy | 2401 | CATACCCTGTGAAGACAATACTATCTACAATTTTTTTCAGGATTATTAAAATCTTCTTTT     | 2460 |
| Db | 2401 | <br>CATACCCTGTGAAGACAATACTATCTACAATTTTTTTCAGGATTATTAAAATCTTCTTTT | 2460 |
| Qy | 2461 | TCATATCGTAGCTTAACTCTGTTTGGTTTTGTCATCTGTAAATACTTACCTACATACA       | 2520 |
|    |      |  |      |

Db 2461 TCACTATCGTAGCTTAAACTCTGTTTGGTTTTGTCATCTGTAAATACTTACCTACATACA 2520  
 Qy 2521 CTGCATGTAGATGATTAAATGAGGGCAGGCCCTGTGCTCATAGCTTTACGATGGAGAGAT 2580  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 2521 CTGCATGTAGATGATTAAATGAGGGCAGGCCCTGTGCTCATAGCTTTACGATGGAGAGAT 2580  
 Qy 2581 GCCAGTGACCTCATAATAAAGACTGTGAACTGCCTGGTGCAGTGTCCACATGACAAAGGG 2640  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 2581 GCCAGTGACCTCATAATAAAGACTGTGAACTGCCTGGTGCAGTGTCCACATGACAAAGGG 2640  
 Qy 2641 GCAGGTAGCACCCCTCTCTACCCATGCTGTGGTTAAAATGGTTTCTAGCATATGTATAAT 2700  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 2641 GCAGGTAGCACCCCTCTCTACCCATGCTGTGGTTAAAATGGTTTCTAGCATATGTATAAT 2700  
 Qy 2701 GCTATAGTTAAAATACTATTTTTTCAAAATCATAACAGATTAGTACATTTAACAGCTACCTG 2760  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 2701 GCTATAGTTAAAATACTATTTTTTCAAAATCATAACAGATTAGTACATTTAACAGCTACCTG 2760  
 Qy 2761 TAAAGCTTATTACTAATTTTTGTATTATTTTTGTAAATAGCCAATAGAAAAGTTTGCTTG 2820  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 2761 TAAAGCTTATTACTAATTTTTGTATTATTTTTGTAAATAGCCAATAGAAAAGTTTGCTTG 2820  
 Qy 2821 ACATGGTGCTTTTCTTTTCATCTAGAGGCAAAACTGCTTTTTGAGACCGTAAGAACCTCTT 2880  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 2821 ACATGGTGCTTTTCTTTTCATCTAGAGGCAAAACTGCTTTTTGAGACCGTAAGAACCTCTT 2880  
 Qy 2881 AGCTTTGTGCGTTCCTGCCTAATTTTTATATCTTCTAAGCAAAGTGCCTTAGGATAGCTT 2940  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 2881 AGCTTTGTGCGTTCCTGCCTAATTTTTATATCTTCTAAGCAAAGTGCCTTAGGATAGCTT 2940  
 Qy 2941 GGGATGAGATGTGTGTGAAAGTATGTACAAGAGAAAACGGAAGAGAGAGGAAATGAGGTG 3000  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 2941 GGGATGAGATGTGTGTGAAAGTATGTACAAGAGAAAACGGAAGAGAGAGGAAATGAGGTG 3000  
 Qy 3001 GGGTTGGAGGAAACCCATGGGGACAGATTCCCATTCTTAGCCTAACGTTTCGTCATTGCCT 3060  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 3001 GGGTTGGAGGAAACCCATGGGGACAGATTCCCATTCTTAGCCTAACGTTTCGTCATTGCCT 3060  
 Qy 3061 CGTCACATCAATGCAAAAGGTCCTGATTTTGTTCAGCAAAACACAGTGCAATGTTCTCA 3120  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 3061 CGTCACATCAATGCAAAAGGTCCTGATTTTGTTCAGCAAAACACAGTGCAATGTTCTCA 3120  
 Qy 3121 GAGTGACTTTTCGAAATAAATTGGGCCCAAGAGCTTTAACTCGGTCTTAAATATGCCCAA 3180  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 3121 GAGTGACTTTTCGAAATAAATTGGGCCCAAGAGCTTTAACTCGGTCTTAAATATGCCCAA 3180  
 Qy 3181 ATTTTTACTTTGTTTTTCTTTTAATAGGCTGGGCCACATGTTGGAAATAAGCTAGTAATG 3240  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 3181 ATTTTTACTTTGTTTTTCTTTTAATAGGCTGGGCCACATGTTGGAAATAAGCTAGTAATG 3240  
 Qy 3241 TTGTTTTCTGTCAATATTGAATGTGATGGTACAGTAAACCAAACCAACAATGTGGCCA 3300  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 3241 TTGTTTTCTGTCAATATTGAATGTGATGGTACAGTAAACCAAACCAACAATGTGGCCA 3300  
 Qy 3301 GAAAGAAAGAGCAATAATAATTAATTCACACACCATATGGATTCTATTTATAAATCACCC 3360  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 3301 GAAAGAAAGAGCAATAATAATTAATTCACACACCATATGGATTCTATTTATAAATCACCC 3360

Qy 3361 ACAAACTTGTTCTTTAATTTTCATCCCAATCACTTTTTTCAGAGGCCTGTTATCATAGAAGT 3420  
 |||  
 Db 3361 ACAAACTTGTTCTTTAATTTTCATCCCAATCACTTTTTTCAGAGGCCTGTTATCATAGAAGT 3420

Qy 3421 CATTTTAGACTCTCAATTTTAAATTAATTTTGAATCACTAATATTTTCACAGTTTATTAA 3480  
 |||  
 Db 3421 CATTTTAGACTCTCAATTTTAAATTAATTTTGAATCACTAATATTTTCACAGTTTATTAA 3480

Qy 3481 TATATTTAATTTCTATTTAAATTTTAGATTATTTTATTACCATGTAATTTTACA 3540  
 |||  
 Db 3481 TATATTTAATTTCTATTTAAATTTTAGATTATTTTATTACCATGTAATTTTACA 3540

Qy 3541 TCCTGATACCCCTTTCCTTCTCCATGTCAGTATCATGTTCTCTAATTATCTTGCCAAATTT 3600  
 |||  
 Db 3541 TCCTGATACCCCTTTCCTTCTCCATGTCAGTATCATGTTCTCTAATTATCTTGCCAAATTT 3600

Qy 3601 TGAAACTACACACAAAAAGCATACTTGCATTATTTATAATAAAATTGCATTTCAGTGGCTT 3660  
 |||  
 Db 3601 TGAAACTACACACAAAAAGCATACTTGCATTATTTATAATAAAATTGCATTTCAGTGGCTT 3660

Qy 3661 TTTAAAAAAATGTTTGATTCAAACCTTTAACATACTGATAAGTAAGAAACAATTATAAT 3720  
 |||  
 Db 3661 TTTAAAAAAATGTTTGATTCAAACCTTTAACATACTGATAAGTAAGAAACAATTATAAT 3720

Qy 3721 TTCTTTACATACTCAAACCAAGATAGAAAAAGGTGCTATCGTTCAACTTCAAACATGT 3780  
 |||  
 Db 3721 TTCTTTACATACTCAAACCAAGATAGAAAAAGGTGCTATCGTTCAACTTCAAACATGT 3780

Qy 3781 TTCCTAGTATTAAGGACTTTAATATAGCAACAGACAAAATTATTGTTAACATGGATGTTA 3840  
 |||  
 Db 3781 TTCCTAGTATTAAGGACTTTAATATAGCAACAGACAAAATTATTGTTAACATGGATGTTA 3840

Qy 3841 CAGCTCAAAGATTTATAAAAGATTTTAACCTATTTTCTCCCTTATTATCCACTGCTAAT 3900  
 |||  
 Db 3841 CAGCTCAAAGATTTATAAAAGATTTTAACCTATTTTCTCCCTTATTATCCACTGCTAAT 3900

Qy 3901 GTGGATGTATGTTCAAACACCTTTTAGTATTGATAGCTTACATATGGCCAAAGGAATACA 3960  
 |||  
 Db 3901 GTGGATGTATGTTCAAACACCTTTTAGTATTGATAGCTTACATATGGCCAAAGGAATACA 3960

Qy 3961 GTTTATAGCAAAACATGGGTATGCTGTAGCTAACTTTATAAAAGTGTAATATAACAATGT 4020  
 |||  
 Db 3961 GTTTATAGCAAAACATGGGTATGCTGTAGCTAACTTTATAAAAGTGTAATATAACAATGT 4020

Qy 4021 AAAAAATTATATATCTGGGAGGATTTTTTGGTTGCCTAAAGTGGCTATAGTTACTGATTT 4080  
 |||  
 Db 4021 AAAAAATTATATATCTGGGAGGATTTTTTGGTTGCCTAAAGTGGCTATAGTTACTGATTT 4080

Qy 4081 TTTATTATGTAAGCAAAACCAATAAAAAATTTAAGTTTTTTTAACAACTACCTTATTTTTC 4140  
 |||  
 Db 4081 TTTATTATGTAAGCAAAACCAATAAAAAATTTAAGTTTTTTTAACAACTACCTTATTTTTC 4140

Qy 4141 ACTGTACAGACACTAATTCATTAAATACTAATTGATTGTTTAAAAGAAATATAAATGTGA 4200  
 |||  
 Db 4141 ACTGTACAGACACTAATTCATTAAATACTAATTGATTGTTTAAAAGAAATATAAATGTGA 4200



QY 4201 CAAGTGGACATTATTTATGTTAAATATACAATTATCAAGCAAGTATGAAGTTATTCAATT 4260  
 |||  
 Db 4201 CAAGTGGACATTATTTATGTTAAATATACAATTATCAAGCAAGTATGAAGTTATTCAATT 4260  
 QY 4261 AAAATGCCACATTTCTGGTCTCTGGG 4286  
 |||  
 Db 4261 AAAATGCCACATTTCTGGTCTCTGGG 4286

RESULT 6

ACC72646

ID ACC72646 standard; cDNA; 4286 BP.

XX

AC ACC72646;

XX

DT 09-JUL-2003 (first entry)

XX

DE Human endothelin receptor type B encoding cDNA.

XX

KW Human; cancer; diagnosis; screening; modulator; leukaemia; ischaemia;  
 KW heart disease; atherosclerosis; endometriosis; gene; ss.

XX

OS Homo sapiens.

XX

PN WO2003025138-A2.

XX

PD 27-MAR-2003.

XX

PF 17-SEP-2002; 2002WO-US029560.

XX

PR 17-SEP-2001; 2001US-0323469P.

PR 20-SEP-2001; 2001US-0323887P.

PR 13-NOV-2001; 2001US-0350666P.

PR 08-FEB-2002; 2002US-0355145P.

PR 08-FEB-2002; 2002US-0355257P.

PR 12-APR-2002; 2002US-0372246P.

XX

PA (EOSB-) EOS BIOTECHNOLOGY INC.

XX

PI Afar D, Aziz N, Gish KC, Hevezi PA, Mack DH, Wilson KE;

PI Zlotnik A;

XX

DR WPI; 2003-354600/33.

DR P-PSDB; ABR58526.

XX

PT New genes that are up-regulated or down-regulated in cancers, useful as  
 PT markers for diagnosing e.g. cancer, ischemia or heart diseases, or as  
 PT therapeutic targets for screening drugs for treating these diseases.

XX

PS Claim 8; Page 143-144; 767pp; English.

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CC The present invention describes an isolated nucleic acid molecule, which  
 CC comprises the sequence of any of the genes that are up-regulated or down-  
 CC regulated in specific cancers (e.g. about 1031 genes up-regulated in  
 CC acute lymphocytic leukemia). ACC72641 to ACC72860 represent cancer  
 CC related gene nucleotide sequences which encode the proteins given in  
 CC ABR58521 to ABR58709. Also described: (1) determining the presence or

CC absence of a pathological cell in a patient; (2) an expression vector  
 CC comprising a nucleic acid molecule described above; (3) a host cell  
 CC comprising the vector; (4) an isolated polypeptide, which is encoded by  
 CC the nucleic acid; (5) an antibody that specifically binds the polypeptide  
 CC of (4); (6) specifically targeting a compound to a pathological cell in a  
 CC patient by administering to the patient the antibody above; and (7) a  
 CC drug screening assay. The nucleic acid is useful as diagnostic markers or  
 CC therapeutic targets. In particular, the nucleic acid is useful for  
 CC diagnosing a pathology, e.g. cancer (e.g. cancer of the bone marrow,  
 CC bladder, brain, breast, cervix, colon/rectum, kidney, lung, ovary,  
 CC pancreas, prostate, skin and uterus), wounds, ischaemia, heart diseases,  
 CC atherosclerosis and endometriosis. The nucleic acid is also useful in  
 CC drug screening, particularly for identifying agents for treating these  
 CC pathologies

XX

SQ Sequence 4286 BP; 1327 A; 829 C; 816 G; 1314 T; 0 U; 0 Other;

Query Match 99.6%; Score 4284.4; DB 7; Length 4286;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 4285; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

|    |     |  |     |
|----|-----|--|-----|
| Qy | 1   | GAGACATTCCGGTGGGGGACTCTGGCCAGCCCAGCAACGTGGATCCTGAGAGCACTCCC  | 60  |
|    |     |  |     |
| Db | 1   | GAGACATTCCGGTGGGGGACTCTGGCCAGCCCAGCAACGTGGATCCTGAGAGCACTCCC  | 60  |
| Qy | 61  | AGGTAGGCATTTGCCCGGTGGGACGCCTTGCCAGAGCAGTGTGTGGCAGGCCCCCGTGG  | 120 |
|    |     |  |     |
| Db | 61  | AGGTAGGCATTTGCCCGGTGGGACGCCTTGCCAGAGCAGTGTGTGGCAGGCCCCCGTGG  | 120 |
| Qy | 121 | AGGATCAACACAGTGGCTGAACACTGGGAAGGAAGTGGTACTTGGAGTCTGGACATCTGA | 180 |
|    |     |  |     |
| Db | 121 | AGGATCAACACAGTGGCTGAACACTGGGAAGGAAGTGGTACTTGGAGTCTGGACATCTGA | 180 |
| Qy | 181 | AACTTGGCTCTGAAACTGCGGAGCGGCCACCGGACGCCTTCTGGAGCAGGTAGCAGCATG | 240 |
|    |     |  |     |
| Db | 181 | AACTTGGCTCTGAAACTGCGGAGCGGCCACCGGACGCCTTCTGGAGCAGGTAGCAGCATG | 240 |
| Qy | 241 | CAGCCGCCTCCAAGTCTGTGCGGACGCGCCCTGGTTGCGCTGGTTCTTGCCTGCGGCCTG | 300 |
|    |     |  |     |
| Db | 241 | CAGCCGCCTCCAAGTCTGTGCGGACGCGCCCTGGTTGCGCTGGTTCTTGCCTGCGGCCTG | 300 |
| Qy | 301 | TCGCGGATCTGGGGAGAGGAGAGAGGCTTCCCGCCTGACAGGGCCACTCCGCTTTTGCAA | 360 |
|    |     |  |     |
| Db | 301 | TCGCGGATCTGGGGAGAGGAGAGAGGCTTCCCGCCTGACAGGGCCACTCCGCTTTTGCAA | 360 |
| Qy | 361 | ACCGCAGAGATAATGACGCCACCCACTAAGACCTTATGGCCCAAGGGTTCCAACGCCAGT | 420 |
|    |     |  |     |
| Db | 361 | ACCGCAGAGATAATGACGCCACCCACTAAGACCTTATGGCCCAAGGGTTCCAACGCCAGT | 420 |
| Qy | 421 | CTGGCGCGGTCGTTGGCACCTGCGGAGGTGCCTAAAGGAGACAGGACGGCAGGATCTCCG | 480 |
|    |     |  |     |
| Db | 421 | CTGGCGCGGTCGTTGGCACCTGCGGAGGTGCCTAAAGGAGACAGGACGGCAGGATCTCCG | 480 |
| Qy | 481 | CCACGCACCATCTCCCCTCCCCCGTGCCAAGGACCCATCGAGATCAAGGAGACTTTCAA  | 540 |
|    |     |  |     |
| Db | 481 | CCACGCACCATCTCCCCTCCCCCGTGCCAAGGACCCATCGAGATCAAGGAGACTTTCAA  | 540 |

Qy 541 TACATCAACACGGTTGTGTCTGCCTTGTGTTCTGTGCTGGGGATCATCGGGAACCTCCACA 600  
 |||  
 Db 541 TACATCAACACGGTTGTGTCTGCCTTGTGTTCTGTGCTGGGGATCATCGGGAACCTCCACA 600  
 |||  
 Qy 601 CTTCTGAGAATTATCTACAAGAACAAGTGCATGCGAAACGGTCCCAATATCTTGATCGCC 660  
 |||  
 Db 601 CTTCTGAGAATTATCTACAAGAACAAGTGCATGCGAAACGGTCCCAATATCTTGATCGCC 660  
 |||  
 Qy 661 AGCTTGGCTCTGGGAGACCTGCTGCACATCGTCATTGACATCCCTATCAATGTCTACAAG 720  
 |||  
 Db 661 AGCTTGGCTCTGGGAGACCTGCTGCACATCGTCATTGACATCCCTATCAATGTCTACAAG 720  
 |||  
 Qy 721 CTGCTGGCAGAGGACTGGCCATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTCATACAG 780  
 |||  
 Db 721 CTGCTGGCAGAGGACTGGCCATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTCATACAG 780  
 |||  
 Qy 781 AAAGCCTCCGTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATATCGA 840  
 |||  
 Db 781 AAAGCCTCCGTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATATCGA 840  
 |||  
 Qy 841 GCTGTTGCTTCTTGGAGTAGAATTAAGGAATTGGGGTTCCAAAATGGACAGCAGTAGAA 900  
 |||  
 Db 841 GCTGTTGCTTCTTGGAGTAGAATTAAGGAATTGGGGTTCCAAAATGGACAGCAGTAGAA 900  
 |||  
 Qy 901 ATTGTTTTGATTTGGGTGGTCTCTGTGGTCTGGCTGTCCCTGAAGCCATAGGTTTTGAT 960  
 |||  
 Db 901 ATTGTTTTGATTTGGGTGGTCTCTGTGGTCTGGCTGTCCCTGAAGCCATAGGTTTTGAT 960  
 |||  
 Qy 961 ATAATTACGATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTTTCAG 1020  
 |||  
 Db 961 ATAATTACGATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTTTCAG 1020  
 |||  
 Qy 1021 AAGACAGCTTTCATGCAGTTTTTACAAGACAGCAAAAGATTGGTGGCTGTTTCACTTTCTAT 1080  
 |||  
 Db 1021 AAGACAGCTTTCATGCAGTTTTTACAAGACAGCAAAAGATTGGTGGCTGTTTCACTTTCTAT 1080  
 |||  
 Qy 1081 TTCTGCTTGCCATTGGCCATCACTGCATTTTTTTTATACACTAATGACCTGTGAAATGTTG 1140  
 |||  
 Db 1081 TTCTGCTTGCCATTGGCCATCACTGCATTTTTTTTATACACTAATGACCTGTGAAATGTTG 1140  
 |||  
 Qy 1141 AGAAAGAAAAGTGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAAGTG 1200  
 |||  
 Db 1141 AGAAAGAAAAGTGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAAGTG 1200  
 |||  
 Qy 1201 GCCAAAACCGTCTTTTGCCTGGTCCTTGTCTTTGCCCTCTGCTGGCTTCCCTTCACCTC 1260  
 |||  
 Db 1201 GCCAAAACCGTCTTTTGCCTGGTCCTTGTCTTTGCCCTCTGCTGGCTTCCCTTCACCTC 1260  
 |||  
 Qy 1261 AGCAGGATTCTGAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGAACCTTTTG 1320  
 |||  
 Db 1261 AGCAGGATTCTGAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGAACCTTTTG 1320  
 |||  
 Qy 1321 AGCTTTCTGTTGGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCCTGCATT 1380  
 |||  
 Db 1321 AGCTTTCTGTTGGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCCTGCATT 1380  
 |||  
 Qy 1381 AACCCAATTGCTCTGTATTTGGTGGAGCAAAAGATTCAAAAAGTCTTTAAGTCATGCTTA 1440

|    |   |      |
|----|---|------|
|    |   |      |
| Db | 1381 AACCCAATTGCTCTGTATTTGGTGAGCAAAAGATTCAAAAAGCTTTAAGTCATGCTTA     | 1440 |
| Qy | 1441 TGCTGCTGGTGCCAGTCATTTGAAGAAAAACAGTCCTTGGAGGAAAAGCAGTCGTGCTTA   | 1500 |
| Db | 1441 TGCTGCTGGTGCCAGTCATTTGAAGAAAAACAGTCCTTGGAGGAAAAGCAGTCGTGCTTA   | 1500 |
| Qy | 1501 AAGTTCAAAGCTAATGATCACGGATATGACAACTTCCGTTCCAGTAATAAATACAGCTCA   | 1560 |
| Db | 1501 AAGTTCAAAGCTAATGATCACGGATATGACAACTTCCGTTCCAGTAATAAATACAGCTCA   | 1560 |
| Qy | 1561 TCTTGAAAGAAGAACTATTTCACTGTATTTTCAATTTCTTTATATTGGACCGAAGTCATTAA | 1620 |
| Db | 1561 TCTTGAAAGAAGAACTATTTCACTGTATTTTCAATTTCTTTATATTGGACCGAAGTCATTAA | 1620 |
| Qy | 1621 AACAAAATGAAACATTTGCCAAAACAAAACAAAACATATGTATTTGCACAGCACACTAT    | 1680 |
| Db | 1621 AACAAAATGAAACATTTGCCAAAACAAAACAAAACATATGTATTTGCACAGCACACTAT    | 1680 |
| Qy | 1681 TAAAAATATTAAGTGTAATTATTTTAACTCACAGCTACATATGACATTTTATGAGCTGT    | 1740 |
| Db | 1681 TAAAAATATTAAGTGTAATTATTTTAACTCACAGCTACATATGACATTTTATGAGCTGT    | 1740 |
| Qy | 1741 TTACGGCATGGAAAGAAAATCAGTGGGAATTAAGAAAGCCTCGTCGTGAAAGCACTTAAT   | 1800 |
| Db | 1741 TTACGGCATGGAAAGAAAATCAGTGGGAATTAAGAAAGCCTCGTCGTGAAAGCACTTAAT   | 1800 |
| Qy | 1801 TTTTACAGTTAGCACTTCAACATAGCTCTTAACAACCTCCAGGATATTCACACAACACT    | 1860 |
| Db | 1801 TTTTACAGTTAGCACTTCAACATAGCTCTTAACAACCTCCAGGATATTCACACAACACT    | 1860 |
| Qy | 1861 TAGGCTTAAAAATGAGCTCACTCAGAATTTCTATTCTTTCTAAAAAGAGATTTATTTT     | 1920 |
| Db | 1861 TAGGCTTAAAAATGAGCTCACTCAGAATTTCTATTCTTTCTAAAAAGAGATTTATTTT     | 1920 |
| Qy | 1921 AATCAATGGGACTCTGATATAAAGGAAGAATAAGTCACTGTAAACAGAACTTTTAAATG    | 1980 |
| Db | 1921 AATCAATGGGACTCTGATATAAAGGAAGAATAAGTCACTGTAAACAGAACTTTTAAATG    | 1980 |
| Qy | 1981 AAGCTTAAATTACTCAATTTAAAAATTTTAAATCCTTTAAACAACCTTTTCAATTAATAT   | 2040 |
| Db | 1981 AAGCTTAAATTACTCAATTTAAAAATTTTAAATCCTTTAAACAACCTTTTCAATTAATAT   | 2040 |
| Qy | 2041 TATCACACTATTATCAGATTGTAATTAGATGCAAATGAGAGAGCAGTTTAGTTGTTGCAT   | 2100 |
| Db | 2041 TATCACACTATTATCAGATTGTAATTAGATGCAAATGAGAGAGCAGTTTAGTTGTTGCAT   | 2100 |
| Qy | 2101 TTTTCGGACACTGGAAACATTTAAATGATCAGGAGGGAGTAACAGAAAGAGCAAGGCTGT   | 2160 |
| Db | 2101 TTTTCGGACACTGGAAACATTTAAATGATCAGGAGGGAGTAACAGAAAGAGCAAGGCTGT   | 2160 |
| Qy | 2161 TTTTGAAATCATTACACTTTCACTAGAGCCCAACCTCAGCATTCTGCAATATGTAAC      | 2220 |
| Db | 2161 TTTTGAAATCATTACACTTTCACTAGAGCCCAACCTCAGCATTCTGCAATATGTAAC      | 2220 |
| Qy | 2221 CAACATGTCACAAACAAGCAGCATGTAACAGACTGGCACATGTGCCAGCTGAATTTAAAA   | 2280 |
|    |   |      |

Db 2221 CAACATGTCACAAACAAGCAGCATGTAACAGACTGGCACATGTGCCAGCTGAATTTAAAA 2280  
 Qy 2281 TATAATACTTTTAAAAAGAAAATTATTACATCCTTTACATTTCAGTTAAGATCAAACCTCA 2340  
 Db 2281 TATAATACTTTTAAAAAGAAAATTATTACATCCTTTACATTTCAGTTAAGATCAAACCTCA 2340  
 Qy 2341 CAAAGAGAAATAGAATGTTTGAAAGGCTATCCCAAAGACTTTTTTTGAATCTGTCATTCA 2400  
 Db 2341 CAAAGAGAAATAGAATGTTTGAAAGGCTATCCCAAAGACTTTTTTTGAATCTGTCATTCA 2400  
 Qy 2401 CATACCCTGTGAAGACAATACTATCTACAATTTTTTTCAGGATTATTAAAATCTTCTTTTT 2460  
 Db 2401 CATACCCTGTGAAGACAATACTATCTACAATTTTTTTCAGGATTATTAAAATCTTCTTTTT 2460  
 Qy 2461 TCACTATCGTAGCTTAAACTCTGTTTGGTTTTGTCATCTGTAAATACTTACCTACATACA 2520  
 Db 2461 TCACTATCGTAGCTTAAACTCTGTTTGGTTTTGTCATCTGTAAATACTTACCTACATACA 2520  
 Qy 2521 CTGCATGTAGATGATTAAATGAGGGCAGGCCCTGTGCTCATAGCTTTACGATGGAGAGAT 2580  
 Db 2521 CTGCATGTAGATGATTAAATGAGGGCAGGCCCTGTGCTCATAGCTTTACGATGGAGAGAT 2580  
 Qy 2581 GCCAGTGACCTCATAATAAAGACTGTGAACTGCCTGGTGCAGTGTCCACATGACAAAGGG 2640  
 Db 2581 GCCAGTGACCTCATAATAAAGACTGTGAACTGCCTGGTGCAGTGTCCACATGACAAAGGG 2640  
 Qy 2641 GCAGGTAGCACCTCTCTCACCCATGCTGTGGTTAAAATGGTTTCTAGCATATGTATAAT 2700  
 Db 2641 GCAGGTAGCACCTCTCTCACCCATGCTGTGGTTAAAATGGTTTCTAGCATATGTATAAT 2700  
 Qy 2701 GCTATAGTTAAAATACTATTTTTCAAATCATAACAGATTAGTACATTTAACAGCTACCTG 2760  
 Db 2701 GCTATAGTTAAAATACTATTTTTCAAATCATAACAGATTAGTACATTTAACAGCTACCTG 2760  
 Qy 2761 TAAAGCTTATTACTAATTTTTGTATTATTTTTGTAAATAGCCAATAGAAAAGTTTGCTTG 2820  
 Db 2761 TAAAGCTTATTACTAATTTTTGTATTATTTTTGTAAATAGCCAATAGAAAAGTTTGCTTG 2820  
 Qy 2821 ACATGGTGCTTTTCTTTCATCTAGAGGCAAAACTGCTTTTTGAGACCGTAAGAACCTCTT 2880  
 Db 2821 ACATGGTGCTTTTCTTTCATCTAGAGGCAAAACTGCTTTTTGAGACCGTAAGAACCTCTT 2880  
 Qy 2881 AGCTTTGTGCGTTCCTGCCTAATTTTTATATCTTCTAAGCAAAGTGCCTTAGGATAGCTT 2940  
 Db 2881 AGCTTTGTGCGTTCCTGCCTAATTTTTATATCTTCTAAGCAAAGTGCCTTAGGATAGCTT 2940  
 Qy 2941 GGGATGAGATGTGTGTGAAAGTATGTACAAGAGAAAACGGAAGAGAGAGGAAATGAGGTG 3000  
 Db 2941 GGGATGAGATGTGTGTGAAAGTATGTACAAGAGAAAACGGAAGAGAGAGGAAATGAGGTG 3000  
 Qy 3001 GGGTTGGAGGAAACCCATGGGGACAGATTTCCCATTCCTTAGCCTAACGTTTCGTCATTGCCT 3060  
 Db 3001 GGGTTGGAGGAAACCCATGGGGACAGATTTCCCATTCCTTAGCCTAACGTTTCGTCATTGCCT 3060  
 Qy 3061 CGTCACATCAATGCAAAGGTCTGATTTTGTTCAGCAAACACAGTGCAATGTTCTCA 3120  
 Db 3061 CGTCACATCAATGCAAAGGTCTGATTTTGTTCAGCAAACACAGTGCAATGTTCTCA 3120

Qy 3121 GAGTGA CTTTCGAAATAAATTGGGCCCAAGAGCTTTAACTCGGTCTTAAATATGCCCAA 3180  
 |||  
 Db 3121 GAGTGA CTTTCGAAATAAATTGGGCCCAAGAGCTTTAACTCGGTCTTAAATATGCCCAA 3180  
 |||  
 Qy 3181 ATTTTACTTTGTTTTCTTTAATAGGCTGGGCCACATGTTGGAAATAAGCTAGTAATG 3240  
 |||  
 Db 3181 ATTTTACTTTGTTTTCTTTAATAGGCTGGGCCACATGTTGGAAATAAGCTAGTAATG 3240  
 |||  
 Qy 3241 TTGTTTTCTGTCAATATTGAATGTGATGGTACAGTAAACCAAAACCAACAATGTGGCCA 3300  
 |||  
 Db 3241 TTGTTTTCTGTCAATATTGAATGTGATGGTACAGTAAACCAAAACCAACAATGTGGCCA 3300  
 |||  
 Qy 3301 GAAAGAAAGAGCAATAATAATTAATTCACACACCATATGGATTCTATTTATAAATCACCC 3360  
 |||  
 Db 3301 GAAAGAAAGAGCAATAATAATTAATTCACACACCATATGGATTCTATTTATAAATCACCC 3360  
 |||  
 Qy 3361 ACAAACTTGTTCTTTAATTTTCATCCCAATCACTTTTTTCAGAGGCCTGTTATCATAGAAGT 3420  
 |||  
 Db 3361 ACAAACTTGTTCTTTAATTTTCATCCCAATCACTTTTTTCAGAGGCCTGTTATCATAGAAGT 3420  
 |||  
 Qy 3421 CATTTTAGACTCTCAATTTTAAATTAATTTTGAATCACTAATATTTTCACAGTTTATTAA 3480  
 |||  
 Db 3421 CATTTTAGACTCTCAATTTTAAATTAATTTTGAATCACTAATATTTTCACAGTTTATTAA 3480  
 |||  
 Qy 3481 TATATTTAATTTCTATTTAAATTTTAGATTATTTTTATTACCATGTACTGAATTTTACA 3540  
 |||  
 Db 3481 TATATTTAATTTCTATTTAAATTTTAGATTATTTTTATTACCATGTACTGAATTTTACA 3540  
 |||  
 Qy 3541 TCCTGATACCCTTTCTTTCTCCATGTCAGTATCATGTTCTCTAATTATCTTGCCAAATTT 3600  
 |||  
 Db 3541 TCCTGATACCCTTTCTTTCTCCATGTCAGTATCATGTTCTCTAATTATCTTGCCAAATTT 3600  
 |||  
 Qy 3601 TGAAACTACACACAAAAGCATACTTGCATTATTTATAATAAAATTGCATTCACTGGCTT 3660  
 |||  
 Db 3601 TGAAACTACACACAAAAGCATACTTGCATTATTTATAATAAAATTGCATTCACTGGCTT 3660  
 |||  
 Qy 3661 TTTAAAAAAATGTTTGATTCAAACTTTAACATACTGATAAGTAAGAAACAATTATAAT 3720  
 |||  
 Db 3661 TTTAAAAAAATGTTTGATTCAAACTTTAACATACTGATAAGTAAGAAACAATTATAAT 3720  
 |||  
 Qy 3721 TTCTTTACATACTCAAAACCAAGATAGAAAAAGGTGCTATCGTTCAACTTCAAAACATGT 3780  
 |||  
 Db 3721 TTCTTTACATACTCAAAACCAAGATAGAAAAAGGTGCTATCGTTCAACTTCAAAACATGT 3780  
 |||  
 Qy 3781 TTCCTAGTATTAAGGACTTTAATATAGCAACAGACAAAATTATTGTTAACATGGATGTTA 3840  
 |||  
 Db 3781 TTCCTAGTATTAAGGACTTTAATATAGCAACAGACAAAATTATTGTTAACATGGATGTTA 3840  
 |||  
 Qy 3841 CAGCTCAAAGATTTATAAAAGATTTTAACCTATTTTCTCCCTTATTATCCACTGCTAAT 3900  
 |||  
 Db 3841 CAGCTCAAAGATTTATAAAAGATTTTAACCTATTTTCTCCCTTATTATCCACTGCTAAT 3900  
 |||  
 Qy 3901 GTGGATGTATGTTCAAACACCTTTTAGTATTGATAGCTTACATATGGCCAAAGGAATACA 3960  
 |||  
 Db 3901 GTGGATGTATGTTCAAACACCTTTTAGTATTGATAGCTTACATATGGCCAAAGGAATACA 3960  
 |||

Qy 3961 GTTTATAGCAAAACATGGGTATGCTGTAGCTAACTTTATAAAAGTGTAATATAACAATGT 4020  
 |||  
 Db 3961 GTTTATAGCAAAACATGGGTATGCTGTAGCTAACTTTATAAAAGTGTAATATAACAATGT 4020  
 Qy 4021 AAAAAATTATATATCTGGGAGGATTTTTTGGTTGCCTAAAGTGGCTATAGTTACTGATTT 4080  
 |||  
 Db 4021 AAAAAATTATATATCTGGGAGGATTTTTTGGTTGCCTAAAGTGGCTATAGTTACTGATTT 4080  
 Qy 4081 TTTATTATGTAAGCAAAACCAATAAAAAATTTAAGTTTTTTTAACTACCTTATTTTTC 4140  
 |||  
 Db 4081 TTTATTATGTAAGCAAAACCAATAAAAAATTTAAGTTTTTTTAACTACCTTATTTTTC 4140  
 Qy 4141 ACTGTACAGACACTAATTCATTAAATACTAATTGATTGTTTAAAGAAATATAAATGTGA 4200  
 |||  
 Db 4141 ACTGTACAGACACTAATTCATTAAATACTAATTGATTGTTTAAAGAAATATAAATGTGA 4200  
 Qy 4201 CAAGTGGACATTATTTATGTTAAATATACAATTATCAAGCAAGTATGAAGTTATTCAATT 4260  
 |||  
 Db 4201 CAAGTGGACATTATTTATGTTAAATATACAATTATCAAGCAAGTATGAAGTTATTCAATT 4260  
 Qy 4261 AAAATGCCACATTTCTGGTCTCTGGG 4286  
 |||  
 Db 4261 AAAATGCCACATTTCTGGTCTCTGGG 4286

RESULT 7

ABZ42661

ID ABZ42661 standard; DNA; 4286 BP.

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AC ABZ42661;

XX

DT 04-MAR-2003 (first entry)

XX

DE Human endothelin B receptor nucleotide SEQ ID NO:113.

XX

KW G protein-coupled receptor; GPCR; antigenic peptide; gene therapy;  
 KW G protein-coupled receptor modulator; antibody; immune-related disease;  
 KW growth-related disease; cell regeneration-related disease; AIDS; cancer;  
 KW immunological-related cell proliferative disease; autoimmune disease;  
 KW Alzheimer's disease; atherosclerosis; infection; osteoarthritis; allergy;  
 KW osteoporosis; cardiomyopathy; inflammation; Crohn's disease; diabetes;  
 KW graft versus host disease; Parkinson's disease; multiple sclerosis; pain;  
 KW psoriasis; anxiety; depression; schizophrenia; dementia; memory loss;  
 KW mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea;  
 KW hypertension; hypotension; renal disorder; rheumatoid arthritis; trauma;  
 KW ulcer; gene; ds.

XX

OS Homo sapiens.

XX

PN WO200261087-A2.

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PD 08-AUG-2002.

XX

PF 19-DEC-2001; 2001WO-US050107.

XX

PR 19-DEC-2000; 2000US-0257144P.

XX

PA (LIFE-) LIFESPAN BIOSCIENCES INC.  
 XX  
 PI Burmer GC, Roush CL, Brown JP;  
 XX  
 DR WPI; 2003-046718/04.  
 DR P-PSDB; ABP81815.  
 XX  
 PT New isolated antigenic peptides e.g., for G protein-coupled receptors  
 PT (GPCR), useful for diagnosing and designing drugs for treating conditions  
 PT in which GPCRs are involved, e.g. AIDS, Alzheimer's disease, cancer or  
 PT autoimmune diseases.  
 XX  
 PS Disclosure; Fig 1; 523pp; English.  
 XX  
 CC The present invention describes antigenic peptides (I) comprising: (a)  
 CC any one of 1601 sequences (see ABP82019 to ABP83619) of 12-24 amino  
 CC acids. Also described: (1) an assay for the detection of a particular G  
 CC protein-coupled receptor (GPCR) or a candidate polypeptide in a sample;  
 CC and (2) an isolated antibody having high specificity and high affinity or  
 CC avidity for a particular GPCR. (I) can be used as GPCR modulators and in  
 CC gene therapy. The antigenic peptides for GPCRs are useful in detecting an  
 CC antibody against a particular GPCR, and in the production of specific  
 CC antibodies. The peptides and antibodies are also useful for detecting the  
 CC presence or absence of corresponding GPCRs. The antigenic peptides for  
 CC GPCRs and antibodies are useful for diagnosing and designing drugs for  
 CC treating immune-related diseases, growth-related diseases, cell  
 CC regeneration-related disease, immunological-related cell proliferative  
 CC diseases, or autoimmune diseases, e.g. AIDS, Alzheimer's disease,  
 CC atherosclerosis, bacterial, fungal, protozoan or viral infections,  
 CC osteoarthritis, osteoporosis, cancer, cardiomyopathy, chronic and acute  
 CC inflammation, allergies, Crohn's disease, diabetes, graft versus host  
 CC disease, Parkinson's disease, multiple sclerosis, pain, psoriasis,  
 CC anxiety, depression, schizophrenia, dementia, mental retardation, memory  
 CC loss, epilepsy, asthma, tuberculosis, obesity, nausea, hypertension,  
 CC hypotension, renal disorders, rheumatoid arthritis, trauma, ulcers, or  
 CC any other disorder in which GPCRs are involved. The antibodies may be  
 CC used in immunoassays and immunodiagnosis. ABZ42523 to ABZ42869 encode  
 CC GPCR proteins given in ABP81675 to ABP82018, which are used in the  
 CC exemplification of the present invention  
 XX  
 SQ Sequence 4286 BP; 1327 A; 829 C; 816 G; 1314 T; 0 U; 0 Other;

Query Match 99.6%; Score 4284.4; DB 7; Length 4286;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 4285; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

|    |     |  |     |
|----|-----|--|-----|
| Qy | 1   | GAGACATTCCGGTGGGGGACTCTGGCCAGCCCAGCAACGTGGATCCTGAGAGCACTCCC  | 60  |
|    |     |  |     |
| Db | 1   | GAGACATTCCGGTGGGGGACTCTGGCCAGCCCAGCAACGTGGATCCTGAGAGCACTCCC  | 60  |
| Qy | 61  | AGGTAGGCATTTGCCCCGGTGGGACGCCTTGCCAGAGCAGTGTGTGGCAGGCCCCCGTGG | 120 |
|    |     |  |     |
| Db | 61  | AGGTAGGCATTTGCCCCGGTGGGACGCCTTGCCAGAGCAGTGTGTGGCAGGCCCCCGTGG | 120 |
| Qy | 121 | AGGATCAACACAGTGGCTGAACACTGGGAAGGAACTGGTACTTGGAGTCTGGACATCTGA | 180 |
|    |     |  |     |
| Db | 121 | AGGATCAACACAGTGGCTGAACACTGGGAAGGAACTGGTACTTGGAGTCTGGACATCTGA | 180 |



|    |     |   |      |
|----|-----|---|------|
| Qy | 181 | AACTTGGCTCTGAAACTGCGGAGCGGCCACCGGACGCCTTCTGGAGCAGGTAGCAGCATG  | 240  |
|    |     |   |      |
| Db | 181 | AACTTGGCTCTGAAACTGCGCAGCGGCCACCGGACGCCTTCTGGAGCAGGTAGCAGCATG  | 240  |
| Qy | 241 | CAGCCGCCTCCAAGTCTGTGCGGACGCGCCCTGGTTGCGCTGGTTCTTGCCTGCGGCCTG  | 300  |
|    |     |   |      |
| Db | 241 | CAGCCGCCTCCAAGTCTGTGCGGACGCGCCCTGGTTGCGCTGGTTCTTGCCTGCGGCCTG  | 300  |
| Qy | 301 | TCGCGGATCTGGGGAGAGGAGAGAGGCTTCCCGCCTGACAGGGCCACTCCGCTTTTGCAA  | 360  |
|    |     |   |      |
| Db | 301 | TCGCGGATCTGGGGAGAGGAGAGAGGCTTCCCGCCTGACAGGGCCACTCCGCTTTTGCAA  | 360  |
| Qy | 361 | ACCGCAGAGATAATGACGCCACCCACTAAGACCTTATGGCCCAAGGGTTCCAACGCCAGT  | 420  |
|    |     |   |      |
| Db | 361 | ACCGCAGAGATAATGACGCCACCCACTAAGACCTTATGGCCCAAGGGTTCCAACGCCAGT  | 420  |
| Qy | 421 | CTGGCGCGGTTCGTTGGCACCTGCGGAGGTGCCTAAAGGAGACAGGACGGCAGGATCTCCG | 480  |
|    |     |   |      |
| Db | 421 | CTGGCGCGGTTCGTTGGCACCTGCGGAGGTGCCTAAAGGAGACAGGACGGCAGGATCTCCG | 480  |
| Qy | 481 | CCACGCACCATCTCCCCTCCCCGTGCCAAGGACCCATCGAGATCAAGGAGACTTTCAA    | 540  |
|    |     |   |      |
| Db | 481 | CCACGCACCATCTCCCCTCCCCGTGCCAAGGACCCATCGAGATCAAGGAGACTTTCAA    | 540  |
| Qy | 541 | TACATCAACACGGTTGTGTCCTGCCTTGTGTTTCGTGCTGGGGATCATCGGGAACCTCACA | 600  |
|    |     |   |      |
| Db | 541 | TACATCAACACGGTTGTGTCCTGCCTTGTGTTTCGTGCTGGGGATCATCGGGAACCTCACA | 600  |
| Qy | 601 | CTTCTGAGAATTATCTACAAGAACAAGTGCATGCGAAACGGTCCCAATATCTTGATCGCC  | 660  |
|    |     |   |      |
| Db | 601 | CTTCTGAGAATTATCTACAAGAACAAGTGCATGCGAAACGGTCCCAATATCTTGATCGCC  | 660  |
| Qy | 661 | AGCTTGGCTCTGGGAGACCTGCTGCACATCGTCATTGACATCCCTATCAATGTCTACAAG  | 720  |
|    |     |   |      |
| Db | 661 | AGCTTGGCTCTGGGAGACCTGCTGCACATCGTCATTGACATCCCTATCAATGTCTACAAG  | 720  |
| Qy | 721 | CTGCTGGCAGAGGACTGGCCATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTCATACAG  | 780  |
|    |     |   |      |
| Db | 721 | CTGCTGGCAGAGGACTGGCCATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTCATACAG  | 780  |
| Qy | 781 | AAAGCCTCCGTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATATCGA  | 840  |
|    |     |   |      |
| Db | 781 | AAAGCCTCCGTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATATCGA  | 840  |
| Qy | 841 | GCTGTTGCTTCTTGGAGTAGAATTAAAGGAATTGGGGTTCCAAAATGGACAGCAGTAGAA  | 900  |
|    |     |   |      |
| Db | 841 | GCTGTTGCTTCTTGGAGTAGAATTAAAGGAATTGGGGTTCCAAAATGGACAGCAGTAGAA  | 900  |
| Qy | 901 | ATTGTTTTGATTTGGGTGGTCTCTGTGGTTCTGGCTGTCCCTGAAGCCATAGGTTTTGAT  | 960  |
|    |     |   |      |
| Db | 901 | ATTGTTTTGATTTGGGTGGTCTCTGTGGTTCTGGCTGTCCCTGAAGCCATAGGTTTTGAT  | 960  |
| Qy | 961 | ATAATTACGATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTTCAG  | 1020 |
|    |     |   |      |
| Db | 961 | ATAATTACGATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTTCAG  | 1020 |

|    |      |  |      |
|----|------|--|------|
| Qy | 1021 | AAGACAGCTTTTCATGCAGTTTTACAAGACAGCAAAAGATTGGTGGCTGTTTCAGTTTCTAT | 1080 |
|    |      |  |      |
| Db | 1021 | AAGACAGCTTTTCATGCAGTTTTACAAGACAGCAAAAGATTGGTGGCTGTTTCAGTTTCTAT | 1080 |
| Qy | 1081 | TTCTGCTTGCCATTGGCCATCACTGCATTTTTTTATACACTAATGACCTGTGAAATGTTG   | 1140 |
|    |      |  |      |
| Db | 1081 | TTCTGCTTGCCATTGGCCATCACTGCATTTTTTTATACACTAATGACCTGTGAAATGTTG   | 1140 |
| Qy | 1141 | AGAAAAGAAAAGTGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAAGTG  | 1200 |
|    |      |  |      |
| Db | 1141 | AGAAAAGAAAAGTGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAAGTG  | 1200 |
| Qy | 1201 | GCCAAAACCGTCTTTTGCCCTGGTCCTTGCTTTGCCCCTCTGCTGGCTTCCCCTTCACCTC  | 1260 |
|    |      |  |      |
| Db | 1201 | GCCAAAACCGTCTTTTGCCCTGGTCCTTGCTTTGCCCCTCTGCTGGCTTCCCCTTCACCTC  | 1260 |
| Qy | 1261 | AGCAGGATTCTGAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGAACTTTTG   | 1320 |
|    |      |  |      |
| Db | 1261 | AGCAGGATTCTGAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGAACTTTTG   | 1320 |
| Qy | 1321 | AGCTTTCTGTTGGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCCTGCATT   | 1380 |
|    |      |  |      |
| Db | 1321 | AGCTTTCTGTTGGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCCTGCATT   | 1380 |
| Qy | 1381 | AACCCAATTGCTCTGTATTTGGTGAGCAAAAGATTCAAAAACCTGCTTTAAGTCATGCTTA  | 1440 |
|    |      |  |      |
| Db | 1381 | AACCCAATTGCTCTGTATTTGGTGAGCAAAAGATTCAAAAACCTGCTTTAAGTCATGCTTA  | 1440 |
| Qy | 1441 | TGCTGCTGGTGCCAGTCATTTGAAGAAAACAGTCCTTGGAGGAAAAGCAGTCGTGCTTA    | 1500 |
|    |      |  |      |
| Db | 1441 | TGCTGCTGGTGCCAGTCATTTGAAGAAAACAGTCCTTGGAGGAAAAGCAGTCGTGCTTA    | 1500 |
| Qy | 1501 | AAGTTCAAAGCTAATGATCACGGATATGACAACTCCGTTCCAGTAATAAATACAGCTCA    | 1560 |
|    |      |  |      |
| Db | 1501 | AAGTTCAAAGCTAATGATCACGGATATGACAACTCCGTTCCAGTAATAAATACAGCTCA    | 1560 |
| Qy | 1561 | TCTTGAAAGAAGAACTATTCACTGTATTTTCACTTTTCTTTATATTGGACCGAAGTCATTAA | 1620 |
|    |      |  |      |
| Db | 1561 | TCTTGAAAGAAGAACTATTCACTGTATTTTCACTTTTCTTTATATTGGACCGAAGTCATTAA | 1620 |
| Qy | 1621 | AACAAAATGAAACATTTGCCAAAACAAAACAAAAACTATGTATTTGCACAGCACACTAT    | 1680 |
|    |      |  |      |
| Db | 1621 | AACAAAATGAAACATTTGCCAAAACAAAACAAAAACTATGTATTTGCACAGCACACTAT    | 1680 |
| Qy | 1681 | TAAAATATTAAGTGTAATTATTTTAACACTCACAGCTACATATGACATTTTATGAGCTGT   | 1740 |
|    |      |  |      |
| Db | 1681 | TAAAATATTAAGTGTAATTATTTTAACACTCACAGCTACATATGACATTTTATGAGCTGT   | 1740 |
| Qy | 1741 | TTACGGCATGGAAAGAAAATCAGTGGGAATTAAGAAAGCCTCGTCGTGAAAGCACTTAAT   | 1800 |
|    |      |  |      |
| Db | 1741 | TTACGGCATGGAAAGAAAATCAGTGGGAATTAAGAAAGCCTCGTCGTGAAAGCACTTAAT   | 1800 |
| Qy | 1801 | TTTTTACAGTTAGCACTTCAACATAGCTCTTAACAACTTCCAGGATATTCACACAACACT   | 1860 |
|    |      |  |      |
| Db | 1801 | TTTTTACAGTTAGCACTTCAACATAGCTCTTAACAACTTCCAGGATATTCACACAACACT   | 1860 |
| Qy | 1861 | TAGGCTTAAAAATGAGCTCACTCAGAATTTCTATTCTTTCTAAAAAGAGATTTATTTT     | 1920 |

|    |      |   |      |
|----|------|---|------|
| Db | 1861 | <br>TAGGCTTAAAAATGAGCTCACTCAGAATTTCTATTCTTTCTAAAAAGAGATTTATTTTTA  | 1920 |
| Qy | 1921 | AATCAATGGGACTCTGATATAAAGGAAGAATAAGTCACTGTAAACAGAACTTTTAAATG       | 1980 |
| Db | 1921 | <br>AATCAATGGGACTCTGATATAAAGGAAGAATAAGTCACTGTAAACAGAACTTTTAAATG   | 1980 |
| Qy | 1981 | AAGCTTAAATTACTCAATTTAAAAATTTTAAATCCTTTAAACAACCTTTTCAATTAATAT      | 2040 |
| Db | 1981 | <br>AAGCTTAAATTACTCAATTTAAAAATTTTAAATCCTTTAAACAACCTTTTCAATTAATAT  | 2040 |
| Qy | 2041 | TATCACACTATTATCAGATTGTAATTAGATGCAAATGAGAGAGCAGTTTAGTTGTTGCAT      | 2100 |
| Db | 2041 | <br>TATCACACTATTATCAGATTGTAATTAGATGCAAATGAGAGAGCAGTTTAGTTGTTGCAT  | 2100 |
| Qy | 2101 | TTTTCGGACACTGGAAACATTTAAATGATCAGGAGGGAGTAACAGAAAGAGCAAGGCTGT      | 2160 |
| Db | 2101 | <br>TTTTCGGACACTGGAAACATTTAAATGATCAGGAGGGAGTAACAGAAAGAGCAAGGCTGT  | 2160 |
| Qy | 2161 | TTTTGAAAATCATTACACTTTCTACTAGAAGCCCAAACCTCAGCATTCTGCAATATGTAAC     | 2220 |
| Db | 2161 | <br>TTTTGAAAATCATTACACTTTCTACTAGAAGCCCAAACCTCAGCATTCTGCAATATGTAAC | 2220 |
| Qy | 2221 | CAACATGTCACAAACAAGCAGCATGTAACAGACTGGCACATGTGCCAGCTGAATTTAAAA      | 2280 |
| Db | 2221 | <br>CAACATGTCACAAACAAGCAGCATGTAACAGACTGGCACATGTGCCAGCTGAATTTAAAA  | 2280 |
| Qy | 2281 | TATAATACTTTTAAAAAGAAAATTATTACATCCTTTACATTCAAGTAAAGATCAAACCTCA     | 2340 |
| Db | 2281 | <br>TATAATACTTTTAAAAAGAAAATTATTACATCCTTTACATTCAAGTAAAGATCAAACCTCA | 2340 |
| Qy | 2341 | CAAAGAGAAATAGAATGTTTGAAAGGCTATCCCAAAGACTTTTTTGAATCTGTCATTCA       | 2400 |
| Db | 2341 | <br>CAAAGAGAAATAGAATGTTTGAAAGGCTATCCCAAAGACTTTTTTGAATCTGTCATTCA   | 2400 |
| Qy | 2401 | CATACCCTGTGAAGACAATACTATCTACAATTTTTTCAGGATTATTAATAATCTTCTTTTT     | 2460 |
| Db | 2401 | <br>CATACCCTGTGAAGACAATACTATCTACAATTTTTTCAGGATTATTAATAATCTTCTTTTT | 2460 |
| Qy | 2461 | TCATATCGTAGCTTAAACTCTGTTTGGTTTTGTCATCTGTAAATACTTACCTACATACA       | 2520 |
| Db | 2461 | <br>TCATATCGTAGCTTAAACTCTGTTTGGTTTTGTCATCTGTAAATACTTACCTACATACA   | 2520 |
| Qy | 2521 | CTGCATGTAGATGATTAAATGAGGGCAGGCCCTGTGCTCATAGCTTTACGATGGAGAGAT      | 2580 |
| Db | 2521 | <br>CTGCATGTAGATGATTAAATGAGGGCAGGCCCTGTGCTCATAGCTTTACGATGGAGAGAT  | 2580 |
| Qy | 2581 | GCCAGTGACCTCATAATAAAGACTGTGAACTGCCTGGTGCAGTGTCCACATGACAAAGGG      | 2640 |
| Db | 2581 | <br>GCCAGTGACCTCATAATAAAGACTGTGAACTGCCTGGTGCAGTGTCCACATGACAAAGGG  | 2640 |
| Qy | 2641 | GCAGGTAGCACCCCTCTCTACCCATGCTGTGGTTAAATGGTTTCTAGCATATGTATAAT       | 2700 |
| Db | 2641 | <br>GCAGGTAGCACCCCTCTCTACCCATGCTGTGGTTAAATGGTTTCTAGCATATGTATAAT   | 2700 |
| Qy | 2701 | GCTATAGTTAAATACTATTTTTTCAAATCATACAGATTAGTACATTTAACAGCTACCTG       | 2760 |
|    |      |   |      |

|    |      |  |      |
|----|------|--|------|
| Db | 2701 | GCTATAGTTAAAATACTATTTTTTCAAATCATACAGATTAGTACATTTAACAGCTACCTG   | 2760 |
| Qy | 2761 | TAAAGCTTATTACTAATTTTTGTATTATTTTTGTAAATAGCCAATAGAAAAGTTTGCTTG   | 2820 |
| Db | 2761 | TAAAGCTTATTACTAATTTTTGTATTATTTTTGTAAATAGCCAATAGAAAAGTTTGCTTG   | 2820 |
| Qy | 2821 | ACATGGTGCTTTTCTTTTCATCTAGAGGCCAAAAGTCTTTTTGAGACCGTAAGAACCTCTT  | 2880 |
| Db | 2821 | ACATGGTGCTTTTCTTTTCATCTAGAGGCCAAAAGTCTTTTTGAGACCGTAAGAACCTCTT  | 2880 |
| Qy | 2881 | AGCTTTGTGCGTTCCTGCCTAATTTTTATATCTTCTAAGCAAAGTGCCTTAGGATAGCTT   | 2940 |
| Db | 2881 | AGCTTTGTGCGTTCCTGCCTAATTTTTATATCTTCTAAGCAAAGTGCCTTAGGATAGCTT   | 2940 |
| Qy | 2941 | GGGATGAGATGTGTGTGAAAGTATGTACAAGAGAAAAACGGAAGAGAGAGGAAATGAGGTG  | 3000 |
| Db | 2941 | GGGATGAGATGTGTGTGAAAGTATGTACAAGAGAAAAACGGAAGAGAGAGGAAATGAGGTG  | 3000 |
| Qy | 3001 | GGGTTGGAGGAAACCCATGGGGACAGATTCCCATCTTAGCCTAACGTTTCGTCATTGCCT   | 3060 |
| Db | 3001 | GGGTTGGAGGAAACCCATGGGGACAGATTCCCATCTTAGCCTAACGTTTCGTCATTGCCT   | 3060 |
| Qy | 3061 | CGTCACATCAATGCAAAAGGTCCTGATTTTGTTCAGCAAAACACAGTGCAATGTTCTCA    | 3120 |
| Db | 3061 | CGTCACATCAATGCAAAAGGTCCTGATTTTGTTCAGCAAAACACAGTGCAATGTTCTCA    | 3120 |
| Qy | 3121 | GAGTGACTTTCGAAATAAATTGGGCCCAAGAGCTTTAACTCGGTCTTAAATATGCCCAA    | 3180 |
| Db | 3121 | GAGTGACTTTCGAAATAAATTGGGCCCAAGAGCTTTAACTCGGTCTTAAATATGCCCAA    | 3180 |
| Qy | 3181 | ATTTTTACTTTGTTTTCTTTTAATAGGCTGGGCCACATGTTGGAAATAAGCTAGTAATG    | 3240 |
| Db | 3181 | ATTTTTACTTTGTTTTCTTTTAATAGGCTGGGCCACATGTTGGAAATAAGCTAGTAATG    | 3240 |
| Qy | 3241 | TTGTTTTCTGTCAATATTGAATGTGATGGTACAGTAAACCAAACCAACAATGTGGCCA     | 3300 |
| Db | 3241 | TTGTTTTCTGTCAATATTGAATGTGATGGTACAGTAAACCAAACCAACAATGTGGCCA     | 3300 |
| Qy | 3301 | GAAAGAAAGAGCAATAATAATTAATTCACACACCATATGGATTCTATTTATAAATCACCC   | 3360 |
| Db | 3301 | GAAAGAAAGAGCAATAATAATTAATTCACACACCATATGGATTCTATTTATAAATCACCC   | 3360 |
| Qy | 3361 | ACAAACTTGTTCTTTAATTTTCATCCCAATCACTTTTTTCAGAGGCCTGTTATCATAGAAGT | 3420 |
| Db | 3361 | ACAAACTTGTTCTTTAATTTTCATCCCAATCACTTTTTTCAGAGGCCTGTTATCATAGAAGT | 3420 |
| Qy | 3421 | CATTTTAGACTCTCAATTTTAAATTAATTTTGAATCACTAATATTTTCACAGTTTATTAA   | 3480 |
| Db | 3421 | CATTTTAGACTCTCAATTTTAAATTAATTTTGAATCACTAATATTTTCACAGTTTATTAA   | 3480 |
| Qy | 3481 | TATATTTAATTTCTATTTAAATTTTAGATTATTTTTATTACCATGTACTGAATTTTACA    | 3540 |
| Db | 3481 | TATATTTAATTTCTATTTAAATTTTAGATTATTTTTATTACCATGTACTGAATTTTACA    | 3540 |
| Qy | 3541 | TCCTGATACCCTTTCTTTCTCCATGTCAGTATCATGTTCTCTAATTATCTTGCCAAATTT   | 3600 |
| Db | 3541 | TCCTGATACCCTTTCTTTCTCCATGTCAGTATCATGTTCTCTAATTATCTTGCCAAATTT   | 3600 |

|    |      |  |      |
|----|------|--|------|
| Qy | 3601 | TGAAACTACACACAAAAAGCATACTTGCATTATTTATAATAAAATTGCATTTCAGTGGCTT  | 3660 |
|    |      |  |      |
| Db | 3601 | TGAAACTACACACAAAAAGCATACTTGCATTATTTATAATAAAATTGCATTTCAGTGGCTT  | 3660 |
| Qy | 3661 | TTTAAAAAAAATGTTTGATTCAAAACTTTAACATACTGATAAGTAAGAAACAATTATAAT   | 3720 |
|    |      |  |      |
| Db | 3661 | TTTAAAAAAAATGTTTGATTCAAAACTTTAACATACTGATAAGTAAGAAACAATTATAAT   | 3720 |
| Qy | 3721 | TTCTTTACATACTCAAACCAAGATAGAAAAAGGTGCTATCGTTCAACTTCAAACATGT     | 3780 |
|    |      |  |      |
| Db | 3721 | TTCTTTACATACTCAAACCAAGATAGAAAAAGGTGCTATCGTTCAACTTCAAACATGT     | 3780 |
| Qy | 3781 | TTCCTAGTATTAAGGACTTTAATATAGCAACAGACAAAATTATTGTTAACATGGATGTTA   | 3840 |
|    |      |  |      |
| Db | 3781 | TTCCTAGTATTAAGGACTTTAATATAGCAACAGACAAAATTATTGTTAACATGGATGTTA   | 3840 |
| Qy | 3841 | CAGCTCAAAGATTTATAAAAGATTTTAACCTATTTTCTCCCTTATTATCCACTGCTAAT    | 3900 |
|    |      |  |      |
| Db | 3841 | CAGCTCAAAGATTTATAAAAGATTTTAACCTATTTTCTCCCTTATTATCCACTGCTAAT    | 3900 |
| Qy | 3901 | GTGGATGTATGTTCAAACACCTTTTAGTATTGATAGCTTACATATGGCCAAAGGAATACA   | 3960 |
|    |      |  |      |
| Db | 3901 | GTGGATGTATGTTCAAACACCTTTTAGTATTGATAGCTTACATATGGCCAAAGGAATACA   | 3960 |
| Qy | 3961 | GTTTATAGCAAACATGGGTATGCTGTAGCTAACTTTATAAAAGTGTAATATAACAATGT    | 4020 |
|    |      |  |      |
| Db | 3961 | GTTTATAGCAAACATGGGTATGCTGTAGCTAACTTTATAAAAGTGTAATATAACAATGT    | 4020 |
| Qy | 4021 | AAAAAATTATATATCTGGGAGGATTTTTTGGTTGCCTAAAGTGGCTATAGTTACTGATTT   | 4080 |
|    |      |  |      |
| Db | 4021 | AAAAAATTATATATCTGGGAGGATTTTTTGGTTGCCTAAAGTGGCTATAGTTACTGATTT   | 4080 |
| Qy | 4081 | TTTATTATGTAAGCAAACCAATAAAAAATTTAAGTTTTTTTAACAACCTACCTTATTTTTTC | 4140 |
|    |      |  |      |
| Db | 4081 | TTTATTATGTAAGCAAACCAATAAAAAATTTAAGTTTTTTTAACAACCTACCTTATTTTTTC | 4140 |
| Qy | 4141 | ACTGTACAGACACTAATTCATTAAATACTAATTGATTGTTTAAAAGAAATATAAATGTGA   | 4200 |
|    |      |  |      |
| Db | 4141 | ACTGTACAGACACTAATTCATTAAATACTAATTGATTGTTTAAAAGAAATATAAATGTGA   | 4200 |
| Qy | 4201 | CAAGTGGACATTATTTATGTTAAATATACAATTATCAAGCAAGTATGAAGTTATTCAATT   | 4260 |
|    |      |  |      |
| Db | 4201 | CAAGTGGACATTATTTATGTTAAATATACAATTATCAAGCAAGTATGAAGTTATTCAATT   | 4260 |
| Qy | 4261 | AAAATGCCACATTTCTGGTCTCTGGG                                     | 4286 |
|    |      |  |      |
| Db | 4261 | AAAATGCCACATTTCTGGTCTCTGGG                                     | 4286 |

RESULT 8

ADB37423

ID ADB37423 standard; DNA; 4286 BP.

XX

AC ADB37423;

XX

DT 04-DEC-2003 (first entry)

XX  
 DE Human cancer associated gene EDNRB polynucleotide #2.  
 XX  
 KW antisense therapy; gene therapy; cytostatic; cancer; Wnt5a; MART-1;  
 KW pirin; HADHB; CD63; ENDRB; PGAM1; HXB; RXRA; integrin b1; syndecan 4;  
 KW tropomyosin 1; AXL; EphA2; GAP43; PFKL; synuclein a; annexin A2; CD20;  
 KW RAB2; tumour; malignant melanoma;  
 KW wingless MMTV integration site family member 5a; human; ds.  
 XX  
 OS Homo sapiens.  
 XX  
 PN US2003152923-A1.  
 XX  
 PD 14-AUG-2003.  
 XX  
 PF 02-AUG-2001; 2001US-00921406.  
 XX  
 PR 02-AUG-2001; 2001US-00921406.  
 XX  
 PA (YAKH/) YAKHINI Z.  
 PA (BITT/) BITTNER M.  
 PA (TREN/) TRENT J.  
 PA (BEND/) BEN-DOR A.  
 PA (MELT/) MELTZER P.  
 PA (CHEN/) CHEN Y.  
 PA (WEER/) WEERARATNA A.  
 PA (JIAN/) JIANG Y.  
 PA (SAMP/) SAMPAS N.  
 PA (DOUG/) DOUGHERTY E.  
 XX  
 PI Yakhini Z, Bittner M, Trent J, Ben-Dor A, Meltzer P, Chen Y;  
 PI Weeraratna A, Jiang Y, Sampas N, Dougherty E;  
 XX  
 DR WPI; 2003-635998/60.  
 XX  
 PT Diagnosing an aggressive form of cancer, comprises detecting expression  
 PT pattern of genes such as Wnt5a, MART-1, pirin, HADHB, CD63, ENDRB, PGAM1,  
 PT synuclein a, annexin A2, CD20, and RAB2.  
 XX  
 PS Disclosure; Page 27-29; 70pp; English.  
 XX  
 CC The invention describes a method of diagnosing an aggressive form of  
 CC cancer comprising: analysing expression of genes Wnt5a, MART-1, pirin,  
 CC HADHB, CD63, ENDRB, PGAM1, HXB, RXRA, integrin b1, syndecan 4,  
 CC tropomyosin 1, AXL, EphA2, GAP43, PFKL, synuclein a, annexin A2, CD20,  
 CC and RAB2 in tumour sample; and identifying the tumour as aggressive or  
 CC non-aggressive based on the expression pattern of the genes. The methods  
 CC are useful for detecting and treating malignant melanoma found to be  
 CC associated with gene markers such as Wnt5a. This sequence represents a  
 CC polynucleotide of a human gene, the expression level of which is used in  
 CC cancer diagnosis.  
 XX  
 SQ Sequence 4286 BP; 1327 A; 829 C; 816 G; 1314 T; 0 U; 0 Other;  
  
 Query Match 99.6%; Score 4284.4; DB 9; Length 4286;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 4285; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

|    |     |   |     |
|----|-----|---|-----|
| Qy | 1   | GAGACATTCCGGTGGGGGACTCTGGCCAGCCCCGAGCAACGTGGATCCTGAGAGCACTCCC | 60  |
| Db | 1   | GAGACATTCCGGTGGGGGACTCTGGCCAGCCCCGAGCAACGTGGATCCTGAGAGCACTCCC | 60  |
| Qy | 61  | AGGTAGGCATTTGCCCCGGTGGGACGCCTTGCCAGAGCAGTGTGTGGCAGGCCCCCGTGG  | 120 |
| Db | 61  | AGGTAGGCATTTGCCCCGGTGGGACGCCTTGCCAGAGCAGTGTGTGGCAGGCCCCCGTGG  | 120 |
| Qy | 121 | AGGATCAACACAGTGGCTGAACACTGGGAAGGAACTGGTACTTGGAGTCTGGACATCTGA  | 180 |
| Db | 121 | AGGATCAACACAGTGGCTGAACACTGGGAAGGAACTGGTACTTGGAGTCTGGACATCTGA  | 180 |
| Qy | 181 | AACTTGGCTCTGAAACTGCGGAGCGGCCACCGACGCCTTCTGGAGCAGGTAGCAGCATG   | 240 |
| Db | 181 | AACTTGGCTCTGAAACTGCGCAGCGGCCACCGACGCCTTCTGGAGCAGGTAGCAGCATG   | 240 |
| Qy | 241 | CAGCCGCCTCCAAGTCTGTGCGGACGCGCCCTGGTTGCGCTGGTTCTTGCCTGCGGCCTG  | 300 |
| Db | 241 | CAGCCGCCTCCAAGTCTGTGCGGACGCGCCCTGGTTGCGCTGGTTCTTGCCTGCGGCCTG  | 300 |
| Qy | 301 | TCGCGGATCTGGGGAGAGGAGAGAGGCTTCCCGCCTGACAGGGCCACTCCGCTTTTGCAA  | 360 |
| Db | 301 | TCGCGGATCTGGGGAGAGGAGAGAGGCTTCCCGCCTGACAGGGCCACTCCGCTTTTGCAA  | 360 |
| Qy | 361 | ACCGCAGAGATAATGACGCCACCCACTAAGACCTTATGGCCCAAGGGTTCCAACGCCAGT  | 420 |
| Db | 361 | ACCGCAGAGATAATGACGCCACCCACTAAGACCTTATGGCCCAAGGGTTCCAACGCCAGT  | 420 |
| Qy | 421 | CTGGCGCGGTTCGTTGGCACCTGCGGAGGTGCCTAAAGGAGACAGGACGGCAGGATCTCCG | 480 |
| Db | 421 | CTGGCGCGGTTCGTTGGCACCTGCGGAGGTGCCTAAAGGAGACAGGACGGCAGGATCTCCG | 480 |
| Qy | 481 | CCACGCACCATCTCCCCTCCCCCGTGCCAAGGACCCATCGAGATCAAGGAGACTTTCAA   | 540 |
| Db | 481 | CCACGCACCATCTCCCCTCCCCCGTGCCAAGGACCCATCGAGATCAAGGAGACTTTCAA   | 540 |
| Qy | 541 | TACATCAACACGGTTGTGTCTGCCTTGTGTTTCGTGCTGGGGATCATCGGGAACCTCCACA | 600 |
| Db | 541 | TACATCAACACGGTTGTGTCTGCCTTGTGTTTCGTGCTGGGGATCATCGGGAACCTCCACA | 600 |
| Qy | 601 | CTTCTGAGAATTATCTACAAGAACAAGTGCATGCGAAACGGTCCCAATATCTTGATCGCC  | 660 |
| Db | 601 | CTTCTGAGAATTATCTACAAGAACAAGTGCATGCGAAACGGTCCCAATATCTTGATCGCC  | 660 |
| Qy | 661 | AGCTTGGCTCTGGGAGACCTGCTGCACATCGTCATTGACATCCCTATCAATGTCTACAAG  | 720 |
| Db | 661 | AGCTTGGCTCTGGGAGACCTGCTGCACATCGTCATTGACATCCCTATCAATGTCTACAAG  | 720 |
| Qy | 721 | CTGCTGGCAGAGGACTGGCCATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTCATACAG  | 780 |
| Db | 721 | CTGCTGGCAGAGGACTGGCCATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTCATACAG  | 780 |
| Qy | 781 | AAAGCCTCCGTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATATCGA  | 840 |
| Db | 781 | AAAGCCTCCGTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATATCGA  | 840 |

|    |      |  |      |
|----|------|--|------|
| Qy | 841  | GCTGTTGCTTCTTGGAGTAGAATTAAAGGAATTGGGGTTCCAAAATGGACAGCAGTAGAA   | 900  |
|    |      |  |      |
| Db | 841  | GCTGTTGCTTCTTGGAGTAGAATTAAAGGAATTGGGGTTCCAAAATGGACAGCAGTAGAA   | 900  |
| Qy | 901  | ATTGTTTTGATTTGGGTGGTCTCTGTGGTTCTGGCTGTCCCTGAAGCCATAGGTTTTGAT   | 960  |
|    |      |  |      |
| Db | 901  | ATTGTTTTGATTTGGGTGGTCTCTGTGGTTCTGGCTGTCCCTGAAGCCATAGGTTTTGAT   | 960  |
| Qy | 961  | ATAATTACGATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTTCAG   | 1020 |
|    |      |  |      |
| Db | 961  | ATAATTACGATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTTCAG   | 1020 |
| Qy | 1021 | AAGACAGCTTTCATGCAGTTTTTACAAGACAGCAAAAGATTGGTGGCTGTTCAAGTTTCTAT | 1080 |
|    |      |  |      |
| Db | 1021 | AAGACAGCTTTCATGCAGTTTTTACAAGACAGCAAAAGATTGGTGGCTGTTCAAGTTTCTAT | 1080 |
| Qy | 1081 | TTCTGCTTGCCATTGGCCATCACTGCATTTTTTTTATACACTAATGACCTGTGAAATGTTG  | 1140 |
|    |      |  |      |
| Db | 1081 | TTCTGCTTGCCATTGGCCATCACTGCATTTTTTTTATACACTAATGACCTGTGAAATGTTG  | 1140 |
| Qy | 1141 | AGAAAGAAAAGTGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAAGTG   | 1200 |
|    |      |  |      |
| Db | 1141 | AGAAAGAAAAGTGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAAGTG   | 1200 |
| Qy | 1201 | GCCAAAACCGTCTTTTGCCTGGTCCTTGTCTTTGCCCTCTGCTGGCTTCCCTTCACCTC    | 1260 |
|    |      |  |      |
| Db | 1201 | GCCAAAACCGTCTTTTGCCTGGTCCTTGTCTTTGCCCTCTGCTGGCTTCCCTTCACCTC    | 1260 |
| Qy | 1261 | AGCAGGATTCTGAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGAACTTTTG   | 1320 |
|    |      |  |      |
| Db | 1261 | AGCAGGATTCTGAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGAACTTTTG   | 1320 |
| Qy | 1321 | AGCTTTCTGTTGGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCCTGCATT   | 1380 |
|    |      |  |      |
| Db | 1321 | AGCTTTCTGTTGGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCCTGCATT   | 1380 |
| Qy | 1381 | AACCCAATTGCTCTGTATTTGGTGAGCAAAAGATTCAAAAAGTCTTTAAGTCATGCTTA    | 1440 |
|    |      |  |      |
| Db | 1381 | AACCCAATTGCTCTGTATTTGGTGAGCAAAAGATTCAAAAAGTCTTTAAGTCATGCTTA    | 1440 |
| Qy | 1441 | TGCTGCTGGTGCCAGTCATTTGAAGAAAAACAGTCCTTGGAGGAAAAGCAGTCGTGCTTA   | 1500 |
|    |      |  |      |
| Db | 1441 | TGCTGCTGGTGCCAGTCATTTGAAGAAAAACAGTCCTTGGAGGAAAAGCAGTCGTGCTTA   | 1500 |
| Qy | 1501 | AAGTTCAAAGCTAATGATCACGGATATGACAACTCCGTTCCAGTAATAAATACAGCTCA    | 1560 |
|    |      |  |      |
| Db | 1501 | AAGTTCAAAGCTAATGATCACGGATATGACAACTCCGTTCCAGTAATAAATACAGCTCA    | 1560 |
| Qy | 1561 | TCTTGAAAGAAGAACTATTCAGTGTATTTTCTTTATATTGGACCGAAGTCATTAA        | 1620 |
|    |      |  |      |
| Db | 1561 | TCTTGAAAGAAGAACTATTCAGTGTATTTTCTTTATATTGGACCGAAGTCATTAA        | 1620 |
| Qy | 1621 | AACAAAATGAAACATTTGCCAAAACAAAACAAAAACTATGTATTTGCACAGCACACTAT    | 1680 |
|    |      |  |      |
| Db | 1621 | AACAAAATGAAACATTTGCCAAAACAAAACAAAAACTATGTATTTGCACAGCACACTAT    | 1680 |
| Qy | 1681 | TAAAATATTAAGTGTAATTATTTTAACTACAGCTACATATGACATTTTATGAGCTGT      | 1740 |



|    |      |   |      |
|----|------|---|------|
|    |      |   |      |
| Db | 1681 | TAAAAATATTAAGTGTAAATTATTTTAACTCACAGCTACATATGACATTTTATGAGCTGT  | 1740 |
| Qy | 1741 | TTACGGCATGGAAAGAAAATCAGTGGGAATTAAGAAAGCCTCGTCGTGAAAGCACTTAAT  | 1800 |
|    |      |   |      |
| Db | 1741 | TTACGGCATGGAAAGAAAATCAGTGGGAATTAAGAAAGCCTCGTCGTGAAAGCACTTAAT  | 1800 |
| Qy | 1801 | TTTTTACAGTTAGCACTTCAACATAGCTCTTAACAACCTCCAGGATATTCACACAACACT  | 1860 |
|    |      |   |      |
| Db | 1801 | TTTTTACAGTTAGCACTTCAACATAGCTCTTAACAACCTCCAGGATATTCACACAACACT  | 1860 |
| Qy | 1861 | TAGGCTTAAAAATGAGCTCACTCAGAATTTCTATTCTTTCTAAAAAGAGATTTATTTT    | 1920 |
|    |      |   |      |
| Db | 1861 | TAGGCTTAAAAATGAGCTCACTCAGAATTTCTATTCTTTCTAAAAAGAGATTTATTTT    | 1920 |
| Qy | 1921 | AATCAATGGGACTCTGATATAAAGGAAGAATAAGTCACTGTAAAACAGAACCTTTTAAATG | 1980 |
|    |      |   |      |
| Db | 1921 | AATCAATGGGACTCTGATATAAAGGAAGAATAAGTCACTGTAAAACAGAACCTTTTAAATG | 1980 |
| Qy | 1981 | AAGCTTAAATTACTCAATTTAAATTTTAAATCCTTTAAACAACCTTTTCAATTAATAT    | 2040 |
|    |      |   |      |
| Db | 1981 | AAGCTTAAATTACTCAATTTAAATTTTAAATCCTTTAAACAACCTTTTCAATTAATAT    | 2040 |
| Qy | 2041 | TATCACACTATTATCAGATTGTAATTAGATGCAAATGAGAGAGCAGTTTAGTTGTTGCAT  | 2100 |
|    |      |   |      |
| Db | 2041 | TATCACACTATTATCAGATTGTAATTAGATGCAAATGAGAGAGCAGTTTAGTTGTTGCAT  | 2100 |
| Qy | 2101 | TTTTCGGACACTGGAAACATTTAAATGATCAGGAGGGAGTAACAGAAAGAGCAAGGCTGT  | 2160 |
|    |      |   |      |
| Db | 2101 | TTTTCGGACACTGGAAACATTTAAATGATCAGGAGGGAGTAACAGAAAGAGCAAGGCTGT  | 2160 |
| Qy | 2161 | TTTTGAAAATCATTACACTTTTACTAGAAGCCCAAACCTCAGCATTCTGCAATATGTAAC  | 2220 |
|    |      |   |      |
| Db | 2161 | TTTTGAAAATCATTACACTTTTACTAGAAGCCCAAACCTCAGCATTCTGCAATATGTAAC  | 2220 |
| Qy | 2221 | CAACATGTCACAAACAAGCAGCATGTAACAGACTGGCACATGTGCCAGCTGAATTTAAAA  | 2280 |
|    |      |   |      |
| Db | 2221 | CAACATGTCACAAACAAGCAGCATGTAACAGACTGGCACATGTGCCAGCTGAATTTAAAA  | 2280 |
| Qy | 2281 | TATAATACTTTTAAAAAGAAAATTATTACATCCTTTACATTAGTTAAGATCAAACCTCA   | 2340 |
|    |      |   |      |
| Db | 2281 | TATAATACTTTTAAAAAGAAAATTATTACATCCTTTACATTAGTTAAGATCAAACCTCA   | 2340 |
| Qy | 2341 | CAAAGAGAAATAGAATGTTTGAAAGGCTATCCCAAAGACTTTTTTGAATCTGTCATTCA   | 2400 |
|    |      |   |      |
| Db | 2341 | CAAAGAGAAATAGAATGTTTGAAAGGCTATCCCAAAGACTTTTTTGAATCTGTCATTCA   | 2400 |
| Qy | 2401 | CATACCCTGTGAAGACAATACTATCTACAATTTTTTCAGGATTATTAAATCTTCTTTTT   | 2460 |
|    |      |   |      |
| Db | 2401 | CATACCCTGTGAAGACAATACTATCTACAATTTTTTCAGGATTATTAAATCTTCTTTTT   | 2460 |
| Qy | 2461 | TCATATCGTAGCTTAAACTCTGTTTGGTTTGTGTCATCTGTAAATACTTACCTACATACA  | 2520 |
|    |      |   |      |
| Db | 2461 | TCATATCGTAGCTTAAACTCTGTTTGGTTTGTGTCATCTGTAAATACTTACCTACATACA  | 2520 |
| Qy | 2521 | CTGCATGTAGATGATTAAATGAGGGCAGGCCCTGTGCTCATAGCTTTACGATGGAGAGAT  | 2580 |
|    |      |   |      |

|    |      |  |      |
|----|------|--|------|
| Db | 2521 | CTGCATGTAGATGATTAAATGAGGGCAGGCCCTGTGCTCATAGCTTTACGATGGAGAGAT   | 2580 |
| Qy | 2581 | GCCAGTGACCTCATAATAAAGACTGTGAACTGCCTGGTGCAGTGTCCACATGACAAAGGG   | 2640 |
|    |      |  |      |
| Db | 2581 | GCCAGTGACCTCATAATAAAGACTGTGAACTGCCTGGTGCAGTGTCCACATGACAAAGGG   | 2640 |
| Qy | 2641 | GCAGGTAGCACCCCTCTCTCACCCATGCTGTGGTTAAAATGGTTTCTAGCATATGTATAAT  | 2700 |
|    |      |  |      |
| Db | 2641 | GCAGGTAGCACCCCTCTCTCACCCATGCTGTGGTTAAAATGGTTTCTAGCATATGTATAAT  | 2700 |
| Qy | 2701 | GCTATAGTTAAAATACTATTTTTCAAAATCATACAGATTAGTACATTTAACAGCTACCTG   | 2760 |
|    |      |  |      |
| Db | 2701 | GCTATAGTTAAAATACTATTTTTCAAAATCATACAGATTAGTACATTTAACAGCTACCTG   | 2760 |
| Qy | 2761 | TAAAGCTTATTACTAATTTTTGTATTATTTTTGTAAATAGCCAATAGAAAAGTTTGCTTG   | 2820 |
|    |      |  |      |
| Db | 2761 | TAAAGCTTATTACTAATTTTTGTATTATTTTTGTAAATAGCCAATAGAAAAGTTTGCTTG   | 2820 |
| Qy | 2821 | ACATGGTGCTTTTCTTTCATCTAGAGGCCAAACTGCTTTTGGAGACCGTAAGAACCTCTT   | 2880 |
|    |      |  |      |
| Db | 2821 | ACATGGTGCTTTTCTTTCATCTAGAGGCCAAACTGCTTTTGGAGACCGTAAGAACCTCTT   | 2880 |
| Qy | 2881 | AGCTTTGTGCGTTCCTGCCTAATTTTTTATATCTTCTAAGCAAAGTGCCTTAGGATAGCTT  | 2940 |
|    |      |  |      |
| Db | 2881 | AGCTTTGTGCGTTCCTGCCTAATTTTTTATATCTTCTAAGCAAAGTGCCTTAGGATAGCTT  | 2940 |
| Qy | 2941 | GGGATGAGATGTGTGTGAAAGTATGTACAAGAGAAAACGGAAGAGAGAGGAAATGAGGTG   | 3000 |
|    |      |  |      |
| Db | 2941 | GGGATGAGATGTGTGTGAAAGTATGTACAAGAGAAAACGGAAGAGAGAGGAAATGAGGTG   | 3000 |
| Qy | 3001 | GGGTTGGAGGAAACCCATGGGGACAGATTCCCATTCTTAGCCTAACGTTTCGTCATTGCCT  | 3060 |
|    |      |  |      |
| Db | 3001 | GGGTTGGAGGAAACCCATGGGGACAGATTCCCATTCTTAGCCTAACGTTTCGTCATTGCCT  | 3060 |
| Qy | 3061 | CGTCACATCAATGCAAAGGTCCTGATTTTGTTCAGCAAAACACAGTGCAATGTTCTCA     | 3120 |
|    |      |  |      |
| Db | 3061 | CGTCACATCAATGCAAAGGTCCTGATTTTGTTCAGCAAAACACAGTGCAATGTTCTCA     | 3120 |
| Qy | 3121 | GAGTGACTTTGAAATAAATTGGGCCCAAGAGCTTTAACTCGGTCTTAAAATATGCCCAA    | 3180 |
|    |      |  |      |
| Db | 3121 | GAGTGACTTTGAAATAAATTGGGCCCAAGAGCTTTAACTCGGTCTTAAAATATGCCCAA    | 3180 |
| Qy | 3181 | ATTTTTACTTTGTTTTCTTTTAAATAGGCTGGGCCACATGTTGGAAATAAGCTAGTAATG   | 3240 |
|    |      |  |      |
| Db | 3181 | ATTTTTACTTTGTTTTCTTTTAAATAGGCTGGGCCACATGTTGGAAATAAGCTAGTAATG   | 3240 |
| Qy | 3241 | TTGTTTTCTGTCAATATTGAATGTGATGGTACAGTAAACCAAACCAACAATGTGGCCA     | 3300 |
|    |      |  |      |
| Db | 3241 | TTGTTTTCTGTCAATATTGAATGTGATGGTACAGTAAACCAAACCAACAATGTGGCCA     | 3300 |
| Qy | 3301 | GAAAGAAAGAGCAATAATAATTAATTCACACACCATATGGATTCTATTTATAAATCACCC   | 3360 |
|    |      |  |      |
| Db | 3301 | GAAAGAAAGAGCAATAATAATTAATTCACACACCATATGGATTCTATTTATAAATCACCC   | 3360 |
| Qy | 3361 | ACAAACTTGTTCTTTAATTTTCATCCCAATCACTTTTTTCAGAGGCCTGTTATCATAGAAGT | 3420 |
|    |      |  |      |
| Db | 3361 | ACAAACTTGTTCTTTAATTTTCATCCCAATCACTTTTTTCAGAGGCCTGTTATCATAGAAGT | 3420 |

|    |      |   |      |
|----|------|---|------|
| Qy | 3421 | CATTTTAGACTCTCAATTTTAAATTAATTTTGAATCACTAATATTTTCACAGTTTATTAA    | 3480 |
|    |      |   |      |
| Db | 3421 | CATTTTAGACTCTCAATTTTAAATTAATTTTGAATCACTAATATTTTCACAGTTTATTAA    | 3480 |
| Qy | 3481 | TATATTTAATTTCTATTTAAATTTTAGATTATTTTATTACCATGTACTGAATTTTACA      | 3540 |
|    |      |   |      |
| Db | 3481 | TATATTTAATTTCTATTTAAATTTTAGATTATTTTATTACCATGTACTGAATTTTACA      | 3540 |
| Qy | 3541 | TCCTGATACCCCTTTCCTTCTCCATGTCTCAGTATCATGTTCTCTAATTATCTTGCCAAATTT | 3600 |
|    |      |   |      |
| Db | 3541 | TCCTGATACCCCTTTCCTTCTCCATGTCTCAGTATCATGTTCTCTAATTATCTTGCCAAATTT | 3600 |
| Qy | 3601 | TGAAACTACACACAAAAAGCATACTTGCATTATTTATAATAAAATTGCATTTCAGTGGCTT   | 3660 |
|    |      |   |      |
| Db | 3601 | TGAAACTACACACAAAAAGCATACTTGCATTATTTATAATAAAATTGCATTTCAGTGGCTT   | 3660 |
| Qy | 3661 | TTTAAAAAAAATGTTTGATTCAAACCTTTAACATACTGATAAGTAAGAAACAATTATAAT    | 3720 |
|    |      |   |      |
| Db | 3661 | TTTAAAAAAAATGTTTGATTCAAACCTTTAACATACTGATAAGTAAGAAACAATTATAAT    | 3720 |
| Qy | 3721 | TTCTTTACATACTCAAACCAAGATAGAAAAAGGTGCTATCGTTCAACTTCAAACATGT      | 3780 |
|    |      |   |      |
| Db | 3721 | TTCTTTACATACTCAAACCAAGATAGAAAAAGGTGCTATCGTTCAACTTCAAACATGT      | 3780 |
| Qy | 3781 | TTCCTAGTATTAAGGACTTTAATATAGCAACAGACAAAATTATTGTTAACATGGATGTTA    | 3840 |
|    |      |   |      |
| Db | 3781 | TTCCTAGTATTAAGGACTTTAATATAGCAACAGACAAAATTATTGTTAACATGGATGTTA    | 3840 |
| Qy | 3841 | CAGCTCAAAGATTTATAAAAGATTTTAACCTATTTTCTCCCTTATTATCCACTGCTAAT     | 3900 |
|    |      |   |      |
| Db | 3841 | CAGCTCAAAGATTTATAAAAGATTTTAACCTATTTTCTCCCTTATTATCCACTGCTAAT     | 3900 |
| Qy | 3901 | GTGGATGTATGTTCAAACACCTTTTAGTATTGATAGCTTACATATGGCCAAAGGAATACA    | 3960 |
|    |      |   |      |
| Db | 3901 | GTGGATGTATGTTCAAACACCTTTTAGTATTGATAGCTTACATATGGCCAAAGGAATACA    | 3960 |
| Qy | 3961 | GTTTATAGCAAACATGGGTATGCTGTAGCTAACTTTATAAAAGTGTAATATAACAATGT     | 4020 |
|    |      |   |      |
| Db | 3961 | GTTTATAGCAAACATGGGTATGCTGTAGCTAACTTTATAAAAGTGTAATATAACAATGT     | 4020 |
| Qy | 4021 | AAAAAATTATATATCTGGGAGGATTTTTTGGTTGCCTAAAGTGGCTATAGTTACTGATTT    | 4080 |
|    |      |   |      |
| Db | 4021 | AAAAAATTATATATCTGGGAGGATTTTTTGGTTGCCTAAAGTGGCTATAGTTACTGATTT    | 4080 |
| Qy | 4081 | TTTATTATGTAAGCAAAACCAATAAAAAATTTAAGTTTTTTTAAACACTACCTTATTTTTC   | 4140 |
|    |      |   |      |
| Db | 4081 | TTTATTATGTAAGCAAAACCAATAAAAAATTTAAGTTTTTTTAAACACTACCTTATTTTTC   | 4140 |
| Qy | 4141 | ACTGTACAGACACTAATTCATTAAATACTAATTGATTGTTTAAAAGAAATATAAATGTGA    | 4200 |
|    |      |   |      |
| Db | 4141 | ACTGTACAGACACTAATTCATTAAATACTAATTGATTGTTTAAAAGAAATATAAATGTGA    | 4200 |
| Qy | 4201 | CAAGTGGACATTATTTATGTTAAATATACAATTATCAAGCAAGTATGAAGTTATTCAATT    | 4260 |
|    |      |   |      |
| Db | 4201 | CAAGTGGACATTATTTATGTTAAATATACAATTATCAAGCAAGTATGAAGTTATTCAATT    | 4260 |

Qy 4261 AAAATGCCACATTTCTGGTCTCTGGG 4286  
|||||  
Db 4261 AAAATGCCACATTTCTGGTCTCTGGG 4286

RESULT 9

ADD18443

ID ADD18443 standard; DNA; 4286 BP.

XX

AC ADD18443;

XX

DT 15-JAN-2004 (first entry)

XX

DE Human prostate cancer diagnosis related DNA sequence SeqID15.

XX

KW prostate tissue; cancer diagnostic; cancer marker; prostate cancer; PCA;  
KW male cancer-related death; serum biomarker; tissue biomarker; cytostatic;  
KW gene therapy; prostate biopsy tissue; AMACR;  
KW alpha-methylacyl-coenzyme A racemase; diagnosing cancer; cell growth;  
KW human; ds.

XX

OS Homo sapiens.

XX

PN WO2003012067-A2.

XX

PD 13-FEB-2003.

XX

PF 02-AUG-2002; 2002WO-US024567.

XX

PR 02-AUG-2001; 2001US-0309581P.

PR 15-NOV-2001; 2001US-0334468P.

PR 01-AUG-2002; 2002US-00210120.

XX

PA (UNMI ) UNIV MICHIGAN.

XX

PI Rubin MA, Chinnaiyan AM, Sreekumar A;

XX

DR WPI; 2003-278396/27.

XX

PT Characterizing prostate tissue comprises providing a prostate tissue  
PT sample from a subject and detecting the presence or absence of expression  
PT of hepsin, pim-1 or EZH2.

XX

PS Disclosure; SEQ ID NO 15; 297pp; English.

XX

CC This invention relates to a novel method of characterising prostate  
CC tissue in a subject and to compositions and methods for cancer  
CC diagnostics, including cancer markers, in particular prostate cancer.  
CC Prostate cancer (PCA) is a leading cause of male cancer-related death.  
CC Additional serum and tissue biomarkers would aid diagnosis. The invention  
CC may provide means of producing compounds with a cytostatic activity or  
CC allow the development of gene therapy. The methods of the invention  
CC useful for characterising prostate tissue in a subject, screening  
CC compounds, characterising inconclusive prostate biopsy tissue in a  
CC subject, detecting AMACR (alpha-methylacyl-coenzyme A racemase)  
CC expression in a bodily fluid, characterising tissue in a subject,  
CC diagnosing cancer in a subject and inhibiting the growth of cells. The

CC present sequence is a DNA sequence which is preferably utilised in the  
CC method of the invention.

XX

SQ Sequence 4286 BP; 1327 A; 829 C; 816 G; 1314 T; 0 U; 0 Other;

Query Match 99.6%; Score 4284.4; DB 9; Length 4286;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 4285; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy      1 GAGACATTCCGGTGGGGGACTCTGGCCAGCCCAGCAACGTGGATCCTGAGAGCACTCCC 60
          |||
Db      1 GAGACATTCCGGTGGGGGACTCTGGCCAGCCCAGCAACGTGGATCCTGAGAGCACTCCC 60

Qy     61 AGGTAGGCATTTGCCCCGGTGGGACGCCTTGCCAGAGCAGTGTGTGGCAGGCCCCCGTGG 120
          |||
Db     61 AGGTAGGCATTTGCCCCGGTGGGACGCCTTGCCAGAGCAGTGTGTGGCAGGCCCCCGTGG 120

Qy    121 AGGATCAACACAGTGGCTGAACACTGGGAAGGAACTGGTACTTGGAGTCTGGACATCTGA 180
          |||
Db    121 AGGATCAACACAGTGGCTGAACACTGGGAAGGAACTGGTACTTGGAGTCTGGACATCTGA 180

Qy    181 AACTTGGCTCTGAAACTGCGGAGCGGCCACCGACGCCTTCTGGAGCAGGTAGCAGCATG 240
          |||
Db    181 AACTTGGCTCTGAAACTGCGCAGCGGCCACCGACGCCTTCTGGAGCAGGTAGCAGCATG 240

Qy    241 CAGCCGCCTCCAAGTCTGTGCGGACGCGCCCTGGTTGCGCTGGTTCTTGCTGCGGCCTG 300
          |||
Db    241 CAGCCGCCTCCAAGTCTGTGCGGACGCGCCCTGGTTGCGCTGGTTCTTGCTGCGGCCTG 300

Qy    301 TCGCGGATCTGGGGAGAGGAGAGAGGCTTCCCGCCTGACAGGGCCACTCCGCTTTTGCAA 360
          |||
Db    301 TCGCGGATCTGGGGAGAGGAGAGAGGCTTCCCGCCTGACAGGGCCACTCCGCTTTTGCAA 360

Qy    361 ACCGCAGAGATAATGACGCCACCCACTAAGACCTTATGGCCCAAGGGTTCCAACGCCAGT 420
          |||
Db    361 ACCGCAGAGATAATGACGCCACCCACTAAGACCTTATGGCCCAAGGGTTCCAACGCCAGT 420

Qy    421 CTGGCGCGGTTCGTTGGCACCTGCGGAGGTGCCTAAAGGAGACAGGACGGCAGGATCTCCG 480
          |||
Db    421 CTGGCGCGGTTCGTTGGCACCTGCGGAGGTGCCTAAAGGAGACAGGACGGCAGGATCTCCG 480

Qy    481 CCACGCACCATCTCCCCTCCCCCGTGCCAAGGACCCATCGAGATCAAGGAGACTTTCAA 540
          |||
Db    481 CCACGCACCATCTCCCCTCCCCCGTGCCAAGGACCCATCGAGATCAAGGAGACTTTCAA 540

Qy    541 TACATCAACACGGTTGTGTCCTGCCTTGTGTTTCGTGCTGGGGATCATCGGGAAGTCCACA 600
          |||
Db    541 TACATCAACACGGTTGTGTCCTGCCTTGTGTTTCGTGCTGGGGATCATCGGGAAGTCCACA 600

Qy    601 CTTCTGAGAATTATCTACAAGAACAAGTGCATGCGAAACGGTCCCAATATCTTGATCGCC 660
          |||
Db    601 CTTCTGAGAATTATCTACAAGAACAAGTGCATGCGAAACGGTCCCAATATCTTGATCGCC 660

Qy    661 AGCTTGGCTCTGGGAGACCTGCTGCACATCGTCATTGACATCCCTATCAATGTCTACAAG 720
          |||
Db    661 AGCTTGGCTCTGGGAGACCTGCTGCACATCGTCATTGACATCCCTATCAATGTCTACAAG 720
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|    |      |   |      |
|----|------|---|------|
| Qy | 721  | CTGCTGGCAGAGGACTGGCCATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTTCATACAG | 780  |
|    |      |   |      |
| Db | 721  | CTGCTGGCAGAGGACTGGCCATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTTCATACAG | 780  |
| Qy | 781  | AAAGCCTCCGTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATATCGA  | 840  |
|    |      |   |      |
| Db | 781  | AAAGCCTCCGTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATATCGA  | 840  |
| Qy | 841  | GCTGTTGCTTCTTGGAGTAGAATTAAAGGAATTGGGGTTCCAAAATGGACAGCAGTAGAA  | 900  |
|    |      |   |      |
| Db | 841  | GCTGTTGCTTCTTGGAGTAGAATTAAAGGAATTGGGGTTCCAAAATGGACAGCAGTAGAA  | 900  |
| Qy | 901  | ATTGTTTTGATTTGGGTGGTCTCTGTGGTTCTGGCTGTCCCTGAAGCCATAGGTTTTGAT  | 960  |
|    |      |   |      |
| Db | 901  | ATTGTTTTGATTTGGGTGGTCTCTGTGGTTCTGGCTGTCCCTGAAGCCATAGGTTTTGAT  | 960  |
| Qy | 961  | ATAATTACGATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTTCAG  | 1020 |
|    |      |   |      |
| Db | 961  | ATAATTACGATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTTCAG  | 1020 |
| Qy | 1021 | AAGACAGCTTTCATGCAGTTTACAAGACAGCAAAGATTGGTGGCTGTTCACTTTCTAT    | 1080 |
|    |      |   |      |
| Db | 1021 | AAGACAGCTTTCATGCAGTTTACAAGACAGCAAAGATTGGTGGCTGTTCACTTTCTAT    | 1080 |
| Qy | 1081 | TTCTGCTTGCCATTGGCCATCACTGCATTTTTTTATACACTAATGACCTGTGAAATGTTG  | 1140 |
|    |      |   |      |
| Db | 1081 | TTCTGCTTGCCATTGGCCATCACTGCATTTTTTTATACACTAATGACCTGTGAAATGTTG  | 1140 |
| Qy | 1141 | AGAAAGAAAAGTGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAAGTG  | 1200 |
|    |      |   |      |
| Db | 1141 | AGAAAGAAAAGTGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAAGTG  | 1200 |
| Qy | 1201 | GCCAAAACCGTCTTTTGCCTGGTCCTTGTCTTTGCCCTCTGCTGGCTTCCCCTTCACCTC  | 1260 |
|    |      |   |      |
| Db | 1201 | GCCAAAACCGTCTTTTGCCTGGTCCTTGTCTTTGCCCTCTGCTGGCTTCCCCTTCACCTC  | 1260 |
| Qy | 1261 | AGCAGGATTCTGAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGAACTTTTG  | 1320 |
|    |      |   |      |
| Db | 1261 | AGCAGGATTCTGAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGAACTTTTG  | 1320 |
| Qy | 1321 | AGCTTTCTGTTGGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCCTGCATT  | 1380 |
|    |      |   |      |
| Db | 1321 | AGCTTTCTGTTGGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCCTGCATT  | 1380 |
| Qy | 1381 | AACCCAATTGCTCTGTATTTGGTGAGCAAAAGATTCAAAAAGTCTTTAAGTCATGCTTA   | 1440 |
|    |      |   |      |
| Db | 1381 | AACCCAATTGCTCTGTATTTGGTGAGCAAAAGATTCAAAAAGTCTTTAAGTCATGCTTA   | 1440 |
| Qy | 1441 | TGCTGCTGGTGCCAGTCATTTGAAGAAAAACAGTCCTTGGAGGAAAAGCAGTCGTGCTTA  | 1500 |
|    |      |   |      |
| Db | 1441 | TGCTGCTGGTGCCAGTCATTTGAAGAAAAACAGTCCTTGGAGGAAAAGCAGTCGTGCTTA  | 1500 |
| Qy | 1501 | AAGTTCAAAGCTAATGATCACGGATATGACAACTCCGTTCCAGTAATAAATACAGCTCA   | 1560 |
|    |      |   |      |
| Db | 1501 | AAGTTCAAAGCTAATGATCACGGATATGACAACTCCGTTCCAGTAATAAATACAGCTCA   | 1560 |
| Qy | 1561 | TCTTGAAAGAAGAACTATTCACCTGTATTTTCTTTTATATTGGACCGAAGTCATTAA     | 1620 |

|    |      |   |      |
|----|------|---|------|
| Db | 1561 | TCTTGAAAGAAGAACTATTCACTGTATTTTCTTTATATTGGACCGAAGTCATTAA       | 1620 |
| Qy | 1621 | AACAAAATGAAACATTTGCCAAAACAAAACAAAAAACTATGTATTTGCACAGCACACTAT  | 1680 |
| Db | 1621 | AACAAAATGAAACATTTGCCAAAACAAAACAAAAAACTATGTATTTGCACAGCACACTAT  | 1680 |
| Qy | 1681 | TAAAATATTAAGTGTAATTATTTTAACACTCACAGCTACATATGACATTTTATGAGCTGT  | 1740 |
| Db | 1681 | TAAAATATTAAGTGTAATTATTTTAACACTCACAGCTACATATGACATTTTATGAGCTGT  | 1740 |
| Qy | 1741 | TTACGGCATGGAAAGAAAATCAGTGGGAATTAAGAAAGCCTCGTCGTGAAAGCACTTAAT  | 1800 |
| Db | 1741 | TTACGGCATGGAAAGAAAATCAGTGGGAATTAAGAAAGCCTCGTCGTGAAAGCACTTAAT  | 1800 |
| Qy | 1801 | TTTTTACAGTTAGCACTTCAACATAGCTCTTAACAACCTTCCAGGATATTCACACAACACT | 1860 |
| Db | 1801 | TTTTTACAGTTAGCACTTCAACATAGCTCTTAACAACCTTCCAGGATATTCACACAACACT | 1860 |
| Qy | 1861 | TAGGCTTAAAAATGAGCTCACTCAGAATTTCTATTCTTTCTAAAAAGAGATTTATTTT    | 1920 |
| Db | 1861 | TAGGCTTAAAAATGAGCTCACTCAGAATTTCTATTCTTTCTAAAAAGAGATTTATTTT    | 1920 |
| Qy | 1921 | AATCAATGGGACTCTGATATAAAGGAAGAATAAGTCACTGTAAAACAGAACTTTTAAATG  | 1980 |
| Db | 1921 | AATCAATGGGACTCTGATATAAAGGAAGAATAAGTCACTGTAAAACAGAACTTTTAAATG  | 1980 |
| Qy | 1981 | AAGCTTAAATTACTCAATTTAAATTTTAAATCCTTTAAACAACCTTTTCAATTAATAT    | 2040 |
| Db | 1981 | AAGCTTAAATTACTCAATTTAAATTTTAAATCCTTTAAACAACCTTTTCAATTAATAT    | 2040 |
| Qy | 2041 | TATCACACTATTATCAGATTGTAATTAGATGCAAATGAGAGAGCAGTTTAGTTGTTGCAT  | 2100 |
| Db | 2041 | TATCACACTATTATCAGATTGTAATTAGATGCAAATGAGAGAGCAGTTTAGTTGTTGCAT  | 2100 |
| Qy | 2101 | TTTTCGGACACTGGAAACATTTAAATGATCAGGAGGGAGTAACAGAAAGAGCAAGGCTGT  | 2160 |
| Db | 2101 | TTTTCGGACACTGGAAACATTTAAATGATCAGGAGGGAGTAACAGAAAGAGCAAGGCTGT  | 2160 |
| Qy | 2161 | TTTTGAAAATCATTACACTTTTACTAGAAGCCCAAACCTCAGCATTCTGCAATATGTAAC  | 2220 |
| Db | 2161 | TTTTGAAAATCATTACACTTTTACTAGAAGCCCAAACCTCAGCATTCTGCAATATGTAAC  | 2220 |
| Qy | 2221 | CAACATGTCACAAACAAGCAGCATGTAACAGACTGGCACATGTGCCAGCTGAATTTAAAA  | 2280 |
| Db | 2221 | CAACATGTCACAAACAAGCAGCATGTAACAGACTGGCACATGTGCCAGCTGAATTTAAAA  | 2280 |
| Qy | 2281 | TATAATACTTTTAAAAAGAAAATTATTACATCCTTTACATTCAAGTAAAGATCAAACCTCA | 2340 |
| Db | 2281 | TATAATACTTTTAAAAAGAAAATTATTACATCCTTTACATTCAAGTAAAGATCAAACCTCA | 2340 |
| Qy | 2341 | CAAAGAGAAAATAGAATGTTTGAAAGGCTATCCCAAAGACTTTTTTGAATCTGTCAATTCA | 2400 |
| Db | 2341 | CAAAGAGAAAATAGAATGTTTGAAAGGCTATCCCAAAGACTTTTTTGAATCTGTCAATTCA | 2400 |
| Qy | 2401 | CATACCCTGTGAAGACAATACTATCTACAATTTTTCAGGATTATTAAAAATCTTCTTTTT  | 2460 |

|    |      |  |      |
|----|------|--|------|
| Db | 2401 | CATACCCTGTGAAGACAATACTATCTACAATTTTTTCAGGATTATTAAAATCTTCTTTTT   | 2460 |
| Qy | 2461 | TCACTATCGTAGCTTAAACTCTGTTTGGTTTTGTCATCTGTAAATACTTACCTACATACA   | 2520 |
|    |      |  |      |
| Db | 2461 | TCACTATCGTAGCTTAAACTCTGTTTGGTTTTGTCATCTGTAAATACTTACCTACATACA   | 2520 |
| Qy | 2521 | CTGCATGTAGATGATTAAATGAGGGCAGGCCCTGTGCTCATAGCTTTACGATGGAGAGAT   | 2580 |
|    |      |  |      |
| Db | 2521 | CTGCATGTAGATGATTAAATGAGGGCAGGCCCTGTGCTCATAGCTTTACGATGGAGAGAT   | 2580 |
| Qy | 2581 | GCCAGTGACCTCATAATAAAGACTGTGAACTGCCTGGTGCAGTGTCCACATGACAAAGGG   | 2640 |
|    |      |  |      |
| Db | 2581 | GCCAGTGACCTCATAATAAAGACTGTGAACTGCCTGGTGCAGTGTCCACATGACAAAGGG   | 2640 |
| Qy | 2641 | GCAGGTAGCACCTCTCTCACCCTGCTGTGGTTAAAATGGTTTCTAGCATATGTATAAT     | 2700 |
|    |      |  |      |
| Db | 2641 | GCAGGTAGCACCTCTCTCACCCTGCTGTGGTTAAAATGGTTTCTAGCATATGTATAAT     | 2700 |
| Qy | 2701 | GCTATAGTTAAAATACTATTTTTTCAAAATCATAACAGATTAGTACATTTAACAGCTACCTG | 2760 |
|    |      |  |      |
| Db | 2701 | GCTATAGTTAAAATACTATTTTTTCAAAATCATAACAGATTAGTACATTTAACAGCTACCTG | 2760 |
| Qy | 2761 | TAAAGCTTATTACTAATTTTTGTATTATTTTTGTAAATAGCCAATAGAAAAGTTTGCTTG   | 2820 |
|    |      |  |      |
| Db | 2761 | TAAAGCTTATTACTAATTTTTGTATTATTTTTGTAAATAGCCAATAGAAAAGTTTGCTTG   | 2820 |
| Qy | 2821 | ACATGGTGCTTTTCTTTCATCTAGAGGCAAACTGCTTTTTGAGACCGTAAGAACCTCTT    | 2880 |
|    |      |  |      |
| Db | 2821 | ACATGGTGCTTTTCTTTCATCTAGAGGCAAACTGCTTTTTGAGACCGTAAGAACCTCTT    | 2880 |
| Qy | 2881 | AGCTTTGTGCGTTCCTGCCTAATTTTTTATATCTTCTAAGCAAAGTGCCTTAGGATAGCTT  | 2940 |
|    |      |  |      |
| Db | 2881 | AGCTTTGTGCGTTCCTGCCTAATTTTTTATATCTTCTAAGCAAAGTGCCTTAGGATAGCTT  | 2940 |
| Qy | 2941 | GGGATGAGATGTGTGTGAAAGTATGTACAAGAGAAAACGGAAGAGAGAGGAAATGAGGTG   | 3000 |
|    |      |  |      |
| Db | 2941 | GGGATGAGATGTGTGTGAAAGTATGTACAAGAGAAAACGGAAGAGAGAGGAAATGAGGTG   | 3000 |
| Qy | 3001 | GGGTTGGAGGAAACCCATGGGGACAGATTCCCATTCTTAGCCTAACGTTTCGTCATTGCCT  | 3060 |
|    |      |  |      |
| Db | 3001 | GGGTTGGAGGAAACCCATGGGGACAGATTCCCATTCTTAGCCTAACGTTTCGTCATTGCCT  | 3060 |
| Qy | 3061 | CGTCACATCAATGCAAAGGTCCTGATTTTGTTCAGCAAAACACAGTGCAATGTTCTCA     | 3120 |
|    |      |  |      |
| Db | 3061 | CGTCACATCAATGCAAAGGTCCTGATTTTGTTCAGCAAAACACAGTGCAATGTTCTCA     | 3120 |
| Qy | 3121 | GAGTGACTTTTCGAAATAAATTGGGCCCAAGAGCTTTAACTCGGTCTTAAAATATGCCCAA  | 3180 |
|    |      |  |      |
| Db | 3121 | GAGTGACTTTTCGAAATAAATTGGGCCCAAGAGCTTTAACTCGGTCTTAAAATATGCCCAA  | 3180 |
| Qy | 3181 | ATTTTTACTTTGTTTTTCTTTTAATAGGCTGGGCCACATGTTGGAAATAAGCTAGTAATG   | 3240 |
|    |      |  |      |
| Db | 3181 | ATTTTTACTTTGTTTTTCTTTTAATAGGCTGGGCCACATGTTGGAAATAAGCTAGTAATG   | 3240 |
| Qy | 3241 | TTGTTTTCTGTCAATATTGAATGTGATGGTACAGTAAACCAAAACCAACAATGTGGCCA    | 3300 |
|    |      |  |      |
| Db | 3241 | TTGTTTTCTGTCAATATTGAATGTGATGGTACAGTAAACCAAAACCAACAATGTGGCCA    | 3300 |



|    |      |  |      |
|----|------|--|------|
| Qy | 3301 | GAAAGAAAGAGCAATAATAATTAATTCACACACCATATGGATTCTATTTATAAATCACCC   | 3360 |
|    |      |  |      |
| Db | 3301 | GAAAGAAAGAGCAATAATAATTAATTCACACACCATATGGATTCTATTTATAAATCACCC   | 3360 |
| Qy | 3361 | ACAAACTTGTTCTTTAATTTTCATCCCAATCACTTTTTTCAGAGGCCTGTTATCATAGAAGT | 3420 |
|    |      |  |      |
| Db | 3361 | ACAAACTTGTTCTTTAATTTTCATCCCAATCACTTTTTTCAGAGGCCTGTTATCATAGAAGT | 3420 |
| Qy | 3421 | CATTTTAGACTCTCAATTTTAAATTAATTTTGAATCACTAATATTTTCACAGTTTATTAA   | 3480 |
|    |      |  |      |
| Db | 3421 | CATTTTAGACTCTCAATTTTAAATTAATTTTGAATCACTAATATTTTCACAGTTTATTAA   | 3480 |
| Qy | 3481 | TATATTTAATTTCTATTTAAATTTTAGATTATTTTATTACCATGTACTGAATTTTACA     | 3540 |
|    |      |  |      |
| Db | 3481 | TATATTTAATTTCTATTTAAATTTTAGATTATTTTATTACCATGTACTGAATTTTACA     | 3540 |
| Qy | 3541 | TCCTGATACCCCTTTCCTTCTCCATGTCAGTATCATGTTCTCTAATTATCTTGCCAAATTT  | 3600 |
|    |      |  |      |
| Db | 3541 | TCCTGATACCCCTTTCCTTCTCCATGTCAGTATCATGTTCTCTAATTATCTTGCCAAATTT  | 3600 |
| Qy | 3601 | TGAAACTACACACAAAAAGCATACTTGCATTATTTATAATAAAATTGCATTCACTGGCTT   | 3660 |
|    |      |  |      |
| Db | 3601 | TGAAACTACACACAAAAAGCATACTTGCATTATTTATAATAAAATTGCATTCACTGGCTT   | 3660 |
| Qy | 3661 | TTTAAAAAAAATGTTTGATTCAAACTTTAACATACTGATAAGTAAGAAACAATTATAAT    | 3720 |
|    |      |  |      |
| Db | 3661 | TTTAAAAAAAATGTTTGATTCAAACTTTAACATACTGATAAGTAAGAAACAATTATAAT    | 3720 |
| Qy | 3721 | TTCTTTACATACTCAAACCAAGATAGAAAAAGGTGCTATCGTTCAACTTCAAACATGT     | 3780 |
|    |      |  |      |
| Db | 3721 | TTCTTTACATACTCAAACCAAGATAGAAAAAGGTGCTATCGTTCAACTTCAAACATGT     | 3780 |
| Qy | 3781 | TTCCTAGTATTAAGGACTTTAATATAGCAACAGACAAAATTATTGTTAACATGGATGTTA   | 3840 |
|    |      |  |      |
| Db | 3781 | TTCCTAGTATTAAGGACTTTAATATAGCAACAGACAAAATTATTGTTAACATGGATGTTA   | 3840 |
| Qy | 3841 | CAGCTCAAAAGATTTATAAAAGATTTTAACTATTTTCTCCCTTATTATCCACTGCTAAT    | 3900 |
|    |      |  |      |
| Db | 3841 | CAGCTCAAAAGATTTATAAAAGATTTTAACTATTTTCTCCCTTATTATCCACTGCTAAT    | 3900 |
| Qy | 3901 | GTGGATGTATGTTCAAACACCTTTTAGTATTGATAGCTTACATATGGCCAAAGGAATACA   | 3960 |
|    |      |  |      |
| Db | 3901 | GTGGATGTATGTTCAAACACCTTTTAGTATTGATAGCTTACATATGGCCAAAGGAATACA   | 3960 |
| Qy | 3961 | GTTTATAGCAAAACATGGGTATGCTGTAGCTAACTTTATAAAAGTGTAATATAACAATGT   | 4020 |
|    |      |  |      |
| Db | 3961 | GTTTATAGCAAAACATGGGTATGCTGTAGCTAACTTTATAAAAGTGTAATATAACAATGT   | 4020 |
| Qy | 4021 | AAAAAATTATATATCTGGGAGGATTTTTTGGTTGCCTAAAGTGGCTATAGTTACTGATTT   | 4080 |
|    |      |  |      |
| Db | 4021 | AAAAAATTATATATCTGGGAGGATTTTTTGGTTGCCTAAAGTGGCTATAGTTACTGATTT   | 4080 |
| Qy | 4081 | TTTATTATGTAAGCAAAACCAATAAAAAATTTAAGTTTTTTTAACTACCTTATTTTTC     | 4140 |
|    |      |  |      |
| Db | 4081 | TTTATTATGTAAGCAAAACCAATAAAAAATTTAAGTTTTTTTAACTACCTTATTTTTC     | 4140 |

Qy 4141 ACTGTACAGACACTAATTCATTAAATACTAATTGATTGTTTAAAAGAAATATAAATGTGA 4200  
 |||  
 Db 4141 ACTGTACAGACACTAATTCATTAAATACTAATTGATTGTTTAAAAGAAATATAAATGTGA 4200  
 Qy 4201 CAAGTGGACATTATTTATGTTAAATATACAATTATCAAGCAAGTATGAAGTTATTCAATT 4260  
 |||  
 Db 4201 CAAGTGGACATTATTTATGTTAAATATACAATTATCAAGCAAGTATGAAGTTATTCAATT 4260  
 Qy 4261 AAAATGCCACATTTCTGGTCTCTGGG 4286  
 |||  
 Db 4261 AAAATGCCACATTTCTGGTCTCTGGG 4286

RESULT 10

AAF21288

ID AAF21288 standard; DNA; 13611 BP.

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AC AAF21288;

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DT 14-MAR-2001 (first entry)

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DE Human low adenosine antisense oligonucleotide related sequence #2855.

XX

KW Low adenosine antisense oligonucleotide; phosphorothioate; allergy;

KW human; airway disorder; bronchoconstriction; lung inflammation;

KW surfactant depletion; respiratory; bronchodilator; antiinflammatory;

KW immunosuppressive; antiasthmatic; analgesic; hypotensive; cytostatic;

KW respiratory obstruction; pulmonary obstruction; impeded respiration;

KW surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;

KW respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;

KW pulmonary hypertension; emphysema; pulmonary transplantation rejection;

KW chronic obstructive pulmonary disease; pulmonary infection; bronchitis;

KW cancer; ss.

XX

OS Homo sapiens.

XX

PN WO200062736-A2.

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PD 26-OCT-2000.

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PF 24-MAR-2000; 2000WO-US008020.

XX

PR 06-APR-1999; 99US-0127958P.

XX

PA (UYEC-) UNIV EAST CAROLINA.

PA (NYCE/) NYCE J W.

XX

PI Nyce JW;

XX

DR WPI; 2000-679539/66.

XX

PT Low adenosine (A) content antisense oligonucleotides which do not trigger

PT adenosine receptors during metabolism, useful e.g. for treating cancers

PT and respiratory obstructions.

XX

PS Disclosure; Page 1277-1280; 1592pp; English.

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CC The present invention describes low adenosine (A) content antisense  
 CC oligonucleotides and compositions (I) comprising them. In the antisense  
 CC oligonucleotides the A is replaced by a 'Universal' or alternative base.  
 CC (I) can have respiratory, bronchodilator, antiinflammatory, analgesic,  
 CC immunosuppressive, antiasthmatic, hypotensive and cytostatic activities.  
 CC The antisense oligonucleotides and (I) can be used to down-regulate the  
 CC expression and or activity of target polypeptides associated with  
 CC lung/respiratory disorders and malignancies, such as stimulating and  
 CC activating peptide factors and transmitters, transcription factors,  
 CC immunoglobulins and antibodies, antibody receptors, cytokines and  
 CC chemokines, endogenously produced specific and non-specific enzymes,  
 CC binding proteins, adhesion molecules and their receptors, cytokine and  
 CC chemokine receptors, adenosine receptors, bradykinin receptors, central  
 CC nervous system (CNS) and peripheral nervous and non-nervous system  
 CC receptors, CNS and peripheral nervous and non-nervous system peptide  
 CC transmitters, defensins, growth factors, vasoactive peptides and  
 CC receptors, binding proteins and malignancy associated proteins. The  
 CC antisense oligonucleotides may be used in this way to treat disorders  
 CC including respiratory obstruction (especially pulmonary obstruction  
 CC and/or bronchoconstriction) and/or lung inflammation, allergy(ies) and/or  
 CC surfactant hypoproduction which are associated with a disease or  
 CC condition selected from pulmonary vasoconstriction, inflammation,  
 CC allergies, asthma, impeded respiration, respiratory distress syndrome  
 CC (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary  
 CC hypertension, emphysema, chronic obstructive pulmonary disease (COPD),  
 CC pulmonary transplantation rejection, pulmonary infections, bronchitis,  
 CC and/or cancer. AAF18434 to AAF21543 represent human polynucleotide  
 CC fragments and antisense oligonucleotides used in the exemplification of  
 CC the present invention

XX

SQ Sequence 13611 BP; 3676 A; 3007 C; 3056 G; 3868 T; 0 U; 4 Other;

Query Match 99.6%; Score 4284.4; DB 3; Length 13611;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 4285; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

|    |      |   |      |
|----|------|---|------|
| Qy | 1    | GAGACATTCCGGTGGGGGACTCTGGCCAGCCCCGAGCAACGTGGATCCTGAGAGCACTCCC | 60   |
|    |      |   |      |
| Db | 1873 | GAGACATTCCGGTGGGGGACTCTGGCCAGCCCCGAGCAACGTGGATCCTGAGAGCACTCCC | 1932 |
| Qy | 61   | AGGTAGGCATTTGCCCCGGTGGGACGCCTTGCCAGAGCAGTGTGTGGCAGGCCCCCGTGG  | 120  |
|    |      |   |      |
| Db | 1933 | AGGTAGGCATTTGCCCCGGTGGGACGCCTTGCCAGAGCAGTGTGTGGCAGGCCCCCGTGG  | 1992 |
| Qy | 121  | AGGATCAACACAGTGGCTGAACACTGGGAAGGAAGTGGTACTTGGAGTCTGGACATCTGA  | 180  |
|    |      |   |      |
| Db | 1993 | AGGATCAACACAGTGGCTGAACACTGGGAAGGAAGTGGTACTTGGAGTCTGGACATCTGA  | 2052 |
| Qy | 181  | AACTTGGCTCTGAAACTGCGGAGCGGCCACCGGACGCCTTCTGGAGCAGGTAGCAGCATG  | 240  |
|    |      |   |      |
| Db | 2053 | AACTTGGCTCTGAAACTGCGGAGCGGCCACCGGACGCCTTCTGGAGCAGGTAGCAGCATG  | 2112 |
| Qy | 241  | CAGCCGCCTCCAAGTCTGTGCGGACGCGCCCTGGTTGCGCTGGTTCTTGCCTGCGGCCTG  | 300  |
|    |      |   |      |
| Db | 2113 | CAGCCGCCTCCAAGTCTGTGCGGACGCGCCCTGGTTGCGCTGGTTCTTGCCTGCGGCCTG  | 2172 |
| Qy | 301  | TCGCGGATCTGGGGAGAGGAGAGAGGCTTCCCGCCTGACAGGGCCACTCCGCTTTTGCAA  | 360  |

|    |      |  |      |
|----|------|--|------|
| Db | 2173 | TCGCGGATCTGGGGAGAGGAGAGAGGCTTCCCGCCTGACAGGGCCACTCCGCTTTTGCAA   | 2232 |
| Qy | 361  | ACCGCAGAGATAATGACGCCACCCACTAAGACCTTATGGCCCAAGGGTTCCAACGCCAGT   | 420  |
| Db | 2233 | ACCGCAGAGATAATGACGCCACCCACTAAGACCTTATGGCCCAAGGGTTCCAACGCCAGT   | 2292 |
| Qy | 421  | CTGGCGCGGTCGTTGGCACCTGCGGAGGTGCCTAAAGGAGACAGGACGGCAGGATCTCCG   | 480  |
| Db | 2293 | CTGGCGCGGTCGTTGGCACCTGCGGAGGTGCCTAAAGGAGACAGGACGGCAGGATCTCCG   | 2352 |
| Qy | 481  | CCACGCACCATCTCCCCCTCCCCCGTGCCAAGGACCCATCGAGATCAAGGAGACTTTCAA   | 540  |
| Db | 2353 | CCACGCACCATCTCCCCCTCCCCCGTGCCAAGGACCCATCGAGATCAAGGAGACTTTCAA   | 2412 |
| Qy | 541  | TACATCAACACGGTTGTGTCCTGCCTTGTGTTCGTGCTGGGGATCATCGGGAACTCCACA   | 600  |
| Db | 2413 | TACATCAACACGGTTGTGTCCTGCCTTGTGTTCGTGCTGGGGATCATCGGGAACTCCACA   | 2472 |
| Qy | 601  | CTTCTGAGAATTATCTACAAGAACAAGTGCATGCGAAACGGTCCCAATATCTTGATCGCC   | 660  |
| Db | 2473 | CTTCTGAGAATTATCTACAAGAACAAGTGCATGCGAAACGGTCCCAATATCTTGATCGCC   | 2532 |
| Qy | 661  | AGCTTGGCTCTGGGAGACCTGCTGCACATCGTCATTGACATCCCTATCAATGTCTACAAG   | 720  |
| Db | 2533 | AGCTTGGCTCTGGGAGACCTGCTGCACATCGTCATTGACATCCCTATCAATGTCTACAAG   | 2592 |
| Qy | 721  | CTGCTGGCAGAGGACTGGCCATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTCATACAG   | 780  |
| Db | 2593 | CTGCTGGCAGAGGACTGGCCATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTCATACAG   | 2652 |
| Qy | 781  | AAAGCCTCCGTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATATCGA   | 840  |
| Db | 2653 | AAAGCCTCCGTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATATCGA   | 2712 |
| Qy | 841  | GCTGTTGCTTCTTGGAGTAGAATTAAAGGAATTGGGGTTCCAAAATGGACAGCAGTAGAA   | 900  |
| Db | 2713 | GCTGTTGCTTCTTGGAGTAGAATTAAAGGAATTGGGGTTCCAAAATGGACAGCAGTAGAA   | 2772 |
| Qy | 901  | ATTGTTTTGATTTGGGTGGTCTCTGTGGTTCTGGCTGTCCCTGAAGCCATAGGTTTTGAT   | 960  |
| Db | 2773 | ATTGTTTTGATTTGGGTGGTCTCTGTGGTTCTGGCTGTCCCTGAAGCCATAGGTTTTGAT   | 2832 |
| Qy | 961  | ATAATTACGATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTTTCA   | 1020 |
| Db | 2833 | ATAATTACGATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTTTCA   | 2892 |
| Qy | 1021 | AAGACAGCTTTCATGCAGTTTTTACAAGACAGCAAAAGATTGGTGGCTGTTTCAGTTTCTAT | 1080 |
| Db | 2893 | AAGACAGCTTTCATGCAGTTTTTACAAGACAGCAAAAGATTGGTGGCTGTTTCAGTTTCTAT | 2952 |
| Qy | 1081 | TTCTGCTTGCCATTGGCCATCACTGCATTTTTTTATACACTAATGACCTGTGAAATGTTG   | 1140 |
| Db | 2953 | TTCTGCTTGCCATTGGCCATCACTGCATTTTTTTATACACTAATGACCTGTGAAATGTTG   | 3012 |
| Qy | 1141 | AGAAAAGAAAAGTGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAAGTG  | 1200 |

|    |      |   |      |
|----|------|---|------|
| Db | 3013 | AGAAAAGAAAAGTGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAAGTG | 3072 |
| Qy | 1201 | GCCAAAACCGTCTTTTGCCTGGTCCTTGTCTTTGCCCTCTGCTGGCTTCCCCCTTCACCTC | 1260 |
|    |      |   |      |
| Db | 3073 | GCCAAAACCGTCTTTTGCCTGGTCCTTGTCTTTGCCCTCTGCTGGCTTCCCCCTTCACCTC | 3132 |
| Qy | 1261 | AGCAGGATTCTGAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGAACTTTTG  | 1320 |
|    |      |   |      |
| Db | 3133 | AGCAGGATTCTGAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGAACTTTTG  | 3192 |
| Qy | 1321 | AGCTTTCTGTTGGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCCTGCATT  | 1380 |
|    |      |   |      |
| Db | 3193 | AGCTTTCTGTTGGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCCTGCATT  | 3252 |
| Qy | 1381 | AACCCAATTGCTCTGTATTTGGTGAGCAAAAGATTCAAAAAGTCTTTAAGTCATGCTTA   | 1440 |
|    |      |   |      |
| Db | 3253 | AACCCAATTGCTCTGTATTTGGTGAGCAAAAGATTCAAAAAGTCTTTAAGTCATGCTTA   | 3312 |
| Qy | 1441 | TGCTGCTGGTGCCAGTCATTTGAAGAAAAACAGTCCTTGGAGGAAAAGCAGTCGTGCTTA  | 1500 |
|    |      |   |      |
| Db | 3313 | TGCTGCTGGTGCCAGTCATTTGAAGAAAAACAGTCCTTGGAGGAAAAGCAGTCGTGCTTA  | 3372 |
| Qy | 1501 | AAGTTCAAAGCTAATGATCACGGATATGACAACCTCCGTTCCAGTAATAAATACAGCTCA  | 1560 |
|    |      |   |      |
| Db | 3373 | AAGTTCAAAGCTAATGATCACGGATATGACAACCTCCGTTCCAGTAATAAATACAGCTCA  | 3432 |
| Qy | 1561 | TCTTGAAAGAAGAACTATTCAGTGTATTTTCAATTTCTTTATATTGGACCGAAGTCATTAA | 1620 |
|    |      |   |      |
| Db | 3433 | TCTTGAAAGAAGAACTATTCAGTGTATTTTCAATTTCTTTATATTGGACCGAAGTCATTAA | 3492 |
| Qy | 1621 | AACAAAATGAAACATTTGCCAAAACAAAACAAAAACTATGTATTTGCACAGCACACTAT   | 1680 |
|    |      |   |      |
| Db | 3493 | AACAAAATGAAACATTTGCCAAAACAAAACAAAAACTATGTATTTGCACAGCACACTAT   | 3552 |
| Qy | 1681 | TAAAATATTAAGTGTAATTATTTTAACTACAGCTACATATGACATTTTATGAGCTGT     | 1740 |
|    |      |   |      |
| Db | 3553 | TAAAATATTAAGTGTAATTATTTTAACTACAGCTACATATGACATTTTATGAGCTGT     | 3612 |
| Qy | 1741 | TTACGGCATGGAAAGAAAATCAGTGGGAATTAAGAAAGCCTCGTCGTGAAAGCACTTAAT  | 1800 |
|    |      |   |      |
| Db | 3613 | TTACGGCATGGAAAGAAAATCAGTGGGAATTAAGAAAGCCTCGTCGTGAAAGCACTTAAT  | 3672 |
| Qy | 1801 | TTTTTACAGTTAGCACTTCAACATAGCTCTTAACAACCTCCAGGATATTCACACAACACT  | 1860 |
|    |      |   |      |
| Db | 3673 | TTTTTACAGTTAGCACTTCAACATAGCTCTTAACAACCTCCAGGATATTCACACAACACT  | 3732 |
| Qy | 1861 | TAGGCTTAAAAATGAGCTCACTCAGAATTTCTATTCTTTCTAAAAAGAGATTTATTTTAA  | 1920 |
|    |      |   |      |
| Db | 3733 | TAGGCTTAAAAATGAGCTCACTCAGAATTTCTATTCTTTCTAAAAAGAGATTTATTTTAA  | 3792 |
| Qy | 1921 | AATCAATGGGACTCTGATATAAAGGAAGAATAAGTCACTGTAAAACAGAACTTTTAAATG  | 1980 |
|    |      |   |      |
| Db | 3793 | AATCAATGGGACTCTGATATAAAGGAAGAATAAGTCACTGTAAAACAGAACTTTTAAATG  | 3852 |
| Qy | 1981 | AAGCTTAAATTACTCAATTTAAATTTTAAATCCTTTAAACAACCTTTTCAATTAATAT    | 2040 |
|    |      |   |      |
| Db | 3853 | AAGCTTAAATTACTCAATTTAAATTTTAAATCCTTTAAACAACCTTTTCAATTAATAT    | 3912 |

|    |      |   |      |
|----|------|---|------|
| Qy | 2041 | TATCACACTATTATCAGATTGTAATTAGATGCAAATGAGAGAGCAGTTTAGTTGTTGCAT  | 2100 |
|    |      |   |      |
| Db | 3913 | TATCACACTATTATCAGATTGTAATTAGATGCAAATGAGAGAGCAGTTTAGTTGTTGCAT  | 3972 |
| Qy | 2101 | TTTTCGGACACTGGAAACATTTAAATGATCAGGAGGGAGTAACAGAAAAGAGCAAGGCTGT | 2160 |
|    |      |   |      |
| Db | 3973 | TTTTCGGACACTGGAAACATTTAAATGATCAGGAGGGAGTAACAGAAAAGAGCAAGGCTGT | 4032 |
| Qy | 2161 | TTTTGAAAATCATTACACTTTCACTAGAAGCCCCAAACCTCAGCATTCTGCAATATGTAAC | 2220 |
|    |      |   |      |
| Db | 4033 | TTTTGAAAATCATTACACTTTCACTAGAAGCCCCAAACCTCAGCATTCTGCAATATGTAAC | 4092 |
| Qy | 2221 | CAACATGTCACAAACAAGCAGCATGTAACAGACTGGCACATGTGCCAGCTGAATTTAAAA  | 2280 |
|    |      |   |      |
| Db | 4093 | CAACATGTCACAAACAAGCAGCATGTAACAGACTGGCACATGTGCCAGCTGAATTTAAAA  | 4152 |
| Qy | 2281 | TATAATACTTTTAAAAAGAAAATTATTACATCCTTTACATTTCAGTTAAGATCAAACCTCA | 2340 |
|    |      |   |      |
| Db | 4153 | TATAATACTTTTAAAAAGAAAATTATTACATCCTTTACATTTCAGTTAAGATCAAACCTCA | 4212 |
| Qy | 2341 | CAAAGAGAAATAGAATGTTTGAAAGGCTATCCCAAAGACTTTTTTGAATCTGTCATTCA   | 2400 |
|    |      |   |      |
| Db | 4213 | CAAAGAGAAATAGAATGTTTGAAAGGCTATCCCAAAGACTTTTTTGAATCTGTCATTCA   | 4272 |
| Qy | 2401 | CATACCCTGTGAAGACAATACTATCTACAATTTTTTCAGGATTATTAAAATCTTCTTTTT  | 2460 |
|    |      |   |      |
| Db | 4273 | CATACCCTGTGAAGACAATACTATCTACAATTTTTTCAGGATTATTAAAATCTTCTTTTT  | 4332 |
| Qy | 2461 | TCACTATCGTAGCTTAAACTCTGTTTGGTTTTGTCATCTGTAAATACTTACCTACATACA  | 2520 |
|    |      |   |      |
| Db | 4333 | TCACTATCGTAGCTTAAACTCTGTTTGGTTTTGTCATCTGTAAATACTTACCTACATACA  | 4392 |
| Qy | 2521 | CTGCATGTAGATGATTAAATGAGGGCAGGCCCTGTGCTCATAGCTTTACGATGGAGAGAT  | 2580 |
|    |      |   |      |
| Db | 4393 | CTGCATGTAGATGATTAAATGAGGGCAGGCCCTGTGCTCATAGCTTTACGATGGAGAGAT  | 4452 |
| Qy | 2581 | GCCAGTGACCTCATAATAAAGACTGTGAACTGCCTGGTGCAGTGTCCACATGACAAAGGG  | 2640 |
|    |      |   |      |
| Db | 4453 | GCCAGTGACCTCATAATAAAGACTGTGAACTGCCTGGTGCAGTGTCCACATGACAAAGGG  | 4512 |
| Qy | 2641 | GCAGGTAGCACCCCTCTCTCACCCATGCTGTGGTTAAATGGTTTCTAGCATATGTATAAT  | 2700 |
|    |      |   |      |
| Db | 4513 | GCAGGTAGCACCCCTCTCTCACCCATGCTGTGGTTAAATGGTTTCTAGCATATGTATAAT  | 4572 |
| Qy | 2701 | GCTATAGTTAAAATACTATTTTTCAAATCATACAGATTAGTACATTTAACAGCTACCTG   | 2760 |
|    |      |   |      |
| Db | 4573 | GCTATAGTTAAAATACTATTTTTCAAATCATACAGATTAGTACATTTAACAGCTACCTG   | 4632 |
| Qy | 2761 | TAAAGCTTATTACTAATTTTTGTATTATTTTTGTAAATAGCCAATAGAAAAGTTTGCTTG  | 2820 |
|    |      |   |      |
| Db | 4633 | TAAAGCTTATTACTAATTTTTGTATTATTTTTGTAAATAGCCAATAGAAAAGTTTGCTTG  | 4692 |
| Qy | 2821 | ACATGGTGCTTTTCTTTCATCTAGAGGCCAAACTGCTTTTTGAGACCGTAAGAACCTCTT  | 2880 |
|    |      |   |      |
| Db | 4693 | ACATGGTGCTTTTCTTTCATCTAGAGGCCAAACTGCTTTTTGAGACCGTAAGAACCTCTT  | 4752 |

|    |      |  |      |
|----|------|--|------|
| Qy | 2881 | AGCTTTGTGCGTTCCTGCCTAATTTTTATATCTTCTAAGCAAAGTGCCTTAGGATAGCTT   | 2940 |
|    |      |  |      |
| Db | 4753 | AGCTTTGTGCGTTCCTGCCTAATTTTTATATCTTCTAAGCAAAGTGCCTTAGGATAGCTT   | 4812 |
| Qy | 2941 | GGGATGAGATGTGTGTGAAAGTATGTACAAGAGAAAACGGAAGAGAGAGGAAATGAGGTG   | 3000 |
|    |      |  |      |
| Db | 4813 | GGGATGAGATGTGTGTGAAAGTATGTACAAGAGAAAACGGAAGAGAGAGGAAATGAGGTG   | 4872 |
| Qy | 3001 | GGGTTGGAGGAAACCCATGGGGACAGATTCCCATTCTTAGCCTAACGTTTCGTCATTGCCT  | 3060 |
|    |      |  |      |
| Db | 4873 | GGGTTGGAGGAAACCCATGGGGACAGATTCCCATTCTTAGCCTAACGTTTCGTCATTGCCT  | 4932 |
| Qy | 3061 | CGTCACATCAATGCAAAAGGTCCTGATTTTGTTCAGCAAAACACAGTGCAATGTTCTCA    | 3120 |
|    |      |  |      |
| Db | 4933 | CGTCACATCAATGCAAAAGGTCCTGATTTTGTTCAGCAAAACACAGTGCAATGTTCTCA    | 4992 |
| Qy | 3121 | GAGTGACTTTCGAAATAAATTGGGCCCCAAGAGCTTTAACTCGGTCTTAAATATGCCCAA   | 3180 |
|    |      |  |      |
| Db | 4993 | GAGTGACTTTCGAAATAAATTGGGCCCCAAGAGCTTTAACTCGGTCTTAAATATGCCCAA   | 5052 |
| Qy | 3181 | ATTTTTACTTTGTTTTCTTTAATAGGCTGGGCCACATGTTGAAATAAGCTAGTAATG      | 3240 |
|    |      |  |      |
| Db | 5053 | ATTTTTACTTTGTTTTCTTTAATAGGCTGGGCCACATGTTGAAATAAGCTAGTAATG      | 5112 |
| Qy | 3241 | TTGTTTTCTGTCAATATTGAATGTGATGGTACAGTAAACCAAACCAACAATGTGGCCA     | 3300 |
|    |      |  |      |
| Db | 5113 | TTGTTTTCTGTCAATATTGAATGTGATGGTACAGTAAACCAAACCAACAATGTGGCCA     | 5172 |
| Qy | 3301 | GAAAGAAAGAGCAATAATAATTAATTCACACACCATATGGATTCTATTTATAAATCACCC   | 3360 |
|    |      |  |      |
| Db | 5173 | GAAAGAAAGAGCAATAATAATTAATTCACACACCATATGGATTCTATTTATAAATCACCC   | 5232 |
| Qy | 3361 | ACAAACTTGTTCTTTAATTTTCATCCCAATCACTTTTTTCAGAGGCCTGTTATCATAGAAGT | 3420 |
|    |      |  |      |
| Db | 5233 | ACAAACTTGTTCTTTAATTTTCATCCCAATCACTTTTTTCAGAGGCCTGTTATCATAGAAGT | 5292 |
| Qy | 3421 | CATTTTAGACTCTCAATTTTAAATTAATTTTGAATCACTAATATTTTCACAGTTTATTAA   | 3480 |
|    |      |  |      |
| Db | 5293 | CATTTTAGACTCTCAATTTTAAATTAATTTTGAATCACTAATATTTTCACAGTTTATTAA   | 5352 |
| Qy | 3481 | TATATTTAATTTCTATTTAAATTTTAGATTATTTTATTACCATGTACTGAATTTTACA     | 3540 |
|    |      |  |      |
| Db | 5353 | TATATTTAATTTCTATTTAAATTTTAGATTATTTTATTACCATGTACTGAATTTTACA     | 5412 |
| Qy | 3541 | TCCTGATACCCTTTCCTTCTCCATGTCAGTATCATGTTCTCTAATTATCTTGCCAAATTT   | 3600 |
|    |      |  |      |
| Db | 5413 | TCCTGATACCCTTTCCTTCTCCATGTCAGTATCATGTTCTCTAATTATCTTGCCAAATTT   | 5472 |
| Qy | 3601 | TGAAACTACACACAAAAAGCATACTTGCATTATTTATAATAAAATTGCATTTCAGTGGCTT  | 3660 |
|    |      |  |      |
| Db | 5473 | TGAAACTACACACAAAAAGCATACTTGCATTATTTATAATAAAATTGCATTTCAGTGGCTT  | 5532 |
| Qy | 3661 | TTTAAAAAAAATGTTTGATTCAAACTTTAACATACTGATAAGTAAGAAACAATTATAAT    | 3720 |
|    |      |  |      |
| Db | 5533 | TTTAAAAAAAATGTTTGATTCAAACTTTAACATACTGATAAGTAAGAAACAATTATAAT    | 5592 |
| Qy | 3721 | TTCTTTACATACTCAAAACCAAGATAGAAAAAGGTGCTATCGTTCAACTTCAAAACATGT   | 3780 |

|    |      |   |      |
|----|------|---|------|
| Db | 5593 | TTTACATACTCAAACCAAGATAGAAAAAGGTGCTATCGTTCAACTTCAAACATGT       | 5652 |
| Qy | 3781 | TTCTTAGTATTAAGGACTTTAATATAGCAACAGACAAAATTATTGTTAACATGGATGTTA  | 3840 |
| Db | 5653 | TTCTTAGTATTAAGGACTTTAATATAGCAACAGACAAAATTATTGTTAACATGGATGTTA  | 5712 |
| Qy | 3841 | CAGCTCAAAGATTTATAAAAGATTTTAACCTATTTTCTCCCTTATTATCCACTGCTAAT   | 3900 |
| Db | 5713 | CAGCTCAAAGATTTATAAAAGATTTTAACCTATTTTCTCCCTTATTATCCACTGCTAAT   | 5772 |
| Qy | 3901 | GTGGATGTATGTTCAAACACCTTTTAGTATTGATAGCTTACATATGGCCAAAGGAATACA  | 3960 |
| Db | 5773 | GTGGATGTATGTTCAAACACCTTTTAGTATTGATAGCTTACATATGGCCAAAGGAATACA  | 5832 |
| Qy | 3961 | GTTTATAGCAAACATGGGTATGCTGTAGCTAACTTTATAAAAGTGTAATATAACAATGT   | 4020 |
| Db | 5833 | GTTTATAGCAAACATGGGTATGCTGTAGCTAACTTTATAAAAGTGTAATATAACAATGT   | 5892 |
| Qy | 4021 | AAAAAATTATATATCTGGGAGGATTTTTTGGTTGCCTAAAGTGGCTATAGTTACTGATTT  | 4080 |
| Db | 5893 | AAAAAATTATATATCTGGGAGGATTTTTTGGTTGCCTAAAGTGGCTATAGTTACTGATTT  | 5952 |
| Qy | 4081 | TTTATTATGTAAGCAAACCAATAAAAAATTTAAGTTTTTTTAACAACCTACCTTATTTTTC | 4140 |
| Db | 5953 | TTTATTATGTAAGCAAACCAATAAAAAATTTAAGTTTTTTTAACAACCTACCTTATTTTTC | 6012 |
| Qy | 4141 | ACTGTACAGACACTAATTCATTAAATACTAATTGATTGTTTAAAAGAAATATAAATGTGA  | 4200 |
| Db | 6013 | ACTGTACAGACACTAATTCATTAAATACTAATTGATTGTTTAAAAGAAATATAAATGTGA  | 6072 |
| Qy | 4201 | CAAGTGGACATTATTTATGTTAAATATACAATTATCAAGCAAGTATGAAGTTATTCAATT  | 4260 |
| Db | 6073 | CAAGTGGACATTATTTATGTTAAATATACAATTATCAAGCAAGTATGAAGTTATTCAATT  | 6132 |
| Qy | 4261 | AAAATGCCACATTTCTGGTCTCTGGG                                    | 4286 |
| Db | 6133 | AAAATGCCACATTTCTGGTCTCTGGG                                    | 6158 |

RESULT 11

ABZ96982

ID ABZ96982 standard; DNA; 13611 BP.

XX

AC ABZ96982;

XX

DT 17-OCT-2003 (first entry)

XX

DE Human nucleic acid sequence.

XX

KW Human; antisense; lung dysfunction; nasal airway dysfunction;  
 KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;  
 KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;  
 KW antisense gene therapy; respiratory; lung; adenosine sensitivity;  
 KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;  
 KW lung inflammation; respiratory disease; ds.

XX





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|----|------|--|------|
| Db | 1933 | AGGTAGGCATTTGCCCCGGTGGGACGCCTTGCCAGAGCAGTGTGTGGCAGGCCCCCGTGG   | 1992 |
| Qy | 121  | AGGATCAACACAGTGGCTGAACACTGGGAAGGAACTGGTACTTGGAGTCTGGACATCTGA   | 180  |
| Db | 1993 | AGGATCAACACAGTGGCTGAACACTGGGAAGGAACTGGTACTTGGAGTCTGGACATCTGA   | 2052 |
| Qy | 181  | AACTTGGCTCTGAAACTGCGGAGCGGCCACCGACGCCTTCTGGAGCAGGTAGCAGCATG    | 240  |
| Db | 2053 | AACTTGGCTCTGAAACTGCGCAGCGGCCACCGACGCCTTCTGGAGCAGGTAGCAGCATG    | 2112 |
| Qy | 241  | CAGCCGCCTCCAAGTCTGTGCGGACGCGCCCTGGTTGCGCTGGTTCTTGCCTGCGGCCTG   | 300  |
| Db | 2113 | CAGCCGCCTCCAAGTCTGTGCGGACGCGCCCTGGTTGCGCTGGTTCTTGCCTGCGGCCTG   | 2172 |
| Qy | 301  | TCGCGGATCTGGGGAGAGGAGAGAGGCTTCCCGCCTGACAGGGCCACTCCGCTTTTGCAA   | 360  |
| Db | 2173 | TCGCGGATCTGGGGAGAGGAGAGAGGCTTCCCGCCTGACAGGGCCACTCCGCTTTTGCAA   | 2232 |
| Qy | 361  | ACCGCAGAGATAATGACGCCACCCACTAAGACCTTATGGCCCAAGGGTTCCAACGCCAGT   | 420  |
| Db | 2233 | ACCGCAGAGATAATGACGCCACCCACTAAGACCTTATGGCCCAAGGGTTCCAACGCCAGT   | 2292 |
| Qy | 421  | CTGGCGCGGTTCGTTGGCACCTGCGGAGGTGCCTAAAGGAGACAGGACGGCAGGATCTCCG  | 480  |
| Db | 2293 | CTGGCGCGGTTCGTTGGCACCTGCGGAGGTGCCTAAAGGAGACAGGACGGCAGGATCTCCG  | 2352 |
| Qy | 481  | CCACGCACCATCTCCCCTCCCCCGTGCCAAGGACCCATCGAGATCAAGGAGACTTTCAA    | 540  |
| Db | 2353 | CCACGCACCATCTCCCCTCCCCCGTGCCAAGGACCCATCGAGATCAAGGAGACTTTCAA    | 2412 |
| Qy | 541  | TACATCAACACGGTTGTGTCCTGCCTTGTGTTTCGTGCTGGGGATCATCGGGAACCTCCACA | 600  |
| Db | 2413 | TACATCAACACGGTTGTGTCCTGCCTTGTGTTTCGTGCTGGGGATCATCGGGAACCTCCACA | 2472 |
| Qy | 601  | CTTCTGAGAATTATCTACAAGAACAAGTGCATGCGAAACGGTCCCAATATCTTGATCGCC   | 660  |
| Db | 2473 | CTTCTGAGAATTATCTACAAGAACAAGTGCATGCGAAACGGTCCCAATATCTTGATCGCC   | 2532 |
| Qy | 661  | AGCTTGGCTCTGGGAGACCTGCTGCACATCGTCATTGACATCCCTATCAATGTCTACAAG   | 720  |
| Db | 2533 | AGCTTGGCTCTGGGAGACCTGCTGCACATCGTCATTGACATCCCTATCAATGTCTACAAG   | 2592 |
| Qy | 721  | CTGCTGGCAGAGGACTGGCCATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTCATACAG   | 780  |
| Db | 2593 | CTGCTGGCAGAGGACTGGCCATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTCATACAG   | 2652 |
| Qy | 781  | AAAGCCTCCGTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATATCGA   | 840  |
| Db | 2653 | AAAGCCTCCGTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATATCGA   | 2712 |
| Qy | 841  | GCTGTTGCTTCTTGGAGTAGAATTAAAGGAATTGGGGTTCCAAAATGGACAGCAGTAGAA   | 900  |
| Db | 2713 | GCTGTTGCTTCTTGGAGTAGAATTAAAGGAATTGGGGTTCCAAAATGGACAGCAGTAGAA   | 2772 |
| Qy | 901  | ATTGTTTTGATTGGGTGGTCTCTGTGGTTCTGGCTGTCCCTGAAGCCATAGGTTTTGAT    | 960  |
| Db | 2773 | ATTGTTTTGATTGGGTGGTCTCTGTGGTTCTGGCTGTCCCTGAAGCCATAGGTTTTGAT    | 2832 |

|    |      |  |      |
|----|------|--|------|
| Qy | 961  | ATAATTACGATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTTCAG   | 1020 |
|    |      |  |      |
| Db | 2833 | ATAATTACGATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTTCAG   | 2892 |
| Qy | 1021 | AAGACAGCTTTCATGCAGTTTACAAGACAGCAAAAGATTGGTGGCTGTTTCAGTTTCTAT   | 1080 |
|    |      |  |      |
| Db | 2893 | AAGACAGCTTTCATGCAGTTTACAAGACAGCAAAAGATTGGTGGCTGTTTCAGTTTCTAT   | 2952 |
| Qy | 1081 | TTCTGCTTGCCATTGGCCATCACTGCATTTTTTTATACACTAATGACCTGTGAAATGTTG   | 1140 |
|    |      |  |      |
| Db | 2953 | TTCTGCTTGCCATTGGCCATCACTGCATTTTTTTATACACTAATGACCTGTGAAATGTTG   | 3012 |
| Qy | 1141 | AGAAAGAAAAGTGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAAGTG   | 1200 |
|    |      |  |      |
| Db | 3013 | AGAAAGAAAAGTGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAAGTG   | 3072 |
| Qy | 1201 | GCCAAAACCGTCTTTTGCCTGGTCCTTGTCTTTGCCCTCTGCTGGCTTCCCCTTCACCTC   | 1260 |
|    |      |  |      |
| Db | 3073 | GCCAAAACCGTCTTTTGCCTGGTCCTTGTCTTTGCCCTCTGCTGGCTTCCCCTTCACCTC   | 3132 |
| Qy | 1261 | AGCAGGATTCTGAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGAACTTTTG   | 1320 |
|    |      |  |      |
| Db | 3133 | AGCAGGATTCTGAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGAACTTTTG   | 3192 |
| Qy | 1321 | AGCTTTCTGTTGGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCCTGCATT   | 1380 |
|    |      |  |      |
| Db | 3193 | AGCTTTCTGTTGGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCCTGCATT   | 3252 |
| Qy | 1381 | AACCCAATTGCTCTGTATTTGGTGAGCAAAAGATTCAAAAAGTCTTTAAGTCATGCTTA    | 1440 |
|    |      |  |      |
| Db | 3253 | AACCCAATTGCTCTGTATTTGGTGAGCAAAAGATTCAAAAAGTCTTTAAGTCATGCTTA    | 3312 |
| Qy | 1441 | TGCTGCTGGTGCCAGTCATTTGAAGAAAAACAGTCCTTGGAGGAAAAGCAGTCGTGCTTA   | 1500 |
|    |      |  |      |
| Db | 3313 | TGCTGCTGGTGCCAGTCATTTGAAGAAAAACAGTCCTTGGAGGAAAAGCAGTCGTGCTTA   | 3372 |
| Qy | 1501 | AAGTTCAAAGCTAATGATCACGGATATGACAACTTCCGTTCCAGTAATAAATACAGCTCA   | 1560 |
|    |      |  |      |
| Db | 3373 | AAGTTCAAAGCTAATGATCACGGATATGACAACTTCCGTTCCAGTAATAAATACAGCTCA   | 3432 |
| Qy | 1561 | TCTTGAAAGAAGAACTATTCACTGTATTTTCACTTTTCTTTATATTGGACCGAAGTCATTAA | 1620 |
|    |      |  |      |
| Db | 3433 | TCTTGAAAGAAGAACTATTCACTGTATTTTCACTTTTCTTTATATTGGACCGAAGTCATTAA | 3492 |
| Qy | 1621 | AACAAAATGAAACATTTGCCAAAACAAAACAAAAAACTATGTATTTGCACAGCACACTAT   | 1680 |
|    |      |  |      |
| Db | 3493 | AACAAAATGAAACATTTGCCAAAACAAAACAAAAAACTATGTATTTGCACAGCACACTAT   | 3552 |
| Qy | 1681 | TAAAATATTAAGTGTAATTATTTTAACACTCACAGCTACATATGACATTTTATGAGCTGT   | 1740 |
|    |      |  |      |
| Db | 3553 | TAAAATATTAAGTGTAATTATTTTAACACTCACAGCTACATATGACATTTTATGAGCTGT   | 3612 |
| Qy | 1741 | TTACGGCATGGAAAGAAAATCAGTGGAATTAAGAAAGCCTCGTCGTGAAAGCACTTAAT    | 1800 |
|    |      |  |      |
| Db | 3613 | TTACGGCATGGAAAGAAAATCAGTGGAATTAAGAAAGCCTCGTCGTGAAAGCACTTAAT    | 3672 |

|    |      |   |      |
|----|------|---|------|
| Qy | 1801 | TTTTTACAGTTAGCACTTCAACATAGCTCTTAACAACCTCCAGGATATTCACACAACACT  | 1860 |
|    |      |   |      |
| Db | 3673 | TTTTTACAGTTAGCACTTCAACATAGCTCTTAACAACCTCCAGGATATTCACACAACACT  | 3732 |
| Qy | 1861 | TAGGCTTAAAAATGAGCTCACTCAGAATTTCTATTCTTTCTAAAAAGAGATTTATTTT    | 1920 |
|    |      |   |      |
| Db | 3733 | TAGGCTTAAAAATGAGCTCACTCAGAATTTCTATTCTTTCTAAAAAGAGATTTATTTT    | 3792 |
| Qy | 1921 | AATCAATGGGACTCTGATATAAAGGAAGAATAAGTCACTGTAAACAGAACTTTTAAATG   | 1980 |
|    |      |   |      |
| Db | 3793 | AATCAATGGGACTCTGATATAAAGGAAGAATAAGTCACTGTAAACAGAACTTTTAAATG   | 3852 |
| Qy | 1981 | AAGCTTAAATTACTCAATTTAAAATTTTAAAATCCTTTAAAACAACCTTTTCAATTAATAT | 2040 |
|    |      |   |      |
| Db | 3853 | AAGCTTAAATTACTCAATTTAAAATTTTAAAATCCTTTAAAACAACCTTTTCAATTAATAT | 3912 |
| Qy | 2041 | TATCACACTATTATCAGATTGTAATTAGATGCAAATGAGAGAGCAGTTTAGTTGTTGCAT  | 2100 |
|    |      |   |      |
| Db | 3913 | TATCACACTATTATCAGATTGTAATTAGATGCAAATGAGAGAGCAGTTTAGTTGTTGCAT  | 3972 |
| Qy | 2101 | TTTTCGGACACTGGAAACATTTAAATGATCAGGAGGGAGTAACAGAAAGAGCAAGGCTGT  | 2160 |
|    |      |   |      |
| Db | 3973 | TTTTCGGACACTGGAAACATTTAAATGATCAGGAGGGAGTAACAGAAAGAGCAAGGCTGT  | 4032 |
| Qy | 2161 | TTTTGAAAATCATTACACTTTTCACTAGAGCCCAAACCTCAGCATTCTGCAATATGTAAC  | 2220 |
|    |      |   |      |
| Db | 4033 | TTTTGAAAATCATTACACTTTTCACTAGAGCCCAAACCTCAGCATTCTGCAATATGTAAC  | 4092 |
| Qy | 2221 | CAACATGTCACAAACAAGCAGCATGTAACAGACTGGCACATGTGCCAGCTGAATTTAAAA  | 2280 |
|    |      |   |      |
| Db | 4093 | CAACATGTCACAAACAAGCAGCATGTAACAGACTGGCACATGTGCCAGCTGAATTTAAAA  | 4152 |
| Qy | 2281 | TATAATACTTTTAAAAAGAAAATTATTACATCCTTTACATTCAGTTAAGATCAAACCTCA  | 2340 |
|    |      |   |      |
| Db | 4153 | TATAATACTTTTAAAAAGAAAATTATTACATCCTTTACATTCAGTTAAGATCAAACCTCA  | 4212 |
| Qy | 2341 | CAAAGAGAAATAGAATGTTTGAAAGGCTATCCCAAAGACTTTTTTGAATCTGTCATTCA   | 2400 |
|    |      |   |      |
| Db | 4213 | CAAAGAGAAATAGAATGTTTGAAAGGCTATCCCAAAGACTTTTTTGAATCTGTCATTCA   | 4272 |
| Qy | 2401 | CATACCCTGTGAAGACAATACTATCTACAATTTTTTCAGGATTATTAAAATCTTCTTTTT  | 2460 |
|    |      |   |      |
| Db | 4273 | CATACCCTGTGAAGACAATACTATCTACAATTTTTTCAGGATTATTAAAATCTTCTTTTT  | 4332 |
| Qy | 2461 | TCACTATCGTAGCTTAAACTCTGTTTGGTTTTGTCATCTGTAAATACTTACCTACATACA  | 2520 |
|    |      |   |      |
| Db | 4333 | TCACTATCGTAGCTTAAACTCTGTTTGGTTTTGTCATCTGTAAATACTTACCTACATACA  | 4392 |
| Qy | 2521 | CTGCATGTAGATGATTAAATGAGGGCAGGCCCTGTGCTCATAGCTTTACGATGGAGAGAT  | 2580 |
|    |      |   |      |
| Db | 4393 | CTGCATGTAGATGATTAAATGAGGGCAGGCCCTGTGCTCATAGCTTTACGATGGAGAGAT  | 4452 |
| Qy | 2581 | GCCAGTGACCTCATAATAAAGACTGTGAACTGCCTGGTGCAGTGTCCACATGACAAAGGG  | 2640 |
|    |      |   |      |
| Db | 4453 | GCCAGTGACCTCATAATAAAGACTGTGAACTGCCTGGTGCAGTGTCCACATGACAAAGGG  | 4512 |
| Qy | 2641 | GCAGGTAGCACCCCTCTCTCACCCATGCTGTGGTTAAAATGGTTTCTAGCATATGTATAAT | 2700 |

|    |      |  |      |
|----|------|--|------|
| Db | 4513 | <br>GCAGGTAGCACCCCTCTCTCACCCATGCTGTGGTTAAAATGGTTTCTAGCATATGTATAAT  | 4572 |
| Qy | 2701 | GCTATAGTTAAAATACTATTTTTCAAATCATACAGATTAGTACATTTAACAGCTACCTG        | 2760 |
| Db | 4573 | <br>GCTATAGTTAAAATACTATTTTTCAAATCATACAGATTAGTACATTTAACAGCTACCTG    | 4632 |
| Qy | 2761 | TAAAGCTTATTACTAATTTTTGTATTATTTTTGTAAATAGCCAATAGAAAAGTTTGCTTG       | 2820 |
| Db | 4633 | <br>TAAAGCTTATTACTAATTTTTGTATTATTTTTGTAAATAGCCAATAGAAAAGTTTGCTTG   | 4692 |
| Qy | 2821 | ACATGGTGCTTTTCTTTTCATCTAGAGGCCAAACTGCTTTTTGAGACCGTAAGAACCTCTT      | 2880 |
| Db | 4693 | <br>ACATGGTGCTTTTCTTTTCATCTAGAGGCCAAACTGCTTTTTGAGACCGTAAGAACCTCTT  | 4752 |
| Qy | 2881 | AGCTTTGTGCGTTCCTGCCTAATTTTTATATCTTCTAAGCAAAGTGCCTTAGGATAGCTT       | 2940 |
| Db | 4753 | <br>AGCTTTGTGCGTTCCTGCCTAATTTTTATATCTTCTAAGCAAAGTGCCTTAGGATAGCTT   | 4812 |
| Qy | 2941 | GGGATGAGATGTGTGTGAAAGTATGTACAAGAGAAAACGGAAGAGAGAGGAAATGAGGTG       | 3000 |
| Db | 4813 | <br>GGGATGAGATGTGTGTGAAAGTATGTACAAGAGAAAACGGAAGAGAGAGGAAATGAGGTG   | 4872 |
| Qy | 3001 | GGGTTGGAGGAAACCCATGGGGACAGATTCCCATTCTTAGCCTAACGTTTCGTCATTGCCT      | 3060 |
| Db | 4873 | <br>GGGTTGGAGGAAACCCATGGGGACAGATTCCCATTCTTAGCCTAACGTTTCGTCATTGCCT  | 4932 |
| Qy | 3061 | CGTCACATCAATGCAAAGGTCCTGATTTTGTTCAGCAAACACAGTGCAATGTTCTCA          | 3120 |
| Db | 4933 | <br>CGTCACATCAATGCAAAGGTCCTGATTTTGTTCAGCAAACACAGTGCAATGTTCTCA      | 4992 |
| Qy | 3121 | GAGTGACTTTTCGAAATAAATTGGGCCCCAAGAGCTTTAACTCGGTCTTAAAATATGCCCAA     | 3180 |
| Db | 4993 | <br>GAGTGACTTTTCGAAATAAATTGGGCCCCAAGAGCTTTAACTCGGTCTTAAAATATGCCCAA | 5052 |
| Qy | 3181 | ATTTTTACTTTGTTTTTCTTTTAATAGGCTGGGCCACATGTTGGAAATAAGCTAGTAATG       | 3240 |
| Db | 5053 | <br>ATTTTTACTTTGTTTTTCTTTTAATAGGCTGGGCCACATGTTGGAAATAAGCTAGTAATG   | 5112 |
| Qy | 3241 | TTGTTTTCTGTCAATATTGAATGTGATGGTACAGTAAACCAAACCAACAATGTGGCCA         | 3300 |
| Db | 5113 | <br>TTGTTTTCTGTCAATATTGAATGTGATGGTACAGTAAACCAAACCAACAATGTGGCCA     | 5172 |
| Qy | 3301 | GAAAGAAAGAGCAATAATAATTAATTCACACACCATATGGATTCTATTTATAAATCACCC       | 3360 |
| Db | 5173 | <br>GAAAGAAAGAGCAATAATAATTAATTCACACACCATATGGATTCTATTTATAAATCACCC   | 5232 |
| Qy | 3361 | ACAAACTTGTTCTTTAATTTTCATCCCAATCACTTTTTTCAGAGGCCTGTTATCATAGAAGT     | 3420 |
| Db | 5233 | <br>ACAAACTTGTTCTTTAATTTTCATCCCAATCACTTTTTTCAGAGGCCTGTTATCATAGAAGT | 5292 |
| Qy | 3421 | CATTTTAGACTCTCAATTTTAAATTAATTTTGAATCACTAATATTTTCACAGTTTATTAA       | 3480 |
| Db | 5293 | <br>CATTTTAGACTCTCAATTTTAAATTAATTTTGAATCACTAATATTTTCACAGTTTATTAA   | 5352 |
| Qy | 3481 | TATATTTAATTTCTATTTAAATTTTAGATTATTTTTATTACCATGTACTGAATTTTTACA       | 3540 |
|    |      |  |      |

Db 5353 TATATTTAATTTCTATTTAAATTTTAGATTATTTTTATTACCATGTACTGAATTTTACA 5412

Qy 3541 TCCTGATACCCTTTTCCTTCTCCATGTCAGTATCATGTTCTCTAATTATCTTGCCAAATTT 3600  
 |||

Db 5413 TCCTGATACCCTTTTCCTTCTCCATGTCAGTATCATGTTCTCTAATTATCTTGCCAAATTT 5472

Qy 3601 TGAAACTACACACAAAAAGCATACTTGCATTATTTATAATAAAATTGCATTCAAGTGGCTT 3660  
 |||

Db 5473 TGAAACTACACACAAAAAGCATACTTGCATTATTTATAATAAAATTGCATTCAAGTGGCTT 5532

Qy 3661 TTTAAAAAAATGTTTGATTCAAAACTTTAACATACTGATAAGTAAGAAACAATTATAAT 3720  
 |||

Db 5533 TTTAAAAAAATGTTTGATTCAAAACTTTAACATACTGATAAGTAAGAAACAATTATAAT 5592

Qy 3721 TTCTTTACATACTCAAACCAAGATAGAAAAAGGTGCTATCGTTCAACTTCAAACATGT 3780  
 |||

Db 5593 TTCTTTACATACTCAAACCAAGATAGAAAAAGGTGCTATCGTTCAACTTCAAACATGT 5652

Qy 3781 TTCCTAGTATTAAGGACTTTAATATAGCAACAGACAAAATTATTGTTAACATGGATGTTA 3840  
 |||

Db 5653 TTCCTAGTATTAAGGACTTTAATATAGCAACAGACAAAATTATTGTTAACATGGATGTTA 5712

Qy 3841 CAGCTCAAAGATTTATAAAAGATTTTAACCTATTTTCTCCCTTATTATCCACTGCTAAT 3900  
 |||

Db 5713 CAGCTCAAAGATTTATAAAAGATTTTAACCTATTTTCTCCCTTATTATCCACTGCTAAT 5772

Qy 3901 GTGGATGTATGTTCAAACACCTTTTAGTATTGATAGCTTACATATGGCCAAAGGAATACA 3960  
 |||

Db 5773 GTGGATGTATGTTCAAACACCTTTTAGTATTGATAGCTTACATATGGCCAAAGGAATACA 5832

Qy 3961 GTTTATAGCAAACATGGGTATGCTGTAGCTAACTTTATAAAAGTGTAATATAACAATGT 4020  
 |||

Db 5833 GTTTATAGCAAACATGGGTATGCTGTAGCTAACTTTATAAAAGTGTAATATAACAATGT 5892

Qy 4021 AAAAAATTATATATCTGGGAGGATTTTTTGGTTGCCTAAAGTGGCTATAGTTACTGATTT 4080  
 |||

Db 5893 AAAAAATTATATATCTGGGAGGATTTTTTGGTTGCCTAAAGTGGCTATAGTTACTGATTT 5952

Qy 4081 TTTATTATGTAAGCAAACCAATAAAAAATTTAAGTTTTTTTAACTACCTTATTTTTTC 4140  
 |||

Db 5953 TTTATTATGTAAGCAAACCAATAAAAAATTTAAGTTTTTTTAACTACCTTATTTTTTC 6012

Qy 4141 ACTGTACAGACACTAATTCATTAAATACTAATTGATTGTTTAAAGAAATATAAATGTGA 4200  
 |||

Db 6013 ACTGTACAGACACTAATTCATTAAATACTAATTGATTGTTTAAAGAAATATAAATGTGA 6072

Qy 4201 CAAGTGGACATTATTTATGTTAAATATACAATTATCAAGCAAGTATGAAGTTATTCAATT 4260  
 |||

Db 6073 CAAGTGGACATTATTTATGTTAAATATACAATTATCAAGCAAGTATGAAGTTATTCAATT 6132

Qy 4261 AAAATGCCACATTTCTGGTCTCTGGG 4286  
 |||

Db 6133 AAAATGCCACATTTCTGGTCTCTGGG 6158

ID AAA35166 standard; DNA; 13612 BP.  
XX  
AC AAA35166;  
XX  
DT 28-JUL-2000 (first entry)  
XX  
DE Human adenosine receptor related polynucleotide 2nd SEQ ID NO:40.  
XX  
KW Human; adenosine receptor; low adenosine antisense oligonucleotide;  
KW phosphorothioate; impaired respiration; inflammation; allergy;  
KW allergic disease; bronchoconstriction; inhibitor; antiinflammatory;  
KW antiallergic; antiasthmatic; cytostatic; analgesic; impaired airway;  
KW lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;  
KW respiratory distress syndrome; pain; cystic fibrosis; emphysema;  
KW pulmonary hypertension; chronic obstructive pulmonary disease; COPD;  
KW cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200009525-A2.  
XX  
PD 24-FEB-2000.  
XX  
PF 03-AUG-1999; 99WO-US017712.  
XX  
PR 03-AUG-1998; 98US-0095212P.  
XX  
PA (UYEC-) UNIV EAST CAROLINA.  
XX  
PI Nyce JW;  
XX  
DR WPI; 2000-205971/18.  
XX  
PT New antisense oligonucleotides useful for treating e.g. pulmonary  
PT vasoconstriction, inflammation, allergies, asthma, hypertension,  
PT bronchitis, emphysema, respiratory distress syndrome, ischemia or  
PT cancers.  
XX  
PS Disclosure; Page 1194-1197; 1343pp; English.  
XX  
CC The present invention describes a new composition comprising an antisense  
CC oligonucleotide (ON) with low adenosine (up to 15%), which targets  
CC nucleic acids involved in bronchoconstriction, allergies, and/or  
CC inflammation. The ON can have antiinflammatory, antiallergic,  
CC antiasthmatic, cytostatic and analgesic activities. The compositions are  
CC useful for the treatment of diseases associated with inflammation,  
CC impaired airways, including lung disease and diseases whose secondary  
CC effects afflict the lungs of a subject. They can be used for treating  
CC e.g. ischaemic conditions, pulmonary vasoconstriction, allergies, asthma,  
CC impeded respiration, respiratory distress syndrome, pain, cystic  
CC fibrosis, pulmonary hypertension, emphysema, chronic obstructive  
CC pulmonary disease (COPD), and cancers such as leukaemias, lymphomas,  
CC carcinomas, and cancers which may metastasise to the lungs, including  
CC breast and prostate cancer. The reduction of the adenosine content of the  
CC ONs reduces side effects. The A-containing ONs break down with the  
CC release of deoxyadenosine which activates adenosine receptors causing  
CC bronchoconstriction and inflammation. AAA32313 to AAA35312 represent the

CC nucleotide sequences given in the sequence listing from the present  
CC invention, which correspond to SEQ ID NO:1 to 2815, and then the last 185  
CC sequences are also called SEQ ID NO:1 to 185, but the sequences differ  
CC from the previously named sequences. SEQ ID NO:11 to 1680 (AAA32323 to  
CC AAA33992) are specifically claimed ONs from the present invention. N.B.  
CC Sequences given in the disclosure of the present invention do not match  
CC up with their corresponding SEQ ID NO: sequences given in the sequence  
CC listing

XX

SQ Sequence 13612 BP; 3677 A; 3007 C; 3056 G; 3868 T; 0 U; 4 Other;

Query Match 99.6%; Score 4284.4; DB 3; Length 13612;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 4285; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy      1 GAGACATTCCGGTGGGGGACTCTGGCCAGCCCAGCAACGTGGATCCTGAGAGCACTCCC 60
      |||
Db    1873 GAGACATTCCGGTGGGGGACTCTGGCCAGCCCAGCAACGTGGATCCTGAGAGCACTCCC 1932

Qy      61 AGGTAGGCATTTGCCCCGGTGGGACGCCTTGCCAGAGCAGTGTGTGGCAGGCCCCCGTGG 120
      |||
Db    1933 AGGTAGGCATTTGCCCCGGTGGGACGCCTTGCCAGAGCAGTGTGTGGCAGGCCCCCGTGG 1992

Qy     121 AGGATCAACACAGTGGCTGAACACTGGGAAGGAACCTGGTACTTGGAGTCTGGACATCTGA 180
      |||
Db    1993 AGGATCAACACAGTGGCTGAACACTGGGAAGGAACCTGGTACTTGGAGTCTGGACATCTGA 2052

Qy     181 AACTTGGCTCTGAAACTGCGGAGCGGCCACCGACGCCTTCTGGAGCAGGTAGCAGCATG 240
      |||
Db    2053 AACTTGGCTCTGAAACTGCGCAGCGGCCACCGACGCCTTCTGGAGCAGGTAGCAGCATG 2112

Qy     241 CAGCCGCCTCCAAGTCTGTGCGGACGCGCCCTGGTTGCGCTGGTTCTTGCCTGCGGCCTG 300
      |||
Db    2113 CAGCCGCCTCCAAGTCTGTGCGGACGCGCCCTGGTTGCGCTGGTTCTTGCCTGCGGCCTG 2172

Qy     301 TCGCGGATCTGGGGAGAGGAGAGAGGCTTCCCGCCTGACAGGGCCACTCCGCTTTTGCAA 360
      |||
Db    2173 TCGCGGATCTGGGGAGAGGAGAGAGGCTTCCCGCCTGACAGGGCCACTCCGCTTTTGCAA 2232

Qy     361 ACCGCAGAGATAATGACGCCACCCACTAAGACCTTATGGCCCAAGGGTTCCAACGCCAGT 420
      |||
Db    2233 ACCGCAGAGATAATGACGCCACCCACTAAGACCTTATGGCCCAAGGGTTCCAACGCCAGT 2292

Qy     421 CTGGCGCGGTTCGTTGGCACCTGCGGAGGTGCCTAAAGGAGACAGGACGGCAGGATCTCCG 480
      |||
Db    2293 CTGGCGCGGTTCGTTGGCACCTGCGGAGGTGCCTAAAGGAGACAGGACGGCAGGATCTCCG 2352

Qy     481 CCACGCACCATCTCCCTCCCCCGTGCCAAGGACCCATCGAGATCAAGGAGACTTTCAAA 540
      |||
Db    2353 CCACGCACCATCTCCCTCCCCCGTGCCAAGGACCCATCGAGATCAAGGAGACTTTCAAA 2412

Qy     541 TACATCAACACGGTTGTGTCTGCTTGTGTTCTGTGCTGGGGATCATCGGGAACCTCACA 600
      |||
Db    2413 TACATCAACACGGTTGTGTCTGCTTGTGTTCTGTGCTGGGGATCATCGGGAACCTCACA 2472

Qy     601 CTTCTGAGAATTATCTACAAGAACAAGTGCATGCGAAACGGTCCCAATATCTTGATCGCC 660
      |||
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Db 2473 CTTCTGAGAATTATCTACAAGAACAAGTGCATGCGAAACGGTCCCAATATCTTGATCGCC 2532  
 Qy 661 AGCTTGGCTCTGGGAGACCTGCTGCACATCGTCATTGACATCCCTATCAATGTCTACAAG 720  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 2533 AGCTTGGCTCTGGGAGACCTGCTGCACATCGTCATTGACATCCCTATCAATGTCTACAAG 2592  
 Qy 721 CTGCTGGCAGAGGACTGGCCATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTCATACAG 780  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 2593 CTGCTGGCAGAGGACTGGCCATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTCATACAG 2652  
 Qy 781 AAAGCCTCCGTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATATCGA 840  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 2653 AAAGCCTCCGTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATATCGA 2712  
 Qy 841 GCTGTTGCTTCTTGGAGTAGAATTAAAGGAATTGGGGTTCCAAAATGGACAGCAGTAGAA 900  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 2713 GCTGTTGCTTCTTGGAGTAGAATTAAAGGAATTGGGGTTCCAAAATGGACAGCAGTAGAA 2772  
 Qy 901 ATTGTTTTGATTTGGGTGGTCTCTGTGGTTCTGGCTGTCCCTGAAGCCATAGGTTTTGAT 960  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 2773 ATTGTTTTGATTTGGGTGGTCTCTGTGGTTCTGGCTGTCCCTGAAGCCATAGGTTTTGAT 2832  
 Qy 961 ATAATTACGATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTTCAG 1020  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 2833 ATAATTACGATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTTCAG 2892  
 Qy 1021 AAGACAGCTTTCATGCAGTTTTTACAAGACAGCAAAAGATTGGTGGCTGTTTCAGTTTCTAT 1080  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 2893 AAGACAGCTTTCATGCAGTTTTTACAAGACAGCAAAAGATTGGTGGCTGTTTCAGTTTCTAT 2952  
 Qy 1081 TTCTGCTTGCCATTGGCCATCACTGCATTTTTTTTATACACTAATGACCTGTGAAATGTTG 1140  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 2953 TTCTGCTTGCCATTGGCCATCACTGCATTTTTTTTATACACTAATGACCTGTGAAATGTTG 3012  
 Qy 1141 AGAAAGAAAAGTGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAAGTG 1200  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 3013 AGAAAGAAAAGTGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAAGTG 3072  
 Qy 1201 GCCAAAACCGTCTTTTGCCTGGTCCTTGTCTTTGCCCTCTGCTGGCTTCCCCTTCACCTC 1260  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 3073 GCCAAAACCGTCTTTTGCCTGGTCCTTGTCTTTGCCCTCTGCTGGCTTCCCCTTCACCTC 3132  
 Qy 1261 AGCAGGATTCTGAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGAACTTTTG 1320  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 3133 AGCAGGATTCTGAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGAACTTTTG 3192  
 Qy 1321 AGCTTTCTGTTGGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCCTGCATT 1380  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 3193 AGCTTTCTGTTGGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCCTGCATT 3252  
 Qy 1381 AACCCAATTGCTCTGTATTTGGTGAGCAAAAGATTCAAAAAGTCTTTAAGTCATGCTTA 1440  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 3253 AACCCAATTGCTCTGTATTTGGTGAGCAAAAGATTCAAAAAGTCTTTAAGTCATGCTTA 3312  
 Qy 1441 TGCTGCTGGTGCCAGTCATTTGAAGAAAAACAGTCCTTGGAGGAAAAGCAGTCGTGCTTA 1500  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 3313 TGCTGCTGGTGCCAGTCATTTGAAGAAAAACAGTCCTTGGAGGAAAAGCAGTCGTGCTTA 3372

|    |      |   |      |
|----|------|---|------|
| Qy | 1501 | AAGTTCAAAGCTAATGATCACGGATATGACAACTTCCGTTCCAGTAATAAATACAGCTCA  | 1560 |
|    |      |   |      |
| Db | 3373 | AAGTTCAAAGCTAATGATCACGGATATGACAACTTCCGTTCCAGTAATAAATACAGCTCA  | 3432 |
| Qy | 1561 | TCTTGAAAGAAGAAGCTATTCACTGTATTTTCTTTATATTGGACCGAAGTCATTAA      | 1620 |
|    |      |   |      |
| Db | 3433 | TCTTGAAAGAAGAAGCTATTCACTGTATTTTCTTTATATTGGACCGAAGTCATTAA      | 3492 |
| Qy | 1621 | AACAAAATGAAACATTTGCCAAAACAAAACAAAAAATATGTATTTGCACAGCACACTAT   | 1680 |
|    |      |   |      |
| Db | 3493 | AACAAAATGAAACATTTGCCAAAACAAAACAAAAAATATGTATTTGCACAGCACACTAT   | 3552 |
| Qy | 1681 | TAAAATATTAAGTGTAATTATTTTAACACTCACAGCTACATATGACATTTTATGAGCTGT  | 1740 |
|    |      |   |      |
| Db | 3553 | TAAAATATTAAGTGTAATTATTTTAACACTCACAGCTACATATGACATTTTATGAGCTGT  | 3612 |
| Qy | 1741 | TTACGGCATGGAAAGAAAATCAGTGGGAATTAAGAAAGCCTCGTCGTGAAAGCACTTAAT  | 1800 |
|    |      |   |      |
| Db | 3613 | TTACGGCATGGAAAGAAAATCAGTGGGAATTAAGAAAGCCTCGTCGTGAAAGCACTTAAT  | 3672 |
| Qy | 1801 | TTTTTACAGTTAGCACTTCAACATAGCTCTTAACAACCTCCAGGATATTCACACAACACT  | 1860 |
|    |      |   |      |
| Db | 3673 | TTTTTACAGTTAGCACTTCAACATAGCTCTTAACAACCTCCAGGATATTCACACAACACT  | 3732 |
| Qy | 1861 | TAGGCTTAAAAATGAGCTCACTCAGAATTTCTATTCTTTCTAAAAAGAGATTTATTTTAA  | 1920 |
|    |      |   |      |
| Db | 3733 | TAGGCTTAAAAATGAGCTCACTCAGAATTTCTATTCTTTCTAAAAAGAGATTTATTTTAA  | 3792 |
| Qy | 1921 | AATCAATGGGACTCTGATATAAAGGAAGAATAAGTCACTGTAAACAGAACTTTTAAATG   | 1980 |
|    |      |   |      |
| Db | 3793 | AATCAATGGGACTCTGATATAAAGGAAGAATAAGTCACTGTAAACAGAACTTTTAAATG   | 3852 |
| Qy | 1981 | AAGCTTAAATTACTCAATTTAAATTTTAAATCCTTTAAACAACCTTTTCAATTAATAT    | 2040 |
|    |      |   |      |
| Db | 3853 | AAGCTTAAATTACTCAATTTAAATTTTAAATCCTTTAAACAACCTTTTCAATTAATAT    | 3912 |
| Qy | 2041 | TATCACACTATTATCAGATTGTAATTAGATGCAAATGAGAGAGCAGTTTAGTTGTTGCAT  | 2100 |
|    |      |   |      |
| Db | 3913 | TATCACACTATTATCAGATTGTAATTAGATGCAAATGAGAGAGCAGTTTAGTTGTTGCAT  | 3972 |
| Qy | 2101 | TTTTCGGACACTGGAAACATTTAAATGATCAGGAGGGAGTAACAGAAAGAGCAAGGCTGT  | 2160 |
|    |      |   |      |
| Db | 3973 | TTTTCGGACACTGGAAACATTTAAATGATCAGGAGGGAGTAACAGAAAGAGCAAGGCTGT  | 4032 |
| Qy | 2161 | TTTTGAAAATCATTACACTTTCACTAGAAGCCCAAACCTCAGCATTCTGCAATATGTAAC  | 2220 |
|    |      |   |      |
| Db | 4033 | TTTTGAAAATCATTACACTTTCACTAGAAGCCCAAACCTCAGCATTCTGCAATATGTAAC  | 4092 |
| Qy | 2221 | CAACATGTCACAAACAAGCAGCATGTAACAGACTGGCACATGTGCCAGCTGAATTTAAAA  | 2280 |
|    |      |   |      |
| Db | 4093 | CAACATGTCACAAACAAGCAGCATGTAACAGACTGGCACATGTGCCAGCTGAATTTAAAA  | 4152 |
| Qy | 2281 | TATAATACTTTTAAAAAGAAAATTATTACATCCTTTACATTTCAGTTAAGATCAAACCTCA | 2340 |
|    |      |   |      |
| Db | 4153 | TATAATACTTTTAAAAAGAAAATTATTACATCCTTTACATTTCAGTTAAGATCAAACCTCA | 4212 |

|    |      |   |      |
|----|------|---|------|
| Qy | 2341 | CAAAGAGAAATAGAATGTTTGAAAGGCTATCCCAAAGACTTTTTTTGAATCTGTCATTCA  | 2400 |
|    |      |   |      |
| Db | 4213 | CAAAGAGAAATAGAATGTTTGAAAGGCTATCCCAAAGACTTTTTTTGAATCTGTCATTCA  | 4272 |
| Qy | 2401 | CATACCCTGTGAAGACAATACTATCTACAATTTTTTCAGGATTATTAAAATCTTCTTTTT  | 2460 |
|    |      |   |      |
| Db | 4273 | CATACCCTGTGAAGACAATACTATCTACAATTTTTTCAGGATTATTAAAATCTTCTTTTT  | 4332 |
| Qy | 2461 | TCACTATCGTAGCTTAAACTCTGTTTGGTTTTGTCATCTGTAAATACTTACCTACATACA  | 2520 |
|    |      |   |      |
| Db | 4333 | TCACTATCGTAGCTTAAACTCTGTTTGGTTTTGTCATCTGTAAATACTTACCTACATACA  | 4392 |
| Qy | 2521 | CTGCATGTAGATGATTAAATGAGGGCAGGCCCTGTGCTCATAGCTTTACGATGGAGAGAT  | 2580 |
|    |      |   |      |
| Db | 4393 | CTGCATGTAGATGATTAAATGAGGGCAGGCCCTGTGCTCATAGCTTTACGATGGAGAGAT  | 4452 |
| Qy | 2581 | GCCAGTGACCTCATAATAAAGACTGTGAACTGCCTGGTGCAGTGTCCACATGACAAAGGG  | 2640 |
|    |      |   |      |
| Db | 4453 | GCCAGTGACCTCATAATAAAGACTGTGAACTGCCTGGTGCAGTGTCCACATGACAAAGGG  | 4512 |
| Qy | 2641 | GCAGGTAGCACCCCTCTCTACCCATGCTGTGGTTAAAATGGTTTCTAGCATATGTATAAT  | 2700 |
|    |      |   |      |
| Db | 4513 | GCAGGTAGCACCCCTCTCTACCCATGCTGTGGTTAAAATGGTTTCTAGCATATGTATAAT  | 4572 |
| Qy | 2701 | GCTATAGTTAAAATACTATTTTTCAAATCATACAGATTAGTACATTTAACAGCTACCTG   | 2760 |
|    |      |   |      |
| Db | 4573 | GCTATAGTTAAAATACTATTTTTCAAATCATACAGATTAGTACATTTAACAGCTACCTG   | 4632 |
| Qy | 2761 | TAAAGCTTATTACTAATTTTTGTATTATTTTTGTAAATAGCCAATAGAAAAGTTTGCTTG  | 2820 |
|    |      |   |      |
| Db | 4633 | TAAAGCTTATTACTAATTTTTGTATTATTTTTGTAAATAGCCAATAGAAAAGTTTGCTTG  | 4692 |
| Qy | 2821 | ACATGGTGCTTTTCTTTCATCTAGAGGCAAACTGCTTTTTGAGACCGTAAGAACCTCTT   | 2880 |
|    |      |   |      |
| Db | 4693 | ACATGGTGCTTTTCTTTCATCTAGAGGCAAACTGCTTTTTGAGACCGTAAGAACCTCTT   | 4752 |
| Qy | 2881 | AGCTTTGTGCGTTCCTGCCTAATTTTTATATCTTCTAAGCAAAGTGCCCTTAGGATAGCTT | 2940 |
|    |      |   |      |
| Db | 4753 | AGCTTTGTGCGTTCCTGCCTAATTTTTATATCTTCTAAGCAAAGTGCCCTTAGGATAGCTT | 4812 |
| Qy | 2941 | GGGATGAGATGTGTGTGAAAGTATGTACAAGAGAAAACGGAAGAGAGAGGAAATGAGGTG  | 3000 |
|    |      |   |      |
| Db | 4813 | GGGATGAGATGTGTGTGAAAGTATGTACAAGAGAAAACGGAAGAGAGAGGAAATGAGGTG  | 4872 |
| Qy | 3001 | GGGTTGGAGGAAACCCATGGGGACAGATTCCCATTCTTAGCCTAACGTTTCGTCATTGCCT | 3060 |
|    |      |   |      |
| Db | 4873 | GGGTTGGAGGAAACCCATGGGGACAGATTCCCATTCTTAGCCTAACGTTTCGTCATTGCCT | 4932 |
| Qy | 3061 | CGTCACATCAATGCAAAAGGTCCTGATTTTGTTCAGCAAAACACAGTGCAATGTTCTCA   | 3120 |
|    |      |   |      |
| Db | 4933 | CGTCACATCAATGCAAAAGGTCCTGATTTTGTTCAGCAAAACACAGTGCAATGTTCTCA   | 4992 |
| Qy | 3121 | GAGTGACTTTCGAAATAAATTGGGCCCCAAGAGCTTTAACTCGGTCTTAAAATATGCCCAA | 3180 |
|    |      |   |      |
| Db | 4993 | GAGTGACTTTCGAAATAAATTGGGCCCCAAGAGCTTTAACTCGGTCTTAAAATATGCCCAA | 5052 |
| Qy | 3181 | ATTTTTACTTTGTTTTTCTTTTAATAGGCTGGGCCACATGTTGGAAATAAGCTAGTAATG  | 3240 |

|    |      |   |      |
|----|------|---|------|
| Db | 5053 | <br>ATTTTACTTTGTTTTCTTTTAATAGGCTGGGCCACATGTTGGAAATAAGCTAGTAATG    | 5112 |
| Qy | 3241 | TTGTTTTCTGTCAATATTGAATGTGATGGTACAGTAAACCAAACCAACAATGTGGCCA        | 3300 |
| Db | 5113 | <br>TTGTTTTCTGTCAATATTGAATGTGATGGTACAGTAAACCAAACCAACAATGTGGCCA    | 5172 |
| Qy | 3301 | GAAAGAAAGAGCAATAATAATTAATTCACACACCATATGGATTCTATTTATAAATCACCC      | 3360 |
| Db | 5173 | <br>GAAAGAAAGAGCAATAATAATTAATTCACACACCATATGGATTCTATTTATAAATCACCC  | 5232 |
| Qy | 3361 | ACAAACTTGTCTTTAATTTTCATCCCAATCACTTTTTTCAGAGGCCTGTTATCATAGAAGT     | 3420 |
| Db | 5233 | <br>ACAAACTTGTCTTTAATTTTCATCCCAATCACTTTTTTCAGAGGCCTGTTATCATAGAAGT | 5292 |
| Qy | 3421 | CATTTTAGACTCTCAATTTTAAATTAATTTTGAATCACTAATATTTTCACAGTTTATTAA      | 3480 |
| Db | 5293 | <br>CATTTTAGACTCTCAATTTTAAATTAATTTTGAATCACTAATATTTTCACAGTTTATTAA  | 5352 |
| Qy | 3481 | TATATTTAATTTCTATTTAAATTTTAGATTATTTTATTACCATGTACTGAATTTTACA        | 3540 |
| Db | 5353 | <br>TATATTTAATTTCTATTTAAATTTTAGATTATTTTATTACCATGTACTGAATTTTACA    | 5412 |
| Qy | 3541 | TCCTGATACCCTTTCCTTCTCCATGTCAGTATCATGTTCTCTAATTATCTTGCCAAATTT      | 3600 |
| Db | 5413 | <br>TCCTGATACCCTTTCCTTCTCCATGTCAGTATCATGTTCTCTAATTATCTTGCCAAATTT  | 5472 |
| Qy | 3601 | TGAAACTACACACAAAAAGCATACTTGCATTATTTATAATAAAATTGCATTCACTGGCTT      | 3660 |
| Db | 5473 | <br>TGAAACTACACACAAAAAGCATACTTGCATTATTTATAATAAAATTGCATTCACTGGCTT  | 5532 |
| Qy | 3661 | TTTAAAAAAATGTTTGATTCAAACCTTTAACATACTGATAAGTAAGAAACAATTATAAT       | 3720 |
| Db | 5533 | <br>TTTAAAAAAATGTTTGATTCAAACCTTTAACATACTGATAAGTAAGAAACAATTATAAT   | 5592 |
| Qy | 3721 | TTCTTTACATACTCAAACCAAGATAGAAAAAGGTGCTATCGTTCAACTTCAAACATGT        | 3780 |
| Db | 5593 | <br>TTCTTTACATACTCAAACCAAGATAGAAAAAGGTGCTATCGTTCAACTTCAAACATGT    | 5652 |
| Qy | 3781 | TTCCTAGTATTAAGGACTTTAATATAGCAACAGACAAAATTATTGTTAACATGGATGTTA      | 3840 |
| Db | 5653 | <br>TTCCTAGTATTAAGGACTTTAATATAGCAACAGACAAAATTATTGTTAACATGGATGTTA  | 5712 |
| Qy | 3841 | CAGCTCAAAGATTTATAAAAGATTTTAACCTATTTTCTCCCTTATTATCCACTGCTAAT       | 3900 |
| Db | 5713 | <br>CAGCTCAAAGATTTATAAAAGATTTTAACCTATTTTCTCCCTTATTATCCACTGCTAAT   | 5772 |
| Qy | 3901 | GTGGATGTATGTTCAAACACCTTTTAGTATTGATAGCTTACATATGGCCAAAGGAATACA      | 3960 |
| Db | 5773 | <br>GTGGATGTATGTTCAAACACCTTTTAGTATTGATAGCTTACATATGGCCAAAGGAATACA  | 5832 |
| Qy | 3961 | GTTTATAGCAAAACATGGGTATGCTGTAGCTAACTTTATAAAAGTGTAATATAACAATGT      | 4020 |
| Db | 5833 | <br>GTTTATAGCAAAACATGGGTATGCTGTAGCTAACTTTATAAAAGTGTAATATAACAATGT  | 5892 |
| Qy | 4021 | AAAAAATTATATATCTGGGAGGATTTTTTGTTGCCTAAAGTGGCTATAGTTACTGATTT       | 4080 |
|    |      |   |      |

Db 5893 AAAAAATTATATATCTGGGAGGATTTTTTGGTTGCCTAAAGTGGCTATAGTTACTGATTT 5952  
 QY 4081 TTTATTATGTAAGCAAAACCAATAAAAAATTTAAGTTTTTTTAACTACCTTATTTTTC 4140  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 5953 TTTATTATGTAAGCAAAACCAATAAAAAATTTAAGTTTTTTTAACTACCTTATTTTTC 6012  
 QY 4141 ACTGTACAGACACTAATTCATTAAATACTAATTGATTGTTTAAAAGAAATATAAATGTGA 4200  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 6013 ACTGTACAGACACTAATTCATTAAATACTAATTGATTGTTTAAAAGAAATATAAATGTGA 6072  
 QY 4201 CAAGTGGACATTATTTATGTTAAATATACAATTATCAAGCAAGTATGAAGTTATTCAATT 4260  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 6073 CAAGTGGACATTATTTATGTTAAATATACAATTATCAAGCAAGTATGAAGTTATTCAATT 6132  
 QY 4261 AAAATGCCACATTTCTGGTCTCTGGG 4286  
 ||||||||||||||||||||||||||||  
 Db 6133 AAAATGCCACATTTCTGGTCTCTGGG 6158

RESULT 13

ACH03911

ID ACH03911 standard; cDNA; 4305 BP.

XX

AC ACH03911;

XX

DT 26-SEP-2003 (first entry)

XX

DE Human cDNA differentially expressed in lung cancer #116.

XX

KW Gene therapy; emphysema; ss; gene; chronic obstructive pulmonary disease;  
 KW respiratory disorder; lung cancer; asthma; human.

XX

OS Homo sapiens.

XX

PN US2003065157-A1.

XX

PD 03-APR-2003.

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PF 04-APR-2002; 2002US-00116802.

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PR 04-APR-2001; 2001US-0281593P.

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PA (LASE/) LASEK A W.

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PI Lasek AW;

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DR WPI; 2003-540803/51.

XX

PT New combination comprising cDNAs that are differentially expressed in  
 PT respiratory disorders, useful for diagnosing or treating respiratory  
 PT disorders e.g., lung cancer, chronic obstructive pulmonary disease,  
 PT emphysema or asthma.

XX

PS Claim 1; Page; 39pp; English.

XX

CC The invention relates to a combination comprising cDNAs or their  
 CC complements that are differentially expressed in respiratory disorder.



|    |      |   |      |
|----|------|---|------|
| Db | 661  | AGCTTGGCTCTGGGAGACCTGCTGCACATCGTCATTGACATCCCTATCAATGTCTACAAG  | 720  |
| Qy | 721  | CTGCTGGCAGAGGACTGGCCATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTCATACAG  | 780  |
|    |      |   |      |
| Db | 721  | CTGCTGGCAGAGGACTGGCCATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTCATACAG  | 780  |
| Qy | 781  | AAAGCCTCCGTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATATCGA  | 840  |
|    |      |   |      |
| Db | 781  | AAAGCCTCCGTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATATCGA  | 840  |
| Qy | 841  | GCTGTTGCTTCTTGGAGTAGAATTAAAGGAATTGGGGTTCCAAAATGGACAGCAGTAGAA  | 900  |
|    |      |   |      |
| Db | 841  | GCTGTTGCTTCTTGGAGTAGAATTAAAGGAATTGGGGTTCCAAAATGGACAGCAGTAGAA  | 900  |
| Qy | 901  | ATTGTTTTGATTTGGGTGGTCTCTGTGGTTCTGGCTGTCCCTGAAGCCATAGTTTTGAT   | 960  |
|    |      |   |      |
| Db | 901  | ATTGTTTTGATTTGGGTGGTCTCTGTGGTTCTGGCTGTCCCTGAAGCCATAGTTTTGAT   | 960  |
| Qy | 961  | ATAATTACGATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTTTCAG | 1020 |
|    |      |   |      |
| Db | 961  | ATAATTACGATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTTTCAG | 1020 |
| Qy | 1021 | AAGACAGCTTTCATGCAGTTTTACAAGACAGCAAAAGATTGGTGGCTGTTTCAGTTTCTAT | 1080 |
|    |      |   |      |
| Db | 1021 | AAGACAGCTTTCATGCAGTTTTACAAGACAGCAAAAGATTGGTGGCTGTTTCAGTTTCTAT | 1080 |
| Qy | 1081 | TTCTGCTTGCCATTGGCCATCACTGCATTTTTTTATACACTAATGACCTGTGAAATGTTG  | 1140 |
|    |      |   |      |
| Db | 1081 | TTCTGCTTGCCATTGGCCATCACTGCATTTTTTTATACACTAATGACCTGTGAAATGTTG  | 1140 |
| Qy | 1141 | AGAAAGAAAAGTGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAAGTG  | 1200 |
|    |      |   |      |
| Db | 1141 | AGAAAGAAAAGTGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAAGTG  | 1200 |
| Qy | 1201 | GCCAAAACCGTCTTTTGCCTGGTCCTTGTCTTTGCCCTCTGCTGGCTTCCCCTTCACCTC  | 1260 |
|    |      |   |      |
| Db | 1201 | GCCAAAACCGTCTTTTGCCTGGTCCTTGTCTTTGCCCTCTGCTGGCTTCCCCTTCACCTC  | 1260 |
| Qy | 1261 | AGCAGGATTCTGAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGAACTTTTG  | 1320 |
|    |      |   |      |
| Db | 1261 | AGCAGGATTCTGAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGAACTTTTG  | 1320 |
| Qy | 1321 | AGCTTTCTGTTGGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCCTGCATT  | 1380 |
|    |      |   |      |
| Db | 1321 | AGCTTTCTGTTGGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCCTGCATT  | 1380 |
| Qy | 1381 | AACCCAATTGCTCTGTATTTGGTGAGCAAAAGATTCAAAAAGTCTTTAAGTCATGCTTA   | 1440 |
|    |      |   |      |
| Db | 1381 | AACCCAATTGCTCTGTATTTGGTGAGCAAAAGATTCAAAAAGTCTTTAAGTCATGCTTA   | 1440 |
| Qy | 1441 | TGCTGCTGGTGCCAGTCATTTGAAGAAAAACAGTCCTTGGAGGAAAAGCAGTCGTGCTTA  | 1500 |
|    |      |   |      |
| Db | 1441 | TGCTGCTGGTGCCAGTCATTTGAAGAAAAACAGTCCTTGGAGGAAAAGCAGTCGTGCTTA  | 1500 |
| Qy | 1501 | AAGTTCAAAGCTAATGATCACGGATATGACAACTTCCGTTCCAGTAATAAATACAGCTCA  | 1560 |
|    |      |   |      |
| Db | 1501 | AAGTTCAAAGCTAATGATCACGGATATGACAACTTCCGTTCCAGTAATAAATACAGCTCA  | 1560 |

|    |      |   |      |
|----|------|---|------|
| Qy | 1561 | TCTTGAAAGAAGAACTATTCACTGTATTTTCATTTTCTTTATATTGGACCGAAGTCATTAA | 1620 |
|    |      |   |      |
| Db | 1561 | TCTTGAAAGAAGAACTATTCACTGTATTTTCATTTTCTTTATATTGGACCGAAGTCATTAA | 1620 |
| Qy | 1621 | AACAAAATGAAACATTTGCCAAAACAAAACAAAAAACTATGTATTGTCACAGCACACTAT  | 1680 |
|    |      |   |      |
| Db | 1621 | AACAAAATGAAACATTTGCCAAAACAAAACAAAAAACTATGTATTGTCACAGCACACTAT  | 1680 |
| Qy | 1681 | TAAAATATTAAGTGTAATTATTTTAACACTCACAGCTACATATGACATTTTATGAGCTGT  | 1740 |
|    |      |   |      |
| Db | 1681 | TAAAATATTAAGTGTAATTATTTTAACACTCACAGCTACATATGACATTTTATGAGCTGT  | 1740 |
| Qy | 1741 | TTACGGCATGGAAAGAAAATCAGTGGGAATTAAGAAAGCCTCGTCGTGAAAGCACTTAAT  | 1800 |
|    |      |   |      |
| Db | 1741 | TTACGGCATGGAAAGAAAATCAGTGGGAATTAAGAAAGCCTCGTCGTGAAAGCACTTAAT  | 1800 |
| Qy | 1801 | TTTTTACAGTTAGCACTTCAACATAGCTCTTAACAACCTCCAGGATATTCACACAACACT  | 1860 |
|    |      |   |      |
| Db | 1801 | TTTTTACAGTTAGCACTTCAACATAGCTCTTAACAACCTCCAGGATATTCACACAACACT  | 1860 |
| Qy | 1861 | TAGGCTTAAAATGAGCTCACTCAGAATTTCTATTCTTTCTAAAAAGAGATTTATTTTTTA  | 1920 |
|    |      |   |      |
| Db | 1861 | TAGGCTTAAAATGAGCTCACTCAGAATTTCTATTCTTTCTAAAAAGAGATTTATTTTTTA  | 1920 |
| Qy | 1921 | AATCAATGGGACTCTGATATAAAGGAAGAATAAGTCACTGTAAAACAGAACTTTTAAATG  | 1980 |
|    |      |   |      |
| Db | 1921 | AATCAATGGGACTCTGATATAAAGGAAGAATAAGTCACTGTAAAACAGAACTTTTAAATG  | 1980 |
| Qy | 1981 | AAGCTTAAATTACTCAATTTAAAATTTTAAAATCCTTTAAAACAACCTTTTCAATTAATAT | 2040 |
|    |      |   |      |
| Db | 1981 | AAGCTTAAATTACTCAATTTAAAATTTTAAAATCCTTTAAAACAACCTTTTCAATTAATAT | 2040 |
| Qy | 2041 | TATCACACTATTATCAGATTGTAATTAGATGCAAATGAGAGAGCAGTTTAGTTGTTGCAT  | 2100 |
|    |      |   |      |
| Db | 2041 | TATCACACTATTATCAGATTGTAATTAGATGCAAATGAGAGAGCAGTTTAGTTGTTGCAT  | 2100 |
| Qy | 2101 | TTTTCGGACACTGGAAACATTTAAATGATCAGGAGGGAGTAACAGAAAGAGCAAGGCTGT  | 2160 |
|    |      |   |      |
| Db | 2101 | TTTTCGGACACTGGAAACATTTAAATGATCAGGAGGGAGTAACAGAAAGAGCAAGGCTGT  | 2160 |
| Qy | 2161 | TTTTGAAAATCATTACACTTTCAC--TAGAAGCCCCAACCTCAGCATT-CTGCAATATGT  | 2217 |
|    |      |   |      |
| Db | 2161 | TTTTGAAAATCATTACACTTTCACCTAGAAGCCCCAACCTCAGCATTCTGCAATATGT    | 2220 |
| Qy | 2218 | AA-CCAACATGTCACAAACAAGCAG--CATGTAACAGACTGGCACATGTG-CCAGCTGAA  | 2273 |
|    |      |   |      |
| Db | 2221 | AACCCAACATGTCACAAACAAGCCAGCCATGTAACAGACTGGCACATGTGCCAGCTGAA   | 2280 |
| Qy | 2274 | TTTAAAATATAATACTTTTAAAAAGAAAATTATTACATCCTTTACATTTCAGTTAAGATCA | 2333 |
|    |      |   |      |
| Db | 2281 | TTTAAAATATAATACTTTTAAAAAGAAAATTATTACATCCTTTACATTTCAGTTAAGATCA | 2340 |
| Qy | 2334 | AACCTCACAAAGAGAAATAGAATGTTTGAAAGGCTATCCCAAAGACTTTTTTGAATCTG   | 2393 |
|    |      |   |      |
| Db | 2341 | AACCTCACAAAGAGAAATAGAATGTTTGAAAGGCTATCCCAAAGACTTTTTTGAATCTG   | 2400 |



|    |      |   |      |
|----|------|---|------|
| Qy | 2394 | TCATTACATACCCTGTGAAGACAATACTATCTACAATTTTTTCAGGATTATTAAAAATCT  | 2453 |
|    |      |   |      |
| Db | 2401 | TCATTACATACCCTGTGAAGACAATACTATCTACAATTTTTTCAGGATTATTAAAAATCT  | 2460 |
| Qy | 2454 | TCTTTTTTCACTATCGTAGCTTAAACTCTGTTTGGTTTTGTCATCTGTAAATACTTACCT  | 2513 |
|    |      |   |      |
| Db | 2461 | TCTTCTTCACTATCGTAGCTTAAACTCTGTTTGGTTTTGTCATCTGTAAATACTTACCT   | 2520 |
| Qy | 2514 | ACATACACTGCATGTAGATGATTAAATGAGGGCAGGCCCTGTGCTCATAGCTTTACGATG  | 2573 |
|    |      |   |      |
| Db | 2521 | ACATACACTGCATGTAGATGATTAAATGAGGGCAGGCCCTGTGCTCATAGCTTTACGATG  | 2580 |
| Qy | 2574 | GAGAGATGCCAGTGACCTCATAATAAAGACTGTGAACTGCCTGGTGCAGTGTCCACATGA  | 2633 |
|    |      |   |      |
| Db | 2581 | GAGAGATGCCAGTGACCTCATAATAAAGACTGTGAACTGCCTGGTGCAGTGTCCACATGA  | 2640 |
| Qy | 2634 | CAAAGGGGCAGGTAGCACCCCTCTCTACCCATGCTGTGGTTAAAAATGGTTTCTAGCATAT | 2693 |
|    |      |   |      |
| Db | 2641 | CAAAGGGGCAGGTAGCACCCCTCTCTACCCATGCTGTGGTTAAAAATGGTTTCTAGCATAT | 2700 |
| Qy | 2694 | GTATAATGCTATAGTTAAATACTATTTTTTCAAATCATACAGATTAGTACATTTAACAG   | 2753 |
|    |      |   |      |
| Db | 2701 | GTATAATGCTATAGTTAAATACTATTTTTTCAAATCATACAGATTAGTACATTTAACAG   | 2760 |
| Qy | 2754 | CTACCTGTAAAGCTTATTACTAATTTTTGTATTATTTTTGTAAATAGCCAATAGAAAAGT  | 2813 |
|    |      |   |      |
| Db | 2761 | CTACCTGTAAAGCTTATTACTAATTTTTGTATTATTTTTGTAAATAGCCAATAGAAAAGT  | 2820 |
| Qy | 2814 | TTGCTTGACATGGTGCTTTTCTTTCATCTAGAGGCAAACTGCTTTTGTAGACCGTAAGA   | 2873 |
|    |      |   |      |
| Db | 2821 | TTGCTTGACATGGTGCTTTTCTTTCATCTAGAGGCAAACTGCTTTTGTAGACCGTAAGA   | 2880 |
| Qy | 2874 | ACCTCTTAGCTTTGTGCGTTCCTGCCTAATTTTTATATCTTCTAAGCAAAGTGCCTTAGG  | 2933 |
|    |      |   |      |
| Db | 2881 | ACCTCTTAGCTTTGTGCGTTCCTGCCTAATTTTTATATCTTCTAAGCAAAGTGCCTTAGG  | 2940 |
| Qy | 2934 | ATAGCTTGGGATGAGATGTGTGTGAAAGTATGTACAAGAGAAAACGGAAGAGAGAGGAAA  | 2993 |
|    |      |   |      |
| Db | 2941 | ATAGCTTGGGATGAGATGTGTGTGAAAGTATGTACAAGAGAAAACGGAAGAGAGAGGAAA  | 3000 |
| Qy | 2994 | TGAGGTGGGGTTGGAGGAAACCCATGGGGACAGATTCCCATTCTTAGCCTAACGTTTCGTC | 3053 |
|    |      |   |      |
| Db | 3001 | TGAGGTGGGGTTGGAGGAAACCCATGGGGACAGATTCCCATTCTTAGCCTAACGTTTCGTC | 3060 |
| Qy | 3054 | ATTGCCTCGTCACATCAATGCAAAGGTCTGATTTTGTTCAGCAAACACAGTGCAAT      | 3113 |
|    |      |   |      |
| Db | 3061 | ATTGCCTCGTCACATCAATGCAAAGGTCTGATTTTGTTCAGCAAACACAGTGCAAT      | 3120 |
| Qy | 3114 | GTTCTCAGAGTGACTTTCGAAATAAATTGGGCCCAAGAGCTTTAACTCGGTCTTAAATA   | 3173 |
|    |      |   |      |
| Db | 3121 | GTTCTCAGAGTGACTTTCGAAATAAATTGGGCCCAAGAGCTTTAACTCGGTCTTAAATA   | 3180 |
| Qy | 3174 | TGCCCAAATTTTACTTTGTTTTCTTTTAATAGGCTGGGCCACATGTTGGAAATAAGCT    | 3233 |
|    |      |   |      |
| Db | 3181 | TGCCCAAATTTTACTTTGTTTTCTTTTAATAGGCTGGGCCACATGTTGGAAATAAGCT    | 3240 |
| Qy | 3234 | AGTAATGTTGTTTTCTGTCAATATTGAATGTGATGGTACAGTAAACCAAAACCAACAAT   | 3293 |

|    |      |   |      |
|----|------|---|------|
| Db | 3241 | <br>AGTAATGTTGTTTTCTGTCAATATTGAATGTGATGGTACAGTAAACCAAAACCCAACAAT  | 3300 |
| Qy | 3294 | GTGGCCAGAAAGAAAGAGCAATAATAATTAATTCACACACCATATGGATTCTATTTATAA      | 3353 |
| Db | 3301 | <br>GTGGCCAGAAAGAAAGAGCAATAATAATTAATTCACACACCATATGGATTCTATTTATAA  | 3360 |
| Qy | 3354 | ATCACCCACAACTTGTTCTTTAATTTTCATCCCAATCACTTTTTTCAGAGGCCTGTTATCA     | 3413 |
| Db | 3361 | <br>ATCACCCACAACTTGTTCTTTAATTTTCATCCCAATCACTTTTTTCAGAGGCCTGTTATCA | 3420 |
| Qy | 3414 | TAGAAGTCATTTTAGACTCTCAATTTTAAATTAATTTTGAATCACTAATATTTTCACAGT      | 3473 |
| Db | 3421 | <br>TAGAAGTCATTTTAGACTCTCAATTTTAAATTAATTTTGAATCACTAATATTTTCACAGT  | 3480 |
| Qy | 3474 | TTATTAATATATTTAATTTCTATTTAAATTTTAGATTATTTTATTACCATGTACTGAAT       | 3533 |
| Db | 3481 | <br>TTATTAATATATTTAATTTCTATTTAAATTTTAGATTATTTTATTACCATGTACTGAAT   | 3540 |
| Qy | 3534 | TTTTACATCCTGATACCCCTTCCTTCTCCATGTCAGTATCATGTTCTCTAATTATCTTGC      | 3593 |
| Db | 3541 | <br>TTTTACATCCTGATACCCCTTCCTTCTCCATGTCAGTATCATGTTCTCTAATTATCTTGC  | 3600 |
| Qy | 3594 | CAAATTTTGAAACTACACACAAAAAGCATACTTGCATTATTTATAATAAAATTGCATTCA      | 3653 |
| Db | 3601 | <br>CAAATTTTGAAACTACACACAAAAAGCATACTTGCATTATTTATAATAAAATTGCATTCA  | 3660 |
| Qy | 3654 | GTGGCTTTTTTAAAAAAATGTTTGATTCAAACTTTAACATACTGATAAGTAAGAAACAA       | 3713 |
| Db | 3661 | <br>GTGGCTTTTTT-AAAAAATGTTTGATTCAAACTTTAACATACTGATAAGTAAGAAACAA   | 3719 |
| Qy | 3714 | TTATAATTTCTTTACATACTCAAACCAAGATAGAAAAAGGTGCTATCGTTCAACTTCAA       | 3773 |
| Db | 3720 | <br>TTATAATTTCTTTACATACTCAAACCAAGATAGAAAAAGGTGCTATCGTTCAACTTCAA   | 3779 |
| Qy | 3774 | AACATGTTTCCTAGTATTAAGGACTTTAATATAGCAACAGACAAAATTATTGTTAACATG      | 3833 |
| Db | 3780 | <br>AACATGTTTCCTAGTATTAAGGACTTTAATATAGCAACAGACAAAATTATTGTTAACATG  | 3839 |
| Qy | 3834 | GATGTTACAGCTCAAAGATTTATAAAAGATTTTAACTATTTTCTCCCTTATTATCCAC        | 3893 |
| Db | 3840 | <br>GATGTTACAGCTCAAAGATTTATAAAAGATTTTAACTATTTTCTCCCTTATTATCCAC    | 3899 |
| Qy | 3894 | TGCTAATGTGGATGTATGTTCAAACACCTTTTAGTATTGATAGCTTACATATGGCCAAAG      | 3953 |
| Db | 3900 | <br>TGCTAATGTGGATGTATGTTCAAACACCTTTTAGTATTGATAGCTTACATATGGCCAAAG  | 3959 |
| Qy | 3954 | GAATACAGTTTATAGCAAAACATGGGTATGCTGTAGCTAACTTTATAAAAGTGTAATATA      | 4013 |
| Db | 3960 | <br>GAATACAGTTTATAGCAAAACATGGGTATGCTGTAGCTAACTTTATAAAAGTGTAATATA  | 4019 |
| Qy | 4014 | ACAATGTAAAAAATTATATATCTGGGAGGATTTTTTGGTTGCCTAAAGTGGCTATAGTTA      | 4073 |
| Db | 4020 | <br>ACAATGTAAAAAATTATATATCTGGGAGGATTTTTTGGTTGCCTAAAGTGGCTATAGTTA  | 4079 |
| Qy | 4074 | CTGATTTTTTTATTATGTAAGCAAAACCAATAAAAAATTTAAGTTTTTTTAACTACCTT       | 4133 |
|    |      |   |      |

Db 4080 CTGATTTTTTATTATGTAAGCAAAACCAATAAAAAATTTAAGTTTTTTTAACTACCTT 4139  
 QY 4134 ATTTTTCACACTGTACAGACACTAATTCATTAAATACTAATTGATTGTTTAAAAGAAATATA 4193  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 4140 ATTTTTCACACTGTACAGACACTAATTCATTAAATACTAATTGATTGTTTAAAAGAAATATA 4199  
 QY 4194 AATGTGACAAGTGGACATTATTTATGTTAAATATACAATTATCAAGCAAGTATGAAGTTA 4253  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 4200 AATGTGACAAGTGGACATTATTTATGTTAAATATACAATTATCAAGCAAGTATGAAGTTA 4259  
 QY 4254 TTCAATTAAAATGCCACATTTCTGGTCTCTGGGAAAAAAAAAAAAA 4299  
 |||||||||||||||||||||||| ||||| |  
 Db 4260 TTCAATTAAAATGCCACATTTCTGGTCAAAAAAAAAAAAAAGNNAGA 4305

RESULT 14

ABK94410

ID ABK94410 standard; DNA; 2972 BP.

XX

AC ABK94410;

XX

DT 27-AUG-2002 (first entry)

XX

DE DNA encoding endothelin receptor B (EDNRB), exon 7.

XX

KW Endothelin; EDN; endothelin converting enzyme; ECE; EDNRB;

KW endothelin receptor B; signaling system; cardiovascular disease;

KW coronary heart disease; hypertension; atherosclerosis; angiogenesis;

KW fatty acid metabolism; diabetes; familial hypercholesterolaemia;

KW forensic marker; transgenic animal; solid support; SNP;

KW cardiovascular regulator; gene; ds; single nucleotide polymorphism.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT variation replace(1048,A)

FT /\*tag= a

FT /standard\_name= "Single nucleotide polymorphism"

FT variation replace(1658,C)

FT /\*tag= b

FT /standard\_name= "Single nucleotide polymorphism"

FT variation replace(1912,T)

FT /\*tag= c

FT /standard\_name= "Single nucleotide polymorphism"

FT variation replace(2130,T)

FT /\*tag= d

FT /standard\_name= "Single nucleotide polymorphism"

XX

PN WO200224747-A2.

XX

PD 28-MAR-2002.

XX

PF 31-AUG-2001; 2001WO-EP010087.

XX

PR 19-SEP-2000; 2000EP-00120123.

XX

PA (EPID-) EPIDAUROS BIOTECHNOLOGIE AG.

XX  
 PI Brinkmann U, Hoffmeyer S;  
 XX  
 DR WPI; 2002-435060/46.  
 XX  
 PT Novel polynucleotide of the endothelin/endothelin converting  
 PT enzyme/receptors of endothelin and endothelin converting enzyme signaling  
 PT system associated with cardiovascular disease, useful for treating the  
 PT disease.  
 XX  
 PS Claim 1; Page; 190pp; English.  
 XX  
 CC The invention describes a polynucleotide (I) of the endothelin  
 CC (EDN)/endothelin converting enzyme (ECE)/receptors of EDN and ECE (EDNR)  
 CC signaling system which is associated with a cardiovascular disease. (I),  
 CC the gene encoding EDN, ECE or EDNR (II) or a vector (III) expressing (I)  
 CC or (II) is useful for producing cells capable of expressing a molecular  
 CC variant polypeptide which is associated with a cardiovascular disease.  
 CC (II), (III), the EDN, ECE or EDNR polypeptide, or a cell expressing a  
 CC molecular variant gene comprising (I) is useful for identifying and  
 CC obtaining a pro-drug or drug capable of modulating the activity of a  
 CC molecular variant of a polypeptide of the EDN/EDNR/ECE signaling system  
 CC or its gene product, or for identifying and obtaining an inhibitor of the  
 CC activity of a molecular variant of a polypeptide of the EDN/EDNR/ECE  
 CC signaling system or its gene product. The isolated proteins and  
 CC polynucleotides encoding them are useful for preparation of a  
 CC pharmaceutical composition for treating a cardiovascular disease such as  
 CC coronary heart disease, hypertension, atherosclerosis, or related to  
 CC abnormal angiogenesis or fatty acid metabolism e.g. diabetes and familial  
 CC hypercholesterolaemia. The gene or a polynucleotide fragment of the  
 CC EDN/ECE/EDNR signaling system are useful as forensic markers, for  
 CC creating a transgenic animal and in creation of a solid support  
 CC comprising polynucleotides, genes, vectors, polypeptides, antibodies or  
 CC host cells of the invention. This sequence encodes a fragment of the  
 CC cardioavascular regulator Endothelin receptor B (EDNRB). Note: This  
 CC sequence does not appear in the specification but has been obtained from  
 CC GenBank using information given in the invention  
 XX  
 SQ Sequence 2972 BP; 1018 A; 499 C; 465 G; 990 T; 0 U; 0 Other;

Query Match 66.4%; Score 2857; DB 6; Length 2972;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 2857; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1430 AGTCATGCTTATGCTGCTGGTGCCAGTCATTTGAAGAAAAACAGTCCTTGGAGGAAAAGC 1489  
 |||  
 Db 9 AGTCATGCTTATGCTGCTGGTGCCAGTCATTTGAAGAAAAACAGTCCTTGGAGGAAAAGC 68  
 Qy 1490 AGTCGTGCTTAAAGTTCAAAGCTAATGATCACGGATATGACAACTTCCGTTCCAGTAATA 1549  
 |||  
 Db 69 AGTCGTGCTTAAAGTTCAAAGCTAATGATCACGGATATGACAACTTCCGTTCCAGTAATA 128  
 Qy 1550 AATACAGCTCATCTTGAAAGAAGAACTATTCACTGTATTTTCTTTTATATTGGACC 1609  
 |||  
 Db 129 AATACAGCTCATCTTGAAAGAAGAACTATTCACTGTATTTTCTTTTATATTGGACC 188  
 Qy 1610 GAAGTCATTAAACAAAATGAAACATTTGCCAAAACAAAACAAAAAACTATGTATTTGCA 1669

|    |      |   |      |
|----|------|---|------|
| Db | 189  | <br>GAAGTCATTAAAACAAAATGAAACATTTGCCAAAACAAAACAAAAA<br>CTATGTATTTGCA | 248  |
| Qy | 1670 | CAGCACACTATTAAATATTAAGTGTAAATTATTTTAACACTCACAGCTACATATGACATT        | 1729 |
| Db | 249  | <br>CAGCACACTATTAAATATTAAGTGTAAATTATTTTAACACTCACAGCTACATATGACATT    | 308  |
| Qy | 1730 | TTATGAGCTGTTTACGGCATGGAAAGAAAATCAGTGGGAATTAAGAAAGCCTCGTCGTGA        | 1789 |
| Db | 309  | <br>TTATGAGCTGTTTACGGCATGGAAAGAAAATCAGTGGGAATTAAGAAAGCCTCGTCGTGA    | 368  |
| Qy | 1790 | AAGCACTTAATTTTTTACAGTTAGCACTTCAACATAGCTCTTAACAACTTCCAGGATATT        | 1849 |
| Db | 369  | <br>AAGCACTTAATTTTTTACAGTTAGCACTTCAACATAGCTCTTAACAACTTCCAGGATATT    | 428  |
| Qy | 1850 | CACACAACACTTAGGCTTAAAAATGAGCTCACTCAGAATTTCTATTCTTTCTAAAAAGAG        | 1909 |
| Db | 429  | <br>CACACAACACTTAGGCTTAAAAATGAGCTCACTCAGAATTTCTATTCTTTCTAAAAAGAG    | 488  |
| Qy | 1910 | ATTTATTTTTTAAATCAATGGGACTCTGATATAAAGGAAGAATAAGTCACTGTAAACAGA        | 1969 |
| Db | 489  | <br>ATTTATTTTTTAAATCAATGGGACTCTGATATAAAGGAAGAATAAGTCACTGTAAACAGA    | 548  |
| Qy | 1970 | ACTTTTAAATGAAGCTTAAATTACTCAATTTAAAATTTTAAAATCCTTTAAAACAACTTT        | 2029 |
| Db | 549  | <br>ACTTTTAAATGAAGCTTAAATTACTCAATTTAAAATTTTAAAATCCTTTAAAACAACTTT    | 608  |
| Qy | 2030 | TCAATTAATATTATCACACTATTATCAGATTGTAATTAGATGCAAATGAGAGAGCAGTTT        | 2089 |
| Db | 609  | <br>TCAATTAATATTATCACACTATTATCAGATTGTAATTAGATGCAAATGAGAGAGCAGTTT    | 668  |
| Qy | 2090 | AGTTGTTGCATTTTTTCGGACACTGGAAACATTTAAATGATCAGGAGGGAGTAACAGAAAG       | 2149 |
| Db | 669  | <br>AGTTGTTGCATTTTTTCGGACACTGGAAACATTTAAATGATCAGGAGGGAGTAACAGAAAG   | 728  |
| Qy | 2150 | AGCAAGGCTGTTTTTGAAAATCATTACACTTTTACTAGAAGCCCAAACCTCAGCATTCTG        | 2209 |
| Db | 729  | <br>AGCAAGGCTGTTTTTGAAAATCATTACACTTTTACTAGAAGCCCAAACCTCAGCATTCTG    | 788  |
| Qy | 2210 | CAATATGTAACCAACATGTCACAAACAAGCAGCATGTAACAGACTGGCACATGTGCCAGC        | 2269 |
| Db | 789  | <br>CAATATGTAACCAACATGTCACAAACAAGCAGCATGTAACAGACTGGCACATGTGCCAGC    | 848  |
| Qy | 2270 | TGAATTTAAAATATAATACTTTTAAAAAGAAAATTATTACATCCTTTACATTTCAGTTAAG       | 2329 |
| Db | 849  | <br>TGAATTTAAAATATAATACTTTTAAAAAGAAAATTATTACATCCTTTACATTTCAGTTAAG   | 908  |
| Qy | 2330 | ATCAAACCTCACAAAGAGAAATAGAATGTTTGAAAGGCTATCCCAAAGACTTTTTTGAA         | 2389 |
| Db | 909  | <br>ATCAAACCTCACAAAGAGAAATAGAATGTTTGAAAGGCTATCCCAAAGACTTTTTTGAA     | 968  |
| Qy | 2390 | TCTGTCATTACATACCCTGTGAAGACAATACTATCTACAATTTTTTTCAGGATTATTAAA        | 2449 |
| Db | 969  | <br>TCTGTCATTACATACCCTGTGAAGACAATACTATCTACAATTTTTTTCAGGATTATTAAA    | 1028 |
| Qy | 2450 | ATCTTCTTTTTTCACTATCGTAGCTTAAACTCTGTTTGGTTTTGTCATCTGTAAATACTT        | 2509 |
|    |      |   |      |

|    |      |   |      |
|----|------|---|------|
| Db | 1029 | ATCTTCTTTTTTCACTATCGTAGCTTAAACTCTGTTTGGTTTTGTCATCTGTAAATACTT  | 1088 |
| Qy | 2510 | ACCTACATACACTGCATGTAGATGATTAAATGAGGGCAGGCCCTGTGCTCATAGCTTTAC  | 2569 |
|    |      |   |      |
| Db | 1089 | ACCTACATACACTGCATGTAGATGATTAAATGAGGGCAGGCCCTGTGCTCATAGCTTTAC  | 1148 |
| Qy | 2570 | GATGGAGAGATGCCAGTGACCTCATAATAAAGACTGTGAACTGCCTGGTGCAGTGTCCAC  | 2629 |
|    |      |   |      |
| Db | 1149 | GATGGAGAGATGCCAGTGACCTCATAATAAAGACTGTGAACTGCCTGGTGCAGTGTCCAC  | 1208 |
| Qy | 2630 | ATGACAAAGGGGCAGGTAGCACCCCTCTCTCACCCATGCTGTGGTTAAAATGGTTTCTAGC | 2689 |
|    |      |   |      |
| Db | 1209 | ATGACAAAGGGGCAGGTAGCACCCCTCTCTCACCCATGCTGTGGTTAAAATGGTTTCTAGC | 1268 |
| Qy | 2690 | ATATGTATAATGCTATAGTTAAAATACTATTTTTTCAAAATCATACAGATTAGTACATTTA | 2749 |
|    |      |   |      |
| Db | 1269 | ATATGTATAATGCTATAGTTAAAATACTATTTTTTCAAAATCATACAGATTAGTACATTTA | 1328 |
| Qy | 2750 | ACAGCTACCTGTAAAGCTTATTACTAATTTTTGTATTATTTTTGTAAATAGCCAATAGAA  | 2809 |
|    |      |   |      |
| Db | 1329 | ACAGCTACCTGTAAAGCTTATTACTAATTTTTGTATTATTTTTGTAAATAGCCAATAGAA  | 1388 |
| Qy | 2810 | AAGTTTGCTTGACATGGTGCTTTTCTTTTCATCTAGAGGCAAACTGCTTTTGAGACCGT   | 2869 |
|    |      |   |      |
| Db | 1389 | AAGTTTGCTTGACATGGTGCTTTTCTTTTCATCTAGAGGCAAACTGCTTTTGAGACCGT   | 1448 |
| Qy | 2870 | AAGAACCTCTTAGCTTTGTGCGTTCCTGCCTAATTTTTTATATCTTCTAAGCAAAGTGCCT | 2929 |
|    |      |   |      |
| Db | 1449 | AAGAACCTCTTAGCTTTGTGCGTTCCTGCCTAATTTTTTATATCTTCTAAGCAAAGTGCCT | 1508 |
| Qy | 2930 | TAGGATAGCTTGGGATGAGATGTGTGTGAAAGTATGTACAAGAGAAAACGGAAGAGAGAG  | 2989 |
|    |      |   |      |
| Db | 1509 | TAGGATAGCTTGGGATGAGATGTGTGTGAAAGTATGTACAAGAGAAAACGGAAGAGAGAG  | 1568 |
| Qy | 2990 | GAAATGAGGTGGGGTTGGAGGAAACCCATGGGGACAGATTCCTTAGCCTAACGTT       | 3049 |
|    |      |   |      |
| Db | 1569 | GAAATGAGGTGGGGTTGGAGGAAACCCATGGGGACAGATTCCTTAGCCTAACGTT       | 1628 |
| Qy | 3050 | CGTCATTGCCTCGTCACATCAATGCAAAGGTCTGATTTTGTTCAGCAAAACACAGTG     | 3109 |
|    |      |   |      |
| Db | 1629 | CGTCATTGCCTCGTCACATCAATGCAAAGGTCTGATTTTGTTCAGCAAAACACAGTG     | 1688 |
| Qy | 3110 | CAATGTTCTCAGAGTGACTTTTGGAAATAAATTGGGCCCAAGAGCTTTAACTCGGTCTTAA | 3169 |
|    |      |   |      |
| Db | 1689 | CAATGTTCTCAGAGTGACTTTTGGAAATAAATTGGGCCCAAGAGCTTTAACTCGGTCTTAA | 1748 |
| Qy | 3170 | AATATGCCCAAATTTTTACTTTGTTTTTCTTTTAATAGGCTGGGCCACATGTTGGAAATA  | 3229 |
|    |      |   |      |
| Db | 1749 | AATATGCCCAAATTTTTACTTTGTTTTTCTTTTAATAGGCTGGGCCACATGTTGGAAATA  | 1808 |
| Qy | 3230 | AGCTAGTAATGTTGTTTTCTGTCAATATTGAATGTGATGGTACAGTAAACCAAACCCAA   | 3289 |
|    |      |   |      |
| Db | 1809 | AGCTAGTAATGTTGTTTTCTGTCAATATTGAATGTGATGGTACAGTAAACCAAACCCAA   | 1868 |
| Qy | 3290 | CAATGTGGCCAGAAAGAAAGAGCAATAATAATTAATTCACACACCATATGGATTCTATTT  | 3349 |
|    |      |   |      |
| Db | 1869 | CAATGTGGCCAGAAAGAAAGAGCAATAATAATTAATTCACACACCATATGGATTCTATTT  | 1928 |

|    |      |  |      |
|----|------|--|------|
| Qy | 3350 | ATAAATCACCCACAAACTTGTTCCTTAATTTTCATCCCAATCACTTTTTTCAGAGGCCTGTT | 3409 |
|    |      |  |      |
| Db | 1929 | ATAAATCACCCACAAACTTGTTCCTTAATTTTCATCCCAATCACTTTTTTCAGAGGCCTGTT | 1988 |
| Qy | 3410 | ATCATAGAAGTCATTTTAGACTCTCAATTTTAAATTAATTTTGAATCACTAATATTTTCA   | 3469 |
|    |      |  |      |
| Db | 1989 | ATCATAGAAGTCATTTTAGACTCTCAATTTTAAATTAATTTTGAATCACTAATATTTTCA   | 2048 |
| Qy | 3470 | CAGTTTATTAATATATTTAATTTCTATTTAAATTTTAGATTATTTTTATTACCATGTACT   | 3529 |
|    |      |  |      |
| Db | 2049 | CAGTTTATTAATATATTTAATTTCTATTTAAATTTTAGATTATTTTTATTACCATGTACT   | 2108 |
| Qy | 3530 | GAATTTTTACATCCTGATACCCTTTCCTTCTCCATGTCAGTATCATGTTCTCTAATTATC   | 3589 |
|    |      |  |      |
| Db | 2109 | GAATTTTTACATCCTGATACCCTTTCCTTCTCCATGTCAGTATCATGTTCTCTAATTATC   | 2168 |
| Qy | 3590 | TTGCCAAATTTTGAAACTACACACAAAAAGCATACCTGCATTATTTATAATAAAATTGCA   | 3649 |
|    |      |  |      |
| Db | 2169 | TTGCCAAATTTTGAAACTACACACAAAAAGCATACCTGCATTATTTATAATAAAATTGCA   | 2228 |
| Qy | 3650 | TTCAGTGGCTTTTTAAAAAAATGTTTGATTCAAACTTTAACATACTGATAAGTAAGAA     | 3709 |
|    |      |  |      |
| Db | 2229 | TTCAGTGGCTTTTTAAAAAAATGTTTGATTCAAACTTTAACATACTGATAAGTAAGAA     | 2288 |
| Qy | 3710 | ACAATTATAATTTCTTTACATACTCAAACCAAGATAGAAAAAGGTGCTATCGTTCAACT    | 3769 |
|    |      |  |      |
| Db | 2289 | ACAATTATAATTTCTTTACATACTCAAACCAAGATAGAAAAAGGTGCTATCGTTCAACT    | 2348 |
| Qy | 3770 | TCAAAACATGTTTCCTAGTATTAAGGACTTTAATATAGCAACAGACAAAATTATTGTTAA   | 3829 |
|    |      |  |      |
| Db | 2349 | TCAAAACATGTTTCCTAGTATTAAGGACTTTAATATAGCAACAGACAAAATTATTGTTAA   | 2408 |
| Qy | 3830 | CATGGATGTTACAGCTCAAAGATTTATAAAAGATTTTAACCTATTTTCTCCCTTATTAT    | 3889 |
|    |      |  |      |
| Db | 2409 | CATGGATGTTACAGCTCAAAGATTTATAAAAGATTTTAACCTATTTTCTCCCTTATTAT    | 2468 |
| Qy | 3890 | CCACTGCTAATGTGGATGTATGTTCAAACACCTTTTAGTATTGATAGCTTACATATGGCC   | 3949 |
|    |      |  |      |
| Db | 2469 | CCACTGCTAATGTGGATGTATGTTCAAACACCTTTTAGTATTGATAGCTTACATATGGCC   | 2528 |
| Qy | 3950 | AAAGGAATACAGTTTATAGCAAAACATGGGTATGCTGTAGCTAACTTTATAAAAGTGTA    | 4009 |
|    |      |  |      |
| Db | 2529 | AAAGGAATACAGTTTATAGCAAAACATGGGTATGCTGTAGCTAACTTTATAAAAGTGTA    | 2588 |
| Qy | 4010 | TATAACAATGTAAAAAATTATATATCTGGGAGGATTTTTTGGTTGCCTAAAGTGGCTATA   | 4069 |
|    |      |  |      |
| Db | 2589 | TATAACAATGTAAAAAATTATATATCTGGGAGGATTTTTTGGTTGCCTAAAGTGGCTATA   | 2648 |
| Qy | 4070 | GTTACTGATTTTTTATTATGTAAGCAAACCAATAAAAATTTAAGTTTTTTTAACTA       | 4129 |
|    |      |  |      |
| Db | 2649 | GTTACTGATTTTTTATTATGTAAGCAAACCAATAAAAATTTAAGTTTTTTTAACTA       | 2708 |
| Qy | 4130 | CCTTATTTTTTCACTGTACAGACACTAATTCATTAAATACTAATTGATTGTTTAAAGAAA   | 4189 |
|    |      |  |      |
| Db | 2709 | CCTTATTTTTTCACTGTACAGACACTAATTCATTAAATACTAATTGATTGTTTAAAGAAA   | 2768 |

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Qy      4190 TATAAATGTGACAAGTGGACATTATTTATGTTAAATATACAATTATCAAGCAAGTATGAA 4249
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2769 TATAAATGTGACAAGTGGACATTATTTATGTTAAATATACAATTATCAAGCAAGTATGAA 2828

Qy      4250 GTTATTCAATTAAAAATGCCACATTTCTGGTCTCTGGG 4286
          ||||||||||||||||||||||||||||||||||
Db      2829 GTTATTCAATTAAAAATGCCACATTTCTGGTCTCTGGG 2865

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RESULT 15

ABQ77402/c

ID ABQ77402 standard; DNA; 183337 BP.

XX

AC ABQ77402;

XX

DT 10-MAY-2003 (first entry)

XX

DE Human EDNRB DNA.

XX

KW Human; EDNRB; vascular disease; cardiant; antiarteriosclerotic; stroke;

KW cerebroprotective; gene therapy; coronary artery disease; ischaemia;

KW myocardial infarction; peripheral vascular disease; pulmonary embolism;

KW venous thromboembolism; forensic; paternity testing; GI12597038; gene;

KW SNP; single nucleotide polymorphism; ds.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT variation replace(75672,t)

FT /\*tag= a

FT /standard\_name= "SNP"

FT /note= "Single nucleotide polymorphism (ID G337a4) which  
 FT does not change the EDNBR protein"

XX

PN WO2003016494-A2.

XX

PD 27-FEB-2003.

XX

PF 16-AUG-2002; 2002WO-US026343.

XX

PR 16-AUG-2001; 2001US-0313097P.

PR 05-OCT-2001; 2001US-0327485P.

PR 14-DEC-2001; 2001US-00020141.

XX

PA (VITI-) VITIVITY INC.

XX

PI Mccarthy J, Ableson A;

XX

DR WPI; 2003-300617/29.

DR P-PSDB; ABG74670.

XX

PT Identifying a subject as a candidate for a particular course of therapy

PT to treat a vascular disease or disorder, e.g. stroke, myocardial

PT infarction or ischemia by determining the identity of the nucleotide

PT present at specific positions.

XX

PS Claim 1; Fig 5; 568pp; English.



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XX
CC   This invention describes a novel method for identifying a subject as a
CC   candidate for a particular course of therapy to treat a vascular disease
CC   or disorder. The method comprises determining the identity of the
CC   nucleotide present at specific positions, or their complements, and
CC   identifying the subject as a candidate for a particular clinical course
CC   of therapy based on the identity of the nucleotide present in that
CC   specific position. The method can be used for identifying a subject who
CC   is a candidate for further diagnostic evaluation of a vascular disease or
CC   disorder and selecting a clinical course of therapy. The products of the
CC   invention have cardiant, antiarteriosclerotic and cerebroprotective
CC   activity and can be used for gene therapy. The methods disclosed are
CC   useful for treating a vascular disease, e.g. atherosclerosis, coronary
CC   artery disease, myocardial infarction, ischaemia, stroke, peripheral
CC   vascular diseases, venous thromboembolism and pulmonary embolism. The DNA
CC   sequences are useful as fingerprint for detecting different individuals
CC   within the same species applicable in forensic studies and paternity
CC   testing. This sequence encodes the human EDNBR gene represented in
CC   GI12597038, used to illustrate the method of the invention
XX
SQ   Sequence 183337 BP; 56451 A; 33595 C; 34663 G; 58628 T; 0 U; 0 Other;

Query Match          66.1%;  Score 2841.8;  DB 7;  Length 183337;
Best Local Similarity 99.9%;  Pred. No. 0;
Matches 2854;  Conservative 0;  Mismatches 2;  Indels 1;  Gaps 1;

Qy      1430 AGTCATGCTTATGCTGCTGGTGCCAGTCATTTGAAGAAAAACAGTCCTTGGAGGAAAAGC 1489
          |||
Db      72830 AGTCATGCTTATGCTGCTGGTGCCAGTCATTTGAAGAAAAACAGTCCTTGGAGGAAAAGC 72771

Qy      1490 AGTCGTGCTTAAAGTTCAAAGCTAATGATCACGGATATGACAACTTCCGTTCCAGTAATA 1549
          |||
Db      72770 AGTCGTGCTTAAAGTTCAAAGCTAATGATCACGGATATGACAACTTCCGTTCCAGTAATA 72711

Qy      1550 AATACAGCTCATCTTGAAAGAAGAACTATTCACTGTATTTTCATTTTCTTTATATTGGACC 1609
          |||
Db      72710 AATACAGCTCATCTTGAAAGAAGAACTATTCACTGTATTTTCATTTTCTTTATATTGGACC 72651

Qy      1610 GAAGTCATTAAAACAAAATGAAACATTTGCCAAAACAAAACAAAAAACTATGTATTTGCA 1669
          |||
Db      72650 GAAGTCATTAAAACAAAATGAAACATTTGCCAAAACAAAACAAAAAACTATGTATTTGCA 72591

Qy      1670 CAGCACACTATTAAATATTAAGTGTAATTATTTTAACACTCACAGCTACATATGACATT 1729
          |||
Db      72590 CAGCACACTATTAAATATTAAGTGTAATTATTTTAACACTCACAGCTACATATGACATT 72531

Qy      1730 TTATGAGCTGTTTACGGCATGGAAAGAAAATCAGTGGGAATTAAGAAAGCCTCGTCGTGA 1789
          |||
Db      72530 TTATGAGCTGTTTACGGCATGGAAAGAAAATCAGTGGGAATTAAGAAAGCCTCGTCGTGA 72471

Qy      1790 AAGCACTTAATTTTTTACAGTTAGCACTTCAACATAGCTCTTAACAACCTCCAGGATATT 1849
          |||
Db      72470 AAGCACTTAATTTTTTACAGTTAGCACTTCAACATAGCTCTTAACAACCTCCAGGATATT 72411

Qy      1850 CACACAACACTTAGGCTTAAAAATGAGCTCACTCAGAATTTCTATTCTTTCTAAAAAGAG 1909
          |||
Db      72410 CACACAACACTTAGGCTTAAAAATGAGCTCACTCAGAATTTCTATTCTTTCTAAAAAGAG 72351

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|    |       |  |       |
|----|-------|--|-------|
| Qy | 1910  | ATTTATTTTAAATCAATGGGACTCTGATATAAAGGAAGAATAAGTCACTGTAAACAGA     | 1969  |
|    |       |  |       |
| Db | 72350 | ATTTATTTTAAATCAATGGGACTCTGATATAAAGGAAGAATAAGTCACTGTAAACAGA     | 72291 |
| Qy | 1970  | ACTTTTAAATGAAGCTTAAATTACTCAATTTAAAATTTTAAAATCCTTTAAAACAACTTT   | 2029  |
|    |       |  |       |
| Db | 72290 | ACTTTTAAATGAAGCTTAAATTACTCAATTTAAAATTTTAAAATCCTTTAAAACAACTTT   | 72231 |
| Qy | 2030  | TCAATTAATATTATCACACTATTATCAGATTGTAATTAGATGCAAATGAGAGAGCAGTTT   | 2089  |
|    |       |  |       |
| Db | 72230 | TCAATTAATATTATCACACTATTATCAGATTGTAATTAGATGCAAATGAGAGAGCAGTTT   | 72171 |
| Qy | 2090  | AGTTGTTGCATTTTTTCGGACACTGGAAACATTTAAATGATCAGGAGGGAGTAACAGAAAAG | 2149  |
|    |       |  |       |
| Db | 72170 | AGTTGTTGCATTTTTTCGGACACTGGAAACATTTAAATGATCAGGAGGGAGTAACAGAAAAG | 72111 |
| Qy | 2150  | AGCAAGGCTGTTTTTGAAAATCATTACACTTTCCTAGTAAGCCCAAACCTCAGCATTCTG   | 2209  |
|    |       |  |       |
| Db | 72110 | AGCAAGGCTGTTTTTGAAAATCATTACACTTTCCTAGTAAGCCCAAACCTCAGCATTCTG   | 72051 |
| Qy | 2210  | CAATATGTAACCAACATGTCACAAACAAGCAGCATGTAACAGACTGGCACATGTGCCAGC   | 2269  |
|    |       |  |       |
| Db | 72050 | CAATATGTAACCAACATGTCACAAACAAGCAGCATGTAACAGACTGGCACATGTGCCAGC   | 71991 |
| Qy | 2270  | TGAATTTAAAATATAATACTTTTAAAAAGAAAATTATTACATCCTTTACATTAGTTAAG    | 2329  |
|    |       |  |       |
| Db | 71990 | TGAATTTAAAATATAATACTTTTAAAAAGAAAATTATTACATCCTTTACATTAGTTAAG    | 71931 |
| Qy | 2330  | ATCAAACCTCACAAAGAGAAATAGAATGTTTGAAAGGCTATCCCAAAGACTTTTTTGAA    | 2389  |
|    |       |  |       |
| Db | 71930 | ATCAAACCTCACAAAGAGAAATAGAATGTTTGAAAGGCTATCCCAAAGACTTTTTTGAA    | 71871 |
| Qy | 2390  | TCTGTCATTACATACCCTGTGAAGACAATACTATCTACAATTTTTTCAGGATTATTTAA    | 2449  |
|    |       |  |       |
| Db | 71870 | TCTGTCATTACATACCCTGTGAAGACAATACTATCTACAATTTTTTCAGGATTATTTAA    | 71811 |
| Qy | 2450  | ATCTTCTTTTTTCACTATCGTAGCTTAAACTCTGTTTGGTTTTGTCATCTGTAAATACTT   | 2509  |
|    |       |  |       |
| Db | 71810 | ATCTTCTTCTTTCACTATCGTAGCTTAAACTCTGTTTGGTTTTGTCATCTGTAAATACTT   | 71751 |
| Qy | 2510  | ACCTACATACACTGCATGTAGATGATTAAATGAGGGCAGGCCCTGTGCTCATAGCTTTAC   | 2569  |
|    |       |  |       |
| Db | 71750 | ACCTACATACACTGCATGTAGATGATTAAATGAGGGCAGGCCCTGTGCTCATAGCTTTAC   | 71691 |
| Qy | 2570  | GATGGAGAGATGCCAGTGACCTCATAATAAAGACTGTGAACTGCCTGGTGCAGTGTCCAC   | 2629  |
|    |       |  |       |
| Db | 71690 | GATGGAGAGATGCCAGTGACCTCATAATAAAGACTGTGAACTGCCTGGTGCAGTGTCCAC   | 71631 |
| Qy | 2630  | ATGACAAAGGGGCAGGTAGCACCCCTCTCTACCCATGCTGTGGTTAAAATGGTTTCTAGC   | 2689  |
|    |       |  |       |
| Db | 71630 | ATGACAAAGGGGCAGGTAGCACCCCTCTCTACCCATGCTGTGGTTAAAATGGTTTCTAGC   | 71571 |
| Qy | 2690  | ATATGTATAATGCTATAGTTAAATACTATTTTTCAAATCATACAGATTAGTACATTTA     | 2749  |
|    |       |  |       |
| Db | 71570 | ATATGTATAATGCTATAGTTAAATACTATTTTTCAAATCATACAGATTAGTACATTTA     | 71511 |

|    |       |  |       |
|----|-------|--|-------|
| Qy | 2750  | ACAGCTACCTGTAAAGCTTATTACTAATTTTTGTATTATTTTGTAAATAGCCAATAGAA    | 2809  |
|    |       |  |       |
| Db | 71510 | ACAGCTACCTGTAAAGCTTATTACTAATTTTTGTATTATTTTGTAAATAGCCAATAGAA    | 71451 |
| Qy | 2810  | AAGTTTGCTTGACATGGTGCTTTTCTTTCATCTAGAGGCAAACTGCTTTTGGAGACCGT    | 2869  |
|    |       |  |       |
| Db | 71450 | AAGTTTGCTTGACATGGTGCTTTTCTTTCATCTAGAGGCAAACTGCTTTTGGAGACCGT    | 71391 |
| Qy | 2870  | AAGAACCTCTTAGCTTTGTGCGTTCCTGCCTAATTTTATATCTTCTAAGCAAAGTGCCT    | 2929  |
|    |       |  |       |
| Db | 71390 | AAGAACCTCTTAGCTTTGTGCGTTCCTGCCTAATTTTATATCTTCTAAGCAAAGTGCCT    | 71331 |
| Qy | 2930  | TAGGATAGCTTGGGATGAGATGTGTGTGAAAGTATGTACAAGAGAAAACGGAAGAGAGAG   | 2989  |
|    |       |  |       |
| Db | 71330 | TAGGATAGCTTGGGATGAGATGTGTGTGAAAGTATGTACAAGAGAAAACGGAAGAGAGAG   | 71271 |
| Qy | 2990  | GAAATGAGGTGGGGTTGGAGGAAACCCATGGGGACAGATTTCCATTCTTAGCCTAACGTT   | 3049  |
|    |       |  |       |
| Db | 71270 | GAAATGAGGTGGGGTTGGAGGAAACCCATGGGGACAGATTTCCATTCTTAGCCTAACGTT   | 71211 |
| Qy | 3050  | CGTCATTGCCTCGTCACATCAATGCAAAGGTCTGATTTTGTTCAGCAAACACAGTG       | 3109  |
|    |       |  |       |
| Db | 71210 | CGTCATTGCCTCGTCACATCAATGCAAAGGTCTGATTTTGTTCAGCAAACACAGTG       | 71151 |
| Qy | 3110  | CAATGTTCTCAGAGTGACTTTTCGAAATAAATTGGGCCCAAGAGCTTTAACTCGGTCTTAA  | 3169  |
|    |       |  |       |
| Db | 71150 | CAATGTTCTCAGAGTGACTTTTCGAAATAAATTGGGCCCAAGAGCTTTAACTCGGTCTTAA  | 71091 |
| Qy | 3170  | AATATGCCCAAATTTTTACTTTGTTTTCTTTTAATAGGCTGGGCCACATGTTGGAAATA    | 3229  |
|    |       |  |       |
| Db | 71090 | AATATGCCCAAATTTTTACTTTGTTTTCTTTTAATAGGCTGGGCCACATGTTGGAAATA    | 71031 |
| Qy | 3230  | AGCTAGTAATGTTGTTTTCTGTCAATATTGAATGTGATGGTACAGTAAACCAAACCCAA    | 3289  |
|    |       |  |       |
| Db | 71030 | AGCTAGTAATGTTGTTTTCTGTCAATATTGAATGTGATGGTACAGTAAACCAAACCCAA    | 70971 |
| Qy | 3290  | CAATGTGGCCAGAAAGAAAGAGCAATAATAATTAATTCACACACCATATGGATTCTATTT   | 3349  |
|    |       |  |       |
| Db | 70970 | CAATGTGGCCAGAAAGAAAGAGCAATAATAATTAATTCACACACCATATGGATTCTATTT   | 70911 |
| Qy | 3350  | ATAAATCACCCACAAACTTGTTCTTTAATTTTCATCCCAATCACTTTTTTCAGAGGCCTGTT | 3409  |
|    |       |  |       |
| Db | 70910 | ATAAATCACCCACAAACTTGTTCTTTAATTTTCATCCCAATCACTTTTTTCAGAGGCCTGTT | 70851 |
| Qy | 3410  | ATCATAGAAGTCATTTTAGACTCTCAATTTTAAATTAATTTTGAATCACTAATATTTTCA   | 3469  |
|    |       |  |       |
| Db | 70850 | ATCATAGAAGTCATTTTAGACTCTCAATTTTAAATTAATTTTGAATCACTAATATTTTCA   | 70791 |
| Qy | 3470  | CAGTTTATTAATATATTTAATTTCTATTTAAATTTTAGATTATTTTATTACCATGTACT    | 3529  |
|    |       |  |       |
| Db | 70790 | CAGTTTATTAATATATTTAATTTCTATTTAAATTTTAGATTATTTTATTACCATGTACT    | 70731 |
| Qy | 3530  | GAATTTTACATCCTGATACCTTTTCTTCCATGTCAGTATCATGTTCTCTAATTATC       | 3589  |
|    |       |  |       |
| Db | 70730 | GAATTTTACATCCTGATACCTTTTCTTCCATGTCAGTATCATGTTCTCTAATTATC       | 70671 |
| Qy | 3590  | TTGCCAAATTTTGAAACTACACACAAAAGCATACTTGCAATTATTTATAATAAAATTGCA   | 3649  |

|    |       |  |       |
|----|-------|--|-------|
| Db | 70670 | <br>TTGCCAAATTTTGAAACTACACACAAAAAGCATACTTGCATTATTTATAATAAAATTGCA | 70611 |
| Qy | 3650  | TTCACTGGCTTTTAAAAAAATGTTTGATTCAAACTTTAACATACTGATAAGTAAGAA        | 3709  |
| Db | 70610 | <br>TTCACTGGCTTTT-AAAAAATGTTTGATTCAAACTTTAACATACTGATAAGTAAGAA    | 70552 |
| Qy | 3710  | ACAATTATAATTTCTTTACATACTCAAAACCAAGATAGAAAAAGGTGCTATCGTTCAACT     | 3769  |
| Db | 70551 | <br>ACAATTATAATTTCTTTACATACTCAAAACCAAGATAGAAAAAGGTGCTATCGTTCAACT | 70492 |
| Qy | 3770  | TCAAAACATGTTTCCTAGTATTAAGGACTTTAATATAGCAACAGACAAAATTATTGTTAA     | 3829  |
| Db | 70491 | <br>TCAAAACATGTTTCCTAGTATTAAGGACTTTAATATAGCAACAGACAAAATTATTGTTAA | 70432 |
| Qy | 3830  | CATGGATGTTACAGCTCAAAAGATTTATAAAAGATTTTAACCTATTTTCTCCCTTATTAT     | 3889  |
| Db | 70431 | <br>CATGGATGTTACAGCTCAAAAGATTTATAAAAGATTTTAACCTATTTTCTCCCTTATTAT | 70372 |
| Qy | 3890  | CCACTGCTAATGTGGATGTATGTTCAAACACCTTTTAGTATTGATAGCTTACATATGGCC     | 3949  |
| Db | 70371 | <br>CCACTGCTAATGTGGATGTATGTTCAAACACCTTTTAGTATTGATAGCTTACATATGGCC | 70312 |
| Qy | 3950  | AAAGGAATACAGTTTATAGCAAAACATGGGTATGCTGTAGCTAACTTTATAAAAGTGTA      | 4009  |
| Db | 70311 | <br>AAAGGAATACAGTTTATAGCAAAACATGGGTATGCTGTAGCTAACTTTATAAAAGTGTA  | 70252 |
| Qy | 4010  | TATAACAATGTAAAAAATTATATATCTGGGAGGATTTTTTGGTTGCCTAAAGTGGCTATA     | 4069  |
| Db | 70251 | <br>TATAACAATGTAAAAAATTATATATCTGGGAGGATTTTTTGGTTGCCTAAAGTGGCTATA | 70192 |
| Qy | 4070  | GTTACTGATTTTTTATTATGTAAGCAAACCAATAAAAATTTAAGTTTTTTTAAACACTA      | 4129  |
| Db | 70191 | <br>GTTACTGATTTTTTATTATGTAAGCAAACCAATAAAAATTTAAGTTTTTTTAAACACTA  | 70132 |
| Qy | 4130  | CCTTATTTTTTCACTGTACAGACACTAATTCATTAAATACTAATTGATTGTTTAAAGAAA     | 4189  |
| Db | 70131 | <br>CCTTATTTTTTCACTGTACAGACACTAATTCATTAAATACTAATTGATTGTTTAAAGAAA | 70072 |
| Qy | 4190  | TATAAATGTGACAAGTGGACATTATTTATGTTAAATATACAATTATCAAGCAAGTATGAA     | 4249  |
| Db | 70071 | <br>TATAAATGTGACAAGTGGACATTATTTATGTTAAATATACAATTATCAAGCAAGTATGAA | 70012 |
| Qy | 4250  | GTTATTCAATTAAAATGCCACATTTCTGGTCTCTGGG                            | 4286  |
| Db | 70011 | <br>GTTATTCAATTAAAATGCCACATTTCTGGTCTCTGGG                        | 69975 |

Search completed: May 14, 2004, 01:25:01  
Job time : 1517.76 secs

OM nucleic - nucleic search, using sw model

Run on: May 14, 2004, 00:25:48 ; Search time 266.574 Seconds  
(without alignments)  
8953.776 Million cell updates/sec

Title: US-09-931-157-2  
Perfect score: 4301  
Sequence: 1 gagacattccggtgggggac.....ctgggaaaaaaaaaaaaaaaa 4301

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued\_Patents\_NA:\*  
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2: /cgn2\_6/ptodata/2/ina/5B\_COMB.seq:\*  
3: /cgn2\_6/ptodata/2/ina/6A\_COMB.seq:\*  
4: /cgn2\_6/ptodata/2/ina/6B\_COMB.seq:\*  
5: /cgn2\_6/ptodata/2/ina/PCTUS\_COMB.seq:\*  
6: /cgn2\_6/ptodata/2/ina/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result<br>No. | %      |       | Query  |    |                    | Description       |
|---------------|--------|-------|--------|----|--------------------|-------------------|
|               | Score  | Match | Length | DB | ID                 |                   |
| 1             | 4301   | 100.0 | 4301   | 4  | US-08-121-446-3    | Sequence 3, Appli |
| 2             | 1691.8 | 39.3  | 1873   | 3  | US-08-910-864-13   | Sequence 13, Appl |
| 3             | 1466.8 | 34.1  | 1470   | 4  | US-09-016-434-1203 | Sequence 1203, Ap |
| 4             | 1070.4 | 24.9  | 1321   | 4  | US-09-175-658B-20  | Sequence 20, Appl |
| 5             | 395.8  | 9.2   | 4079   | 4  | US-09-016-434-1257 | Sequence 1257, Ap |
| 6             | 395.8  | 9.2   | 4105   | 4  | US-08-121-446-1    | Sequence 1, Appli |
| 7             | 132.2  | 3.1   | 1700   | 5  | PCT-US92-02091-1   | Sequence 1, Appli |
| 8             | 114.6  | 2.7   | 246240 | 2  | US-08-724-394A-20  | Sequence 20, Appl |
| 9             | 114.6  | 2.7   | 246240 | 2  | US-08-724-394A-21  | Sequence 21, Appl |
| 10            | 114.6  | 2.7   | 246240 | 2  | US-08-724-394A-22  | Sequence 22, Appl |
| 11            | 108.8  | 2.5   | 1584   | 5  | PCT-US92-02091-5   | Sequence 5, Appli |

|   |    |       |     |        |   |                    |                   |
|---|----|-------|-----|--------|---|--------------------|-------------------|
| c | 12 | 107.2 | 2.5 | 801    | 4 | US-09-175-658B-25  | Sequence 25, Appl |
|   | 13 | 106.6 | 2.5 | 1205   | 3 | US-09-120-772-1    | Sequence 1, Appli |
|   | 14 | 106.6 | 2.5 | 1413   | 4 | US-09-016-434-1275 | Sequence 1275, Ap |
|   | 15 | 106   | 2.5 | 1726   | 4 | US-09-016-434-1215 | Sequence 1215, Ap |
|   | 16 | 106   | 2.5 | 1726   | 5 | PCT-US92-02091-3   | Sequence 3, Appli |
|   | 17 | 101.6 | 2.4 | 1352   | 4 | US-09-016-434-1233 | Sequence 1233, Ap |
|   | 18 | 101.6 | 2.4 | 1352   | 5 | PCT-US92-02091-7   | Sequence 7, Appli |
|   | 19 | 98.6  | 2.3 | 1563   | 1 | US-08-279-590A-1   | Sequence 1, Appli |
|   | 20 | 98.6  | 2.3 | 1563   | 1 | US-08-910-092-1    | Sequence 1, Appli |
|   | 21 | 89.6  | 2.1 | 259    | 4 | US-09-016-434-921  | Sequence 921, App |
|   | 22 | 88    | 2.0 | 1842   | 4 | US-09-170-496D-91  | Sequence 91, Appl |
|   | 23 | 88    | 2.0 | 1842   | 4 | US-09-170-496D-211 | Sequence 211, App |
|   | 24 | 88    | 2.0 | 4953   | 4 | US-09-620-312D-240 | Sequence 240, App |
|   | 25 | 84.8  | 2.0 | 4156   | 1 | US-08-465-687A-1   | Sequence 1, Appli |
|   | 26 | 84.8  | 2.0 | 4156   | 3 | US-09-030-970-1    | Sequence 1, Appli |
|   | 27 | 84.8  | 2.0 | 4156   | 4 | US-09-520-210-1    | Sequence 1, Appli |
|   | 28 | 84.8  | 2.0 | 4156   | 5 | PCT-US94-11843-1   | Sequence 1, Appli |
|   | 29 | 80.6  | 1.9 | 1443   | 3 | US-08-959-381A-3   | Sequence 3, Appli |
|   | 30 | 80.6  | 1.9 | 1446   | 4 | US-09-170-496D-81  | Sequence 81, Appl |
|   | 31 | 80.6  | 1.9 | 1446   | 4 | US-09-170-496D-207 | Sequence 207, App |
|   | 32 | 80.6  | 1.9 | 1626   | 3 | US-08-959-381A-4   | Sequence 4, Appli |
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| c | 34 | 63.4  | 1.5 | 20674  | 4 | US-09-641-638-651  | Sequence 651, App |
|   | 35 | 63.2  | 1.5 | 595    | 1 | US-08-784-289-1    | Sequence 1, Appli |
|   | 36 | 62.8  | 1.5 | 1652   | 4 | US-09-721-870-17   | Sequence 17, Appl |
|   | 37 | 61.8  | 1.4 | 1605   | 4 | US-09-676-970-1    | Sequence 1, Appli |
|   | 38 | 61.8  | 1.4 | 1605   | 4 | US-09-676-972B-1   | Sequence 1, Appli |
|   | 39 | 61.8  | 1.4 | 1605   | 4 | US-09-016-434-1231 | Sequence 1231, Ap |
|   | 40 | 61.8  | 1.4 | 1605   | 4 | US-09-676-941A-1   | Sequence 1, Appli |
|   | 41 | 61.8  | 1.4 | 1605   | 4 | US-10-013-846-3    | Sequence 3, Appli |
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|   | 43 | 61.8  | 1.4 | 4571   | 1 | US-08-232-144-5    | Sequence 5, Appli |
|   | 44 | 60.8  | 1.4 | 511    | 4 | US-09-175-658B-22  | Sequence 22, Appl |
| c | 45 | 60.6  | 1.4 | 1864   | 4 | US-09-468-265-4    | Sequence 4, Appli |

#### ALIGNMENTS

#### RESULT 1

US-08-121-446-3

; Sequence 3, Application US/08121446

; Patent No. 6313276

; GENERAL INFORMATION:

; APPLICANT: IMURA, HIROO

; APPLICANT: NAKAO, KAZUWA

; APPLICANT: NAKANISHI, SHIGETADA

; TITLE OF INVENTION: A HUMAN ENDOTHELIN RECEPTOR

; NUMBER OF SEQUENCES: 4

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: MORRISON & FOERSTER

; STREET: 755 Page Mill Road

; CITY: Palo Alto

; STATE: California

; COUNTRY: USA

; ZIP: 94304-1018

; COMPUTER READABLE FORM:

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; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/121,446
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/911,684
; FILING DATE: 10-JUL-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: CIOTTI, THOMAS E.
; REGISTRATION NUMBER: 21,013
; REFERENCE/DOCKET NUMBER: 29900-20324.00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4301 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 238..1566
US-08-121-446-3

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Query Match          100.0%; Score 4301; DB 4; Length 4301;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4301; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 GAGACATTCCGGTGGGGGACTCTGGCCAGCCCAGCAACGTGGATCCTGAGAGCACTCCC 60
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Db      1 GAGACATTCCGGTGGGGGACTCTGGCCAGCCCAGCAACGTGGATCCTGAGAGCACTCCC 60

Qy     61 AGGTAGGCATTTGCCCCGGTGGGACGCCTTGCCAGAGCAGTGTGTGGCAGGCCCGCTGG 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy    121 AGGATCAACACAGTGGCTGAACACTGGGAAGGAACTGGTACTTGGAGTCTGGACATCTGA 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 AGGATCAACACAGTGGCTGAACACTGGGAAGGAACTGGTACTTGGAGTCTGGACATCTGA 180

Qy    181 AACTTGGCTCTGAAACTGCGGAGCGGCCACCGGACGCCTTCTGGAGCAGGTAGCAGCATG 240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 AACTTGGCTCTGAAACTGCGGAGCGGCCACCGGACGCCTTCTGGAGCAGGTAGCAGCATG 240

Qy    241 CAGCCGCCTCCAAGTCTGTGCGGACGCGCCCTGGTTGCGCTGGTTCTTGCCTGCGGCCTG 300
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 CAGCCGCCTCCAAGTCTGTGCGGACGCGCCCTGGTTGCGCTGGTTCTTGCCTGCGGCCTG 300

Qy    301 TCGCGGATCTGGGGAGAGGAGAGAGGCTTCCCGCCTGACAGGGCCACTCCGCTTTTGCAA 360
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|    |      |   |      |
|----|------|---|------|
| Qy | 361  | ACCGCAGAGATAATGACGCCACCCACTAAGACCTTATGGCCCAAGGGTTCCAACGCCAGT    | 420  |
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| Db | 361  | ACCGCAGAGATAATGACGCCACCCACTAAGACCTTATGGCCCAAGGGTTCCAACGCCAGT    | 420  |
| Qy | 421  | CTGGCGCGGTTCGTTGGCACCTGCGGAGGTGCCTAAAGGAGACAGGACGGCAGGATCTCCG   | 480  |
|    |      |   |      |
| Db | 421  | CTGGCGCGGTTCGTTGGCACCTGCGGAGGTGCCTAAAGGAGACAGGACGGCAGGATCTCCG   | 480  |
| Qy | 481  | CCACGCACCATCTCCCCTCCCCCGTGCCAAGGACCCATCGAGATCAAGGAGACTTTCAA     | 540  |
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| Db | 481  | CCACGCACCATCTCCCCTCCCCCGTGCCAAGGACCCATCGAGATCAAGGAGACTTTCAA     | 540  |
| Qy | 541  | TACATCAACACGGTTGTGTCTGCCTTGTGTTTCGTGCTGGGGATCATCGGGAAGTCCACA    | 600  |
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| Qy | 601  | CTTCTGAGAATTATCTACAAGAACAAGTGCATGCGAAACGGTCCCAATATCTTGATCGCC    | 660  |
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| Db | 601  | CTTCTGAGAATTATCTACAAGAACAAGTGCATGCGAAACGGTCCCAATATCTTGATCGCC    | 660  |
| Qy | 661  | AGCTTGGCTCTGGGAGACCTGCTGCACATCGTCATTGACATCCCTATCAATGTCTACAAG    | 720  |
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| Db | 661  | AGCTTGGCTCTGGGAGACCTGCTGCACATCGTCATTGACATCCCTATCAATGTCTACAAG    | 720  |
| Qy | 721  | CTGCTGGCAGAGGACTGGCCATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTCATACAG    | 780  |
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| Qy | 781  | AAAGCCTCCGTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATATCGA    | 840  |
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| Db | 781  | AAAGCCTCCGTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATATCGA    | 840  |
| Qy | 841  | GCTGTTGCTTCTTGGAGTAGAATTAAAGGAATTGGGGTTCCAAAATGGACAGCAGTAGAA    | 900  |
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| Db | 841  | GCTGTTGCTTCTTGGAGTAGAATTAAAGGAATTGGGGTTCCAAAATGGACAGCAGTAGAA    | 900  |
| Qy | 901  | ATTGTTTTGATTTGGGTGGTCTCTGTGGTTCTGGCTGTCCCTGAAGCCATAGGTTTTGAT    | 960  |
|    |      |   |      |
| Db | 901  | ATTGTTTTGATTTGGGTGGTCTCTGTGGTTCTGGCTGTCCCTGAAGCCATAGGTTTTGAT    | 960  |
| Qy | 961  | ATAATTACGATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTTTCTAG  | 1020 |
|    |      |   |      |
| Db | 961  | ATAATTACGATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTTTCTAG  | 1020 |
| Qy | 1021 | AAGACAGCTTTCATGCAGTTTTTACAAGACAGCAAAAGATTGGTGGCTGTTTCTAGTTTCTAT | 1080 |
|    |      |   |      |
| Db | 1021 | AAGACAGCTTTCATGCAGTTTTTACAAGACAGCAAAAGATTGGTGGCTGTTTCTAGTTTCTAT | 1080 |
| Qy | 1081 | TTCTGCTTGCCATTGGCCATCACTGCATTTTTTTTATACACTAATGACCTGTGAAATGTTG   | 1140 |
|    |      |   |      |
| Db | 1081 | TTCTGCTTGCCATTGGCCATCACTGCATTTTTTTTATACACTAATGACCTGTGAAATGTTG   | 1140 |
| Qy | 1141 | AGAAAGAAAAGTGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAAGTG    | 1200 |
|    |      |   |      |
| Db | 1141 | AGAAAGAAAAGTGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAAGTG    | 1200 |



|    |      |  |      |
|----|------|--|------|
| Qy | 1201 | GCCAAAACCGTCTTTTGCCTGGTCCTTGTCTTTGCCCTCTGCTGGCTTCCCCTTCACCTC   | 1260 |
| Db | 1201 | GCCAAAACCGTCTTTTGCCTGGTCCTTGTCTTTGCCCTCTGCTGGCTTCCCCTTCACCTC   | 1260 |
| Qy | 1261 | AGCAGGATTCTGAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGAACTTTTG   | 1320 |
| Db | 1261 | AGCAGGATTCTGAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGAACTTTTG   | 1320 |
| Qy | 1321 | AGCTTCTGTTGGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCCTGCATT    | 1380 |
| Db | 1321 | AGCTTCTGTTGGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCCTGCATT    | 1380 |
| Qy | 1381 | AACCCAATTGCTCTGTATTTGGTGAGCAAAAGATTCAAAAAGCTTTAAGTCATGCTTA     | 1440 |
| Db | 1381 | AACCCAATTGCTCTGTATTTGGTGAGCAAAAGATTCAAAAAGCTTTAAGTCATGCTTA     | 1440 |
| Qy | 1441 | TGCTGCTGGTGCCAGTCATTTGAAGAAAAACAGTCCTTGGAGGAAAAGCAGTCGTGCTTA   | 1500 |
| Db | 1441 | TGCTGCTGGTGCCAGTCATTTGAAGAAAAACAGTCCTTGGAGGAAAAGCAGTCGTGCTTA   | 1500 |
| Qy | 1501 | AAGTTCAAAGCTAATGATCACGGATATGACAACTCCGTTCAGTAATAAATACAGCTCA     | 1560 |
| Db | 1501 | AAGTTCAAAGCTAATGATCACGGATATGACAACTCCGTTCAGTAATAAATACAGCTCA     | 1560 |
| Qy | 1561 | TCTTGAAAGAAGAACTATTCAGTGTATTTTCTTTATATTGGACCGAAGTCATTAA        | 1620 |
| Db | 1561 | TCTTGAAAGAAGAACTATTCAGTGTATTTTCTTTATATTGGACCGAAGTCATTAA        | 1620 |
| Qy | 1621 | AACAAAATGAAACATTTGCCAAAACAAAACAAAAACTATGTATTTGCACAGCACACTAT    | 1680 |
| Db | 1621 | AACAAAATGAAACATTTGCCAAAACAAAACAAAAACTATGTATTTGCACAGCACACTAT    | 1680 |
| Qy | 1681 | TAAAATATTAAGTGTAATTATTTTAACACTCACAGCTACATATGACATTTTATGAGCTGT   | 1740 |
| Db | 1681 | TAAAATATTAAGTGTAATTATTTTAACACTCACAGCTACATATGACATTTTATGAGCTGT   | 1740 |
| Qy | 1741 | TTACGGCATGGAAAGAAAATCAGTGGGAATTAAGAAAGCCTCGTCGTGAAAGCACTTAAT   | 1800 |
| Db | 1741 | TTACGGCATGGAAAGAAAATCAGTGGGAATTAAGAAAGCCTCGTCGTGAAAGCACTTAAT   | 1800 |
| Qy | 1801 | TTTTTACAGTTAGCACTTCAACATAGCTCTTAACAACCTCCAGGATATTCACACAACACT   | 1860 |
| Db | 1801 | TTTTTACAGTTAGCACTTCAACATAGCTCTTAACAACCTCCAGGATATTCACACAACACT   | 1860 |
| Qy | 1861 | TAGGCTTAAAAATGAGCTCACTCAGAATTTCTATTCTTTCTAAAAAGAGATTTATTTTAA   | 1920 |
| Db | 1861 | TAGGCTTAAAAATGAGCTCACTCAGAATTTCTATTCTTTCTAAAAAGAGATTTATTTTAA   | 1920 |
| Qy | 1921 | AATCAATGGGACTCTGATATAAAGGAAGAATAAGTCACTGTAAAAACAGAACTTTTAAATG  | 1980 |
| Db | 1921 | AATCAATGGGACTCTGATATAAAGGAAGAATAAGTCACTGTAAAAACAGAACTTTTAAATG  | 1980 |
| Qy | 1981 | AAGCTTAAATTACTCAATTTAAAAATTTAAAAATCCTTTAAAAACAACTTTTCAATTAATAT | 2040 |
| Db | 1981 | AAGCTTAAATTACTCAATTTAAAAATTTAAAAATCCTTTAAAAACAACTTTTCAATTAATAT | 2040 |
| Qy | 2041 | TATCACACTATTATCAGATTGTAATTAGATGCAAATGAGAGAGCAGTTTAGTTGTTGCAT   | 2100 |

|    |      |  |  |  |      |
|----|------|--|--|--|------|
| Db | 2041 |  | TATC   | ACTATTATCAGATTGTAATTAGATGCAAATGAGAGAGCAGTTTAGTTGTTGCAT     | 2100 |
| Qy | 2101 |  | TTTTCGG  | ACTGGAAACATTTAAATGATCAGGAGGGAGTAACAGAAAGAGCAAGGCTGT        | 2160 |
| Db | 2101 |  | TTTTCGG  | ACTGGAAACATTTAAATGATCAGGAGGGAGTAACAGAAAGAGCAAGGCTGT        | 2160 |
| Qy | 2161 |  | TTT  | TGAAAATCATTACACTTTCACTAGAAAGCCCAAACCTCAGCATTCTGCAATATGTAAC | 2220 |
| Db | 2161 |  | TTT  | TGAAAATCATTACACTTTCACTAGAAAGCCCAAACCTCAGCATTCTGCAATATGTAAC | 2220 |
| Qy | 2221 |  | CAACATGT   | CACAAACAAGCAGCATGTAACAGACTGGCACATGTGCCAGCTGAATTTAAAA       | 2280 |
| Db | 2221 |  | CAACATGT   | CACAAACAAGCAGCATGTAACAGACTGGCACATGTGCCAGCTGAATTTAAAA       | 2280 |
| Qy | 2281 |  | TATAATACTTTTAAAAA  | GAAAATTATTACATCCTTTACATTTCAGTTAAGATCAAACCTCA               | 2340 |
| Db | 2281 |  | TATAATACTTTTAAAAA  | GAAAATTATTACATCCTTTACATTTCAGTTAAGATCAAACCTCA               | 2340 |
| Qy | 2341 |  | CAAAGAGAAATAG  | AATGTTTGAAAGGCTATCCCAAAGACTTTTTTGAATCTGTCATTCA             | 2400 |
| Db | 2341 |  | CAAAGAGAAATAG  | AATGTTTGAAAGGCTATCCCAAAGACTTTTTTGAATCTGTCATTCA             | 2400 |
| Qy | 2401 |  | CATACCCTGTGAAGACA  | ATACTATCTACAATTTTTTCAGGATTATTTAAATCTTCTTTTT                | 2460 |
| Db | 2401 |  | CATACCCTGTGAAGACA  | ATACTATCTACAATTTTTTCAGGATTATTTAAATCTTCTTTTT                | 2460 |
| Qy | 2461 |  | TC   | ACTATCGTAGCTTAAACTCTGTTTGGTTTTGTCATCTGTAAATACTTACCTACATACA | 2520 |
| Db | 2461 |  | TC   | ACTATCGTAGCTTAAACTCTGTTTGGTTTTGTCATCTGTAAATACTTACCTACATACA | 2520 |
| Qy | 2521 |  | CTGCATGTAGATGATTAAATGAGGGCAGGCCCTGTGCTCATAGCTTTACGATGGAGAGAT | 2580   |      |
| Db | 2521 |  | CTGCATGTAGATGATTAAATGAGGGCAGGCCCTGTGCTCATAGCTTTACGATGGAGAGAT | 2580   |      |
| Qy | 2581 |  | GCCAGTGACCTCATAATAAAGACTGTGAACTGCCTGGTGCAGTGTCCACATGACAAAGGG | 2640   |      |
| Db | 2581 |  | GCCAGTGACCTCATAATAAAGACTGTGAACTGCCTGGTGCAGTGTCCACATGACAAAGGG | 2640   |      |
| Qy | 2641 |  | GCAGGTAGCACCCTCTCTCACCCATGCTGTGGTTAAATGGTTTCTAGCATATGTATAAT  | 2700   |      |
| Db | 2641 |  | GCAGGTAGCACCCTCTCTCACCCATGCTGTGGTTAAATGGTTTCTAGCATATGTATAAT  | 2700   |      |
| Qy | 2701 |  | GCTATAGTTAAAATACTATTTTTCAAATCATACAGATTAGTACATTTAACAGCTACCTG  | 2760   |      |
| Db | 2701 |  | GCTATAGTTAAAATACTATTTTTCAAATCATACAGATTAGTACATTTAACAGCTACCTG  | 2760   |      |
| Qy | 2761 |  | TAAAGCTTATTACTAATTTTTGTATTATTTTTGTAAATAGCCAATAGAAAAGTTTGCTTG | 2820   |      |
| Db | 2761 |  | TAAAGCTTATTACTAATTTTTGTATTATTTTTGTAAATAGCCAATAGAAAAGTTTGCTTG | 2820   |      |
| Qy | 2821 |  | ACATGGTGCTTTTCTTTCATCTAGAGGC                                 | AAAACCTGCTTTTGGAGACCGTAAGAACCTCTT                          | 2880 |
| Db | 2821 |  | ACATGGTGCTTTTCTTTCATCTAGAGGC                                 | AAAACCTGCTTTTGGAGACCGTAAGAACCTCTT                          | 2880 |
| Qy | 2881 |  | AGCTTTGTGCGTTCCTGCCTAATTTTTATATCTTCTAAGCAAAGTGCCTTAGGATAGCTT | 2940   |      |

|    |      |   |      |
|----|------|---|------|
| Db | 2881 | AGCTTTGTGCGTTCCTGCCTAATTTTTATATCTTCTAAGCAAAGTGCCTTAGGATAGCTT  | 2940 |
| Qy | 2941 | GGGATGAGATGTGTGTGAAAGTATGTACAAGAGAAAACGGAAGAGAGAGGAAATGAGGTG  | 3000 |
|    |      |   |      |
| Db | 2941 | GGGATGAGATGTGTGTGAAAGTATGTACAAGAGAAAACGGAAGAGAGAGGAAATGAGGTG  | 3000 |
| Qy | 3001 | GGGTTGGAGGAAACCCATGGGGACAGATTCCCATTCTTAGCCTAACGTTTCGTCATTGCCT | 3060 |
|    |      |   |      |
| Db | 3001 | GGGTTGGAGGAAACCCATGGGGACAGATTCCCATTCTTAGCCTAACGTTTCGTCATTGCCT | 3060 |
| Qy | 3061 | CGTCACATCAATGCAAAAGGTCTTGATTTTGTTCAGCAAAACACAGTGCAATGTTCTCA   | 3120 |
|    |      |   |      |
| Db | 3061 | CGTCACATCAATGCAAAAGGTCTTGATTTTGTTCAGCAAAACACAGTGCAATGTTCTCA   | 3120 |
| Qy | 3121 | GAGTGACTTTCGAAATAAATTGGGCCCAAGAGCTTTAACTCGGTCTTAAAAATATGCCCAA | 3180 |
|    |      |   |      |
| Db | 3121 | GAGTGACTTTCGAAATAAATTGGGCCCAAGAGCTTTAACTCGGTCTTAAAAATATGCCCAA | 3180 |
| Qy | 3181 | ATTTTACTTTGTTTTTCTTTAATAGGCTGGGCCACATGTTGGAAATAAGCTAGTAATG    | 3240 |
|    |      |   |      |
| Db | 3181 | ATTTTACTTTGTTTTTCTTTAATAGGCTGGGCCACATGTTGGAAATAAGCTAGTAATG    | 3240 |
| Qy | 3241 | TTGTTTTCTGTCAATATTGAATGTGATGGTACAGTAAACCAAACCAACAATGTGGCCA    | 3300 |
|    |      |   |      |
| Db | 3241 | TTGTTTTCTGTCAATATTGAATGTGATGGTACAGTAAACCAAACCAACAATGTGGCCA    | 3300 |
| Qy | 3301 | GAAAGAAAGAGCAATAATAATTAATTCACACACCATATGGATTCTATTTATAAATCACCC  | 3360 |
|    |      |   |      |
| Db | 3301 | GAAAGAAAGAGCAATAATAATTAATTCACACACCATATGGATTCTATTTATAAATCACCC  | 3360 |
| Qy | 3361 | ACAACTTGTTCTTTAATTTTCATCCCAATCACTTTTTTCAGAGGCCTGTTATCATAGAAGT | 3420 |
|    |      |   |      |
| Db | 3361 | ACAACTTGTTCTTTAATTTTCATCCCAATCACTTTTTTCAGAGGCCTGTTATCATAGAAGT | 3420 |
| Qy | 3421 | CATTTTAGACTCTCAATTTTAAATTAATTTTGAATCACTAATATTTTCACAGTTTATTAA  | 3480 |
|    |      |   |      |
| Db | 3421 | CATTTTAGACTCTCAATTTTAAATTAATTTTGAATCACTAATATTTTCACAGTTTATTAA  | 3480 |
| Qy | 3481 | TATATTTAATTTCTATTTAAATTTTAGATTATTTTATTACCATGTACTGAATTTTTACA   | 3540 |
|    |      |   |      |
| Db | 3481 | TATATTTAATTTCTATTTAAATTTTAGATTATTTTATTACCATGTACTGAATTTTTACA   | 3540 |
| Qy | 3541 | TCCTGATACCCCTTTCCTTCTCCATGTCAGTATCATGTTCTCTAATTATCTTGCCAAATTT | 3600 |
|    |      |   |      |
| Db | 3541 | TCCTGATACCCCTTTCCTTCTCCATGTCAGTATCATGTTCTCTAATTATCTTGCCAAATTT | 3600 |
| Qy | 3601 | TGAAACTACACACAAAAAGCATACTTGCATTATTTATAATAAAATTGCATTTCAGTGGCTT | 3660 |
|    |      |   |      |
| Db | 3601 | TGAAACTACACACAAAAAGCATACTTGCATTATTTATAATAAAATTGCATTTCAGTGGCTT | 3660 |
| Qy | 3661 | TTTAAAAAAATGTTTGATTCAAAACTTTAACATACTGATAAGTAAGAAACAATTATAAT   | 3720 |
|    |      |   |      |
| Db | 3661 | TTTAAAAAAATGTTTGATTCAAAACTTTAACATACTGATAAGTAAGAAACAATTATAAT   | 3720 |
| Qy | 3721 | TTCTTTACATACTCAAAACCAAGATAGAAAAAGGTGCTATCGTTCAACTTCAAACATGT   | 3780 |
|    |      |   |      |
| Db | 3721 | TTCTTTACATACTCAAAACCAAGATAGAAAAAGGTGCTATCGTTCAACTTCAAACATGT   | 3780 |

Qy 3781 TTCCTAGTATTAAGGACTTTAATATAGCAACAGACAAAATTATTGTAAACATGGATGTTA 3840  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 3781 TTCCTAGTATTAAGGACTTTAATATAGCAACAGACAAAATTATTGTAAACATGGATGTTA 3840  
 Qy 3841 CAGCTCAAAAGATTTATAAAAGATTTTAACCTATTTTCTCCCTTATTATCCACTGCTAAT 3900  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 3841 CAGCTCAAAAGATTTATAAAAGATTTTAACCTATTTTCTCCCTTATTATCCACTGCTAAT 3900  
 Qy 3901 GTGGATGTATGTTCAAACACCTTTTAGTATTGATAGCTTACATATGGCCAAAGGAATACA 3960  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 3901 GTGGATGTATGTTCAAACACCTTTTAGTATTGATAGCTTACATATGGCCAAAGGAATACA 3960  
 Qy 3961 GTTTATAGCAAAACATGGGTATGCTGTAGCTAACTTTATAAAAGTGTAATATAACAATGT 4020  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 3961 GTTTATAGCAAAACATGGGTATGCTGTAGCTAACTTTATAAAAGTGTAATATAACAATGT 4020  
 Qy 4021 AAAAAATTATATATCTGGGAGGATTTTTTGGTTGCCTAAAGTGGCTATAGTTACTGATTT 4080  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 4021 AAAAAATTATATATCTGGGAGGATTTTTTGGTTGCCTAAAGTGGCTATAGTTACTGATTT 4080  
 Qy 4081 TTTATTATGTAAGCAAAACCAATAAAAAATTTAAGTTTTTTTAACAACCTACCTTATTTTTC 4140  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 4081 TTTATTATGTAAGCAAAACCAATAAAAAATTTAAGTTTTTTTAACAACCTACCTTATTTTTC 4140  
 Qy 4141 ACTGTACAGACACTAATTCATTAAATACTAATTGATTGTTTAAAAGAAATATAAATGTGA 4200  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 4141 ACTGTACAGACACTAATTCATTAAATACTAATTGATTGTTTAAAAGAAATATAAATGTGA 4200  
 Qy 4201 CAAGTGGACATTATTTATGTTAAATATACAATTATCAAGCAAGTATGAAGTTATTCAATT 4260  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 4201 CAAGTGGACATTATTTATGTTAAATATACAATTATCAAGCAAGTATGAAGTTATTCAATT 4260  
 Qy 4261 AAAATGCCACATTTCTGGTCTCTGGGAAAAAAAAAAAAAAAAAAAA 4301  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 4261 AAAATGCCACATTTCTGGTCTCTGGGAAAAAAAAAAAAAAAAAAAA 4301

RESULT 2

US-08-910-864-13

; Sequence 13, Application US/08910864

; Patent No. 6280931

; GENERAL INFORMATION:

; APPLICANT: SAKAMOTO, AIJI

; APPLICANT: HANAOKA, FUMIO

; TITLE OF INVENTION: METHOD FOR SPECIFICALLY AMPLIFYING A cDNA OF AN  
 EXTREMELY

; TITLE OF INVENTION: SMALL QUANTITY

; NUMBER OF SEQUENCES: 13

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: FISH & RICHARDSON P.C.

; STREET: 4225 EXECUTIVE SQUARE, SUITE 1400

; CITY: LA JOLLA

; STATE: CA

; COUNTRY: USA

; ZIP: 92037

; COMPUTER READABLE FORM:

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; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/910,864
; FILING DATE: 13-AUG-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 216506/1996
; FILING DATE: 16-AUG-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: HAILE, LISA A.
; REGISTRATION NUMBER: 38,347
; REFERENCE/DOCKET NUMBER: 07898/017001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-678-5070
; TELEFAX: 619-678-5099
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1873 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 231..1556
US-08-910-864-13

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Query Match          39.3%; Score 1691.8; DB 3; Length 1873;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 1696; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

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Qy      178 TGAAACTTGGCTCTGAAACTGCGGAGCGGCCACCGGACGCCTTCTGGAGCAGGTAGCAGC 237
      || || |||||
Db      171 TGTCTCTAGGCTCTGAAACTGCGGAGCGGCCACCGGACGCCTTCTGGAGCAGGTAGCAGC 230

Qy      238 ATGCAGCCGCCTCCAAGTCTGTGCGGACGCGCCCTGGTTGCGCTGGTTCTTGCCTGCGGC 297
      |||||
Db      231 ATGCAGCCGCCTCCAAGTCTGTGCGGACGCGCCCTGGTTGCGCTGGTTCTTGCCTGCGGC 290

Qy      298 CTGTCGCGGATCTGGGGAGAGGAGAGAGGCTTCCCGCCTGACAGGGCCACTCCGCTTTTG 357
      |||||
Db      291 CTGTCGCGGATCTGGGGAGAGGAGAGAGGCTTCCCGCCTGACAGGGCCACTCCGCTTTTG 350

Qy      358 CAAACCGCAGAGATAATGACGCCACCCACTAAGACCTTATGGCCCAAGGGTTCCAACGCC 417
      |||||
Db      351 CAAACCGCAGAGATAATGACGCCACCCACTAAGACCTTATGGCCCAAGGGTTCCAACGCC 410

Qy      418 AGTCTGGCGCGGTCGTTGGCACCTGCGGAGGTGCCTAAAGGAGACAGGACGGCAGGATCT 477
      |||||
Db      411 AGTCTGGCGCGGTCGTTGGCACCTGCGGAGGTGCCTAAAGGAGACAGGACGGCAGGATCT 470

Qy      478 CCGCCACGCACCATCTCCCCTCCCCCGTGCCAAGGACCCATCGAGATCAAGGAGACTTTC 537
      |||||
Db      471 CCGCCACGCACCATCTCCCCTCCCCCGTGCCAAGGACCCATCGAGATCAAGGAGACTTTC 530

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|    |      |  |      |
|----|------|--|------|
| Qy | 538  | AAATACATCAACACGGTTGTGTCCTGCCTTGTGTTTCGTGCTGGGGATCATCGGGAACCTCC | 597  |
|    |      |  |      |
| Db | 531  | AAATACATCAACACGGTTGTGTCCTGCCTTGTGTTTCGTGCTGGGGATCATCGGGAACCTCC | 590  |
| Qy | 598  | ACACTTCTGAGAATTATCTACAAGAACAAGTGCATGCGAAACGGTCCCAATATCTTGATC   | 657  |
|    |      |  |      |
| Db | 591  | ACACTTCTGAGAATTATCTACAAGAACAAGTGCATGCGAAACGGTCCCAATATCTTGATC   | 650  |
| Qy | 658  | GCCAGCTTGGCTCTGGGAGACCTGCTGCACATCGTCATTGACATCCCTATCAATGTCTAC   | 717  |
|    |      |  |      |
| Db | 651  | GCCAGCTTGGCTCTGGGAGACCTGCTGCACATCGTCATTGACATCCCTATCAATGTCTAC   | 710  |
| Qy | 718  | AAGCTGCTGGCAGAGGACTGGCCATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTCATA   | 777  |
|    |      |  |      |
| Db | 711  | AAGCTGCTGGCAGAGGACTGGCCATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTCATA   | 770  |
| Qy | 778  | CAGAAAGCCTCCGTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATAT   | 837  |
|    |      |  |      |
| Db | 771  | CAGAAAGCCTCCGTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATAT   | 830  |
| Qy | 838  | CGAGCTGTTGCTTCTTGGAGTAGAATTAAAGGAATTGGGGTTCCAAAATGGACAGCAGTA   | 897  |
|    |      |  |      |
| Db | 831  | CGAGCTGTTGCTTCTTGGAGTAGAATTAAAGGAATTGGGGTTCCAAAATGGACAGCAGTA   | 890  |
| Qy | 898  | GAAATTGTTTTGATTTGGGTGGTCTCTGTGGTTCTGGCTGTCCCTGAAGCCATAGGTTTT   | 957  |
|    |      |  |      |
| Db | 891  | GAAATTGTTTTGATTTGGGTGGTCTCTGTGGTTCTGGCTGTCCCTGAAGCCATAGGTTTT   | 950  |
| Qy | 958  | GATATAATTACGATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTT   | 1017 |
|    |      |  |      |
| Db | 951  | GATATAATTACGATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTT   | 1010 |
| Qy | 1018 | CAGAAGACAGCTTTCATGCAGTTTTACAAGACAGCAAAGATTGGTGGCTGTTTCAGTTTC   | 1077 |
|    |      |  |      |
| Db | 1011 | CAGAAGACAGCTTTCATGCAGTTTTACAAGACAGCAAAGATTGGTGGCTATTCAGTTTC    | 1070 |
| Qy | 1078 | TATTTCTGCTTGCCATTGGCCATCACTGCATTTTTTTTATACACTAATGACCTGTGAAATG  | 1137 |
|    |      |  |      |
| Db | 1071 | TATTTCTGCTTGCCATTGGCCATCACTGCATTTTTTTTATACACTAATGACCTGTGAAATG  | 1130 |
| Qy | 1138 | TTGAGAAAGAAAAGTGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAA   | 1197 |
|    |      |  |      |
| Db | 1131 | TTGAGAAAGAAAAGTGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAA   | 1190 |
| Qy | 1198 | GTGGCCAAAACCGTCTTTTGCCTGGTCTTGTCTTTGCCCTCTGCTGGCTTCCCCTTCAC    | 1257 |
|    |      |  |      |
| Db | 1191 | GTGGCCAAAACCGTCTTTTGCCTGGTCTTGTCTTTGCCCTCTGCTGGCTTCCCCTTCAC    | 1250 |
| Qy | 1258 | CTCAGCAGGATTCTGAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGAACCT   | 1317 |
|    |      |  |      |
| Db | 1251 | CTCAGCAGGATTCTGAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGAACCT   | 1310 |
| Qy | 1318 | TTGAGCTTTCTGTTGGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCCTGC   | 1377 |
|    |      |  |      |
| Db | 1311 | TTGAGCTTTCTGTTGGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCCTGC   | 1370 |

|    |      |   |      |
|----|------|---|------|
| Qy | 1378 | ATTAACCCAATTGCTCTGTATTTGGTGAGCAAAAGATTCAAAAAGCTGCTTTAAGTCATGC | 1437 |
|    |      |   |      |
| Db | 1371 | ATTAACCCAATTGCTCTGTATTTGGTGAGCAAAAGATTCAAAAAGCTGCTTTAAGTCATGC | 1430 |
| Qy | 1438 | TTATGCTGCTGGTGCCAGTCATTTGAAGAAAAACAGTCCTTGGAGGAAAAGCAGTCGTGC  | 1497 |
|    |      |   |      |
| Db | 1431 | TTATGCTGCTGGTGCCAGTCATTTGAAGAAAAACAGTCCTTGGAGGAAAAGCAGTCGTGC  | 1490 |
| Qy | 1498 | TTAAAGTTCAAAGCTAATGATCACGGATATGACAACTTCCGTTCCAGTAATAAATACAGC  | 1557 |
|    |      |   |      |
| Db | 1491 | TTAAAGTTCAAAGCTAATGATCACGGATATGACAACTTCCGTTCCAGTAATAAATACAGC  | 1550 |
| Qy | 1558 | TCATCTTGAAAGAAGAACTATTCAGTGTATTTTCTTTATATTGGACCGAAGTCAT       | 1617 |
|    |      |   |      |
| Db | 1551 | TCATCTTGAAAGAAGAACTATTCAGTGTATTTTCTTTATATTGGACCGAAGTCAT       | 1610 |
| Qy | 1618 | TAAAACAAAATGAAACATTTGCCAAAACAAAACAAAAAACTATGTATTTGCACAGCACAC  | 1677 |
|    |      |   |      |
| Db | 1611 | TAAAACAAAATGAAACATTTGCCAAAACAAAACAAAAAACTATGTATTTGCACAGCACAC  | 1670 |
| Qy | 1678 | TATTAATAATTAAGTGTAATTATTTTAACACTCACAGCTACATATGACATTTTATGAGC   | 1737 |
|    |      |   |      |
| Db | 1671 | TATTAATAATTAAGTGTAATTATTTTAACACTCACAGCTACATATGACATTTTATGAGC   | 1730 |
| Qy | 1738 | TGTTTACGGCATGGAAAGAAAATCAGTGGAATTAAGAAAGCCTCGTCGTGAAAGCACTT   | 1797 |
|    |      |   |      |
| Db | 1731 | TGTTTACGGCATGGAAAGAAAATCAGTGGAATTAAGAAAGCCTCGTCGTGAAAGCACTT   | 1790 |
| Qy | 1798 | AATTTTTTACAGTTAGCACTTCAACATAGCTCTTAACAACTTCCAGGATATTCACACAAC  | 1857 |
|    |      |   |      |
| Db | 1791 | AATTTTTTACAGTTAGCACTTCAACATAGCTCTTAACAACTTCCAGGATATTCACACAAC  | 1850 |
| Qy | 1858 | ACTTAGGCTTAAAAATGAGCTCA                                       | 1880 |
|    |      |   |      |
| Db | 1851 | ACTTAGGCTTAAAAATGAGCTCA                                       | 1873 |

# RESULT 3

US-09-016-434-1203

; Sequence 1203, Application US/09016434

; Patent No. 6500938

; GENERAL INFORMATION:

; APPLICANT: Janice Au-Young

; APPLICANT: Jeffrey J. Seilhamer

; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING

; TITLE OF INVENTION: PATHWAY GENE EXPRESSION

; NUMBER OF SEQUENCES: 1490

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.

; STREET: 3174 PORTER DRIVE

; CITY: PALO ALTO

; STATE: CALIFORNIA

; COUNTRY: USA

; ZIP: 94304

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

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;   OPERATING SYSTEM:  PC-DOS/MS-DOS
;   SOFTWARE:  Word Perfect 6.1 for Windows/MS-DOS 6.2
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER:  US/09/016,434
;   FILING DATE:  HERewith
;   CLASSIFICATION:
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER:
;   FILING DATE:
;   CLASSIFICATION:
;   ATTORNEY/AGENT INFORMATION:
;   NAME:  Zeller, Karen J.
;   REGISTRATION NUMBER:  37,071
;   REFERENCE/DOCKET NUMBER:  PA-0002 US
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE:  (650) 855-0555
;   TELEFAX:  (650) 845-4166
;   INFORMATION FOR SEQ ID NO:  1203:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH:  1470 base pairs
;   TYPE:  nucleic acid
;   STRANDEDNESS:  single
;   TOPOLOGY:  linear
;   IMMEDIATE SOURCE:
;   LIBRARY:  GENBANK
;   CLONE:  g182275
US-09-016-434-1203

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Query Match          34.1%;  Score 1466.8;  DB 4;  Length 1470;
Best Local Similarity 99.9%;  Pred. No. 0;
Matches 1468;  Conservative 0;  Mismatches 2;  Indels 0;  Gaps 0;

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Qy      192 GAAACTGCGGAGCGGCCACCGGACGCCTTCTGGAGCAGGTAGCAGCATGCAGCCGCCTCC 251
          |||
Db      1   GAAACTGCGGACGGGCCACCGGACGCCTTCTGGAGCAGGTAGCAGCATGCAGCCGCCTCC 60

Qy      252 AAGTCTGTGCGGACGCGCCCTGGTTGCGCTGGTTCTTGCCTGCGGCCTGTCGCGGATCTG 311
          |||
Db      61 AAGTCTGTGCGGACGCGCCCTGGTTGCGCTGGTTCTTGCCTGCGGCCTGTCGCGGATCTG 120

Qy      312 GGGAGAGGAGAGAGGCTTCCCGCCTGACAGGGCCACTCCGCTTTTGCAAACCGCAGAGAT 371
          |||
Db      121 GGGAGAGGAGAGAGGCTTCCCGCCTGACAGGGCCACTCCGCTTTTGCAAACCGCAGAGAT 180

Qy      372 AATGACGCCACCCACTAAGACCTTATGGCCCAAGGGTTCCAACGCCAGTCTGGCGCGGTC 431
          |||
Db      181 AATGACGCCACCCACTAAGACCTTATGGCCCAAGGGTTCCAACGCCAGTCTGGCGCGGTC 240

Qy      432 GTTGGCACCTGCGGAGGTGCCTAAAGGAGACAGGACGGCAGGATCTCCGCCACGCACCAT 491
          |||
Db      241 GTTGGCACCTGCGGAGGTGCCTAAAGGAGACAGGACGGCAGGATCTCCGCCACGCACCAT 300

Qy      492 CTCCCCCTCCCCCGTGCCAAGGACCCATCGAGATCAAGGAGACTTTCAAATACATCAACAC 551
          |||
Db      301 CTCCCCCTCCCCCGTGCCAAGGACCCATCGAGATCAAGGAGACTTTCAAATACATCAACAC 360

Qy      552 GGTTGTGTCTCTGCCTTGTGTTCTGCTGGGGATCATCGGGAAGTCCACACTTCTGAGAAT 611

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|    |      |  |  |      |
|----|------|--|--|------|
| Db | 361  |  | GGTTGTGTCCTGCCTTGTGTTTCGTGCTGGGGATCATCGGGAACCTCCACACTTCTGAGAAT | 420  |
| Qy | 612  |  | TATCTACAAGAACAAGTGCATGCGAAACGGTCCCAATATCTTGATCGCCAGCTTGGCTCT   | 671  |
| Db | 421  |  | TATCTACAAGAACAAGTGCATGCGAAACGGTCCCAATATCTTGATCGCCAGCTTGGCTCT   | 480  |
| Qy | 672  |  | GGGAGACCTGCTGCACATCGTCATTGACATCCCTATCAATGTCTACAAGCTGCTGGCAGA   | 731  |
| Db | 481  |  | GGGAGACCTGCTGCACATCGTCATTGACATCCCTATCAATGTCTACAAGCTGCTGGCAGA   | 540  |
| Qy | 732  |  | GGACTGGCCATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTCATACAGAAAGCCTCCGT   | 791  |
| Db | 541  |  | GGACTGGCCATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTCATACAGAAAGCCTCCGT   | 600  |
| Qy | 792  |  | GGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATATCGAGCTGTTGCTTC   | 851  |
| Db | 601  |  | GGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATATCGAGCTGTTGCTTC   | 660  |
| Qy | 852  |  | TTGGAGTAGAATTAAAGGAATTGGGGTTCCAAAATGGACAGCAGTAGAAATTGTTTTGAT   | 911  |
| Db | 661  |  | TTGGAGTAGAATTAAAGGAATTGGGGTTCCAAAATGGACAGCAGTAGAAATTGTTTTGAT   | 720  |
| Qy | 912  |  | TTGGGTGGTCTCTGTGGTTCTGGCTGTCCCTGAAGCCATAGGTTTTGATATAAATTACGAT  | 971  |
| Db | 721  |  | TTGGGTGGTCTCTGTGGTTCTGGCTGTCCCTGAAGCCATAGGTTTTGATATAAATTACGAT  | 780  |
| Qy | 972  |  | GGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTTCAGAAGACAGCTTT   | 1031 |
| Db | 781  |  | GGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTTCAGAAGACAGCTTT   | 840  |
| Qy | 1032 |  | CATGCAGTTTTACAAGACAGCAAAAGATTGGTGGCTGTTCAAGTTTCTATTTCTGCTTGCC  | 1091 |
| Db | 841  |  | CATGCAGTTTTACAAGACAGCAAAAGATTGGTGGCTGTTCAAGTTTCTATTTCTGCTTGCC  | 900  |
| Qy | 1092 |  | ATTGGCCATCACTGCATTTTTTTTATACACTAATGACCTGTGAAATGTTGAGAAAGAAAAG  | 1151 |
| Db | 901  |  | ATTGGCCATCACTGCATTTTTTTTATACACTAATGACCTGTGAAATGTTGAGAAAGAAAAG  | 960  |
| Qy | 1152 |  | TGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAAGTGGCCAAAACCGT   | 1211 |
| Db | 961  |  | TGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAAGTGGCCAAAACCGT   | 1020 |
| Qy | 1212 |  | CTTTTGCCTGGTCCTTGTCTTTGCCCTCTGCTGGCTTCCCCTTCACCTCAGCAGGATTCT   | 1271 |
| Db | 1021 |  | CTTTTGCCTGGTCCTTGTCTTTGCCCTCTGCTGGCTTCCCCTTCACCTCAGCAGGATTCT   | 1080 |
| Qy | 1272 |  | GAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGAACTTTTGAGCTTTCTGTT   | 1331 |
| Db | 1081 |  | GAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGAACTTTTGAGCTTTCTGTT   | 1140 |
| Qy | 1332 |  | GGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCCTGCATTAACCCAATTGC   | 1391 |
| Db | 1141 |  | GGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCCTGCATTAACCCAATTGC   | 1200 |
| Qy | 1392 |  | TCTGTATTTGGTGAGCAAAAGATTCAAAAACCTGCTTTAAGTCATGCTTATGCTGCTGGTG  | 1451 |
|    |      |  |  |      |

Db 1201 TCTGTATTTGGTGAGCAAAAGATTCAAAAAGCTTTAAGTCATGCTTATGCTGCTGGTG 1260

Qy 1452 CCAGTCATTTGAAGAAAAACAGTCCTTGGAGGAAAAGCAGTCGTGCTTAAAGTTCAAAGC 1511  
 |||

Db 1261 CCAGTCATTTGAAGAAAAACAGTCCTTGGAGGAAAAGCAGTCGTGCTTAAAGTTCAAAGC 1320

Qy 1512 TAATGATCACGGATATGACAACCTCCGTTCCAGTAATAAATACAGCTCATCTTGAAAGAA 1571  
 |||

Db 1321 TAATGATCACGGATATGACAACCTCCGTTCCAGTAATAAATACAGCTCATCTTGAAAGAA 1380

Qy 1572 GAACTATTCACTGTATTTTCTTTATATTGGACCGAAGTCATTAAACAAAATGAA 1631  
 |||

Db 1381 GAACTATTCACTGTATTTTCTTTATATTGGACCGAAGTCATTAAACAAAATGAA 1440

Qy 1632 ACATTTGCCAAAACAAAACAAAAAACTATG 1661  
 |||

Db 1441 ACATTTGCCAAAACAAAACAAAAAACTATG 1470

#### RESULT 4

US-09-175-658B-20

; Sequence 20, Application US/09175658B

; Patent No. 6372900

; GENERAL INFORMATION:

; APPLICANT: METALLINOS, DANIKA

; APPLICANT: RINE, JASPER

; APPLICANT: BOWLING, ANN

; TITLE OF INVENTION: HORSE ENDOTHELIN-B RECEPTOR GENE AND GENE PRODUCTS

; FILE REFERENCE: GOBR-110

; CURRENT APPLICATION NUMBER: US/09/175,658B

; CURRENT FILING DATE: 1998-10-20

; PRIOR APPLICATION NUMBER: 60/062,562

; PRIOR FILING DATE: 1997-10-21

; NUMBER OF SEQ ID NOS: 25

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 20

; LENGTH: 1321

; TYPE: DNA

; ORGANISM: Horse

US-09-175-658B-20

Query Match 24.9%; Score 1070.4; DB 4; Length 1321;  
 Best Local Similarity 88.7%; Pred. No. 1.5e-256;  
 Matches 1171; Conservative 0; Mismatches 146; Indels 3; Gaps 1;

Qy 227 CAGGTAGCAGCATGCAGCCGCTCCAAGTCTGTGCGGACGCGCCCTGGTTGCGCTGGTTC 286  
 |||

Db 1 CAGGTAGCAGCATGCAGCCTCTGCCAACCTGTGTGGACGCGTTCTGGTGGCGCTGATCC 60

Qy 287 TTGCCTGCGGCCTGTGCGGGATCTGGGGAGAGGAGAGAGGCTTCCCGCCTGACAGGGCCA 346  
 |||

Db 61 TTGCCTGCGGCGTGGCAGGGGTCCAGGGAGAAGAGAGGAGATTCCCGCCGGCCAGGGCCA 120

Qy 347 CTCCG---CTTTTGCAAACCGCAGAGATAATGACGCCACCCACTAAGACCTTATGGCCCA 403  
 |||

Db 121 CTCCGCCACTTCTGGGGTCTGAAGAGATAATGACGCCCCGACTAAGACCTCCTGGCCGA 180

|    |      |  |      |
|----|------|--|------|
| QY | 404  | AGGGTTCCAACGCCAGTCTGGCGCGGTTCGTTGGCACCTGCGGAGGTGCCTAAAGGAGACA  | 463  |
| Db | 181  | CGGGGTCCAACGCCAGCGTGCCGCGGTTCATCAGCACCTCCGCAAATGCCTAAAGCAGGGA  | 240  |
| QY | 464  | GGACGGCAGGATCTCCGCCACGCACCATCTCCCTCCCCCGTGCCAAGGACCCATCGAGA    | 523  |
| Db | 241  | GGACGGCGGGAGCCCAGCGACGCACCCTCCCTCCTCCCCCGTGCGAAAGAACCATCGAGA   | 300  |
| QY | 524  | TCAAGGAGACTTTCAAATACATCAACACGGTTGTGTCTGCCTTGTGTTTCGTGCTGGGGA   | 583  |
| Db | 301  | TCAAGGAGACTTTCAAGTACATCAACACAGTAGTGTCTGCCTAGTGTTTCGTGCTGGGCA   | 360  |
| QY | 584  | TCATCGGGAACCTCCACACTTCTGAGAATTATCTACAAGAACAAGTGCATGCGAAACGGTC  | 643  |
| Db | 361  | TCATCGGAAACTCCACACTGCTGAGAATCATTTACAAGAACAAGTGCATGCGGAACGGCC   | 420  |
| QY | 644  | CCAATATCTTGATCGCCAGCTTGGCTCTGGGAGACCTGCTGCACATCGTCATTGACATCC   | 703  |
| Db | 421  | CTAATATCTTGATCGCCAGCCTGGCTCTCCGAGACCTGCTGCAAATCATCATTGACGTCC   | 480  |
| QY | 704  | CTATCAATGTCTACAAGCTGCTGGCAGAGGACTGGCCATTTGGAGCTGAGATGTGTAAGC   | 763  |
| Db | 481  | CCATCAATGTCTACAAGCTGCTGGCTGAGGACTGGCCCTTTGGAGTCGAGATGTGTAAGC   | 540  |
| QY | 764  | TGGTGCCTTTTCATACAGAAAGCCTCCGTGGGAATCACTGTGCTGAGTCTATGTGCTCTGA  | 823  |
| Db | 541  | TGGTGCCTTTTCATACAGAAGGCCTCCGTGGGCATCACTGTGCTGAGTCTGTGTGCTCTAA  | 600  |
| QY | 824  | GTATTGACAGATATCGAGCTGTTGCTTCTTGGAGTAGAATTAAAGGAATTGGGGTTCCAA   | 883  |
| Db | 601  | GTATTGACAGATATCGAGCTGTTGCTTCCCTTGGAGCGAATTAAAGGAATTCGGGTTCAA   | 660  |
| QY | 884  | AATGGACAGCAGTAGAAATTGTTTTGATTTGGGTGGTCTCTGTGGTTCTGGCTGTCCCTG   | 943  |
| Db | 661  | AATGGACAGCAGTAGAAATTGTTTTAATTTGGGTGGTCTCTGTGGTTCTGGCTGTCCCTG   | 720  |
| QY | 944  | AAGCCATAGGTTTTTGATATAATTACGATGGACTACAAAGGAAGTTATCTGCGAATCTGCT  | 1003 |
| Db | 721  | AAGCCGTGGGTTTTTGATATGATTACCGCTGACTACAAAGGAAGTTATCTGCGAATCTGCC  | 780  |
| QY | 1004 | TGCTTCATCCCGTTTCAGAAGACAGCTTTCATGCAGTTTACAAAGACAGCAAAAGATTGGT  | 1063 |
| Db | 781  | TGCTTCATCCCACTCAGAAAACAGCCTTCATGCAGTTTACAAAGATGCTAAGGACTGGT    | 840  |
| QY | 1064 | GGCTGTTTCAGTTTCTATTTCTGCTTGCCATTGGCCATCACTGCATTTTTTTTATACACTAA | 1123 |
| Db | 841  | GGCTATTTAGTTTCTATTTCTGCTTGCCATTGGCCATCACTGCATTTTTTTTATACCTTGA  | 900  |
| QY | 1124 | TGACCTGTGAAATGTTGAGAAAGAAAAGTGGCATGCAGATTGCTTTAAATGATCACCTAA   | 1183 |
| Db | 901  | TGACCTGTGAAATGTTGAGAAAGAAGAGTGGCATGCAAATTGCTTTAAATGATCACTTAA   | 960  |
| QY | 1184 | AGCAGAGACGGGAAGTGGCCAAAACCGTCTTTTGCCTGGTCCTTGTCTTTGCCCTCTGCT   | 1243 |
| Db | 961  | AGCAGAGAAGGGAAGTGGCGAAAACAGTATTCTGCCTGGTCCTTGTCTTTGCCCTGTGCT   | 1020 |
| QY | 1244 | GGCTTCCCCTTCACCTCAGCAGGATTCTGAAGCTCACTCTTTATAATCAGAATGATCCCA   | 1303 |

|    |      |  |   |      |
|----|------|--|---|------|
| Db | 1021 |  | GGCTTCCTCTTCACCTCAGCAGGATTTTGAAACACACTCTTTATGATCAGAATGATCCCC  | 1080 |
| Qy | 1304 |  | ATAGATGTGAACTTTTGAGCTTTCTGTTGGTATTGGACTATATTGGTATCAACATGGCTT  | 1363 |
| Db | 1081 |  | ATAGATGTGAACTTTTGAGCTTTTGTGTTGGTATTGGACTACATTGGCATCAACATGGCCT | 1140 |
| Qy | 1364 |  | CACTGAATTCCTGCATTAACCCAATTGCTCTGTATTTGGTGAGCAAAAGATTCAAAAACT  | 1423 |
| Db | 1141 |  | CCCTGAATTCCTGCATTAATCCAATAGCTCTGTATTTGGTGAGCAAAAGATTCAAAAACT  | 1200 |
| Qy | 1424 |  | GCTTTAAGTCATGCTTATGCTGCTGGTGCCAGTCATTTGAAGAAAAACAGTCCTTGGAGG  | 1483 |
| Db | 1201 |  | GCTTTAAGTCGTGCTTATGCTGCTGGTGCCAATCATTTGAAGAAAAACAGTCCTTGGAGG  | 1260 |
| Qy | 1484 |  | AAAAGCAGTCGTGCTTAAAGTTCAAAGCTAATGATCACGGATATGACAACTTCCGTTCCA  | 1543 |
| Db | 1261 |  | ACAAGCAGTCATGCTTAAAGTTCAAAGCTAATGATCACGGATATGACAACTTCCGTTCCA  | 1320 |

RESULT 5

US-09-016-434-1257

; Sequence 1257, Application US/09016434

; Patent No. 6500938

; GENERAL INFORMATION:

; APPLICANT: Janice Au-Young

; APPLICANT: Jeffrey J. Seilhamer

; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING

; TITLE OF INVENTION: PATHWAY GENE EXPRESSION

; NUMBER OF SEQUENCES: 1490

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.

; STREET: 3174 PORTER DRIVE

; CITY: PALO ALTO

; STATE: CALIFORNIA

; COUNTRY: USA

; ZIP: 94304

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/016,434

; FILING DATE: HEREWITH

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER:

; FILING DATE:

; CLASSIFICATION:

; ATTORNEY/AGENT INFORMATION:

; NAME: Zeller, Karen J.

; REGISTRATION NUMBER: 37,071

; REFERENCE/DOCKET NUMBER: PA-0002 US

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (650) 855-0555

; TELEFAX: (650) 845-4166

```
; INFORMATION FOR SEQ ID NO: 1257:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 4079 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
; IMMEDIATE SOURCE:
;   LIBRARY: GENBANK
;   CLONE: g219649
US-09-016-434-1257
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Query Match          9.2%; Score 395.8; DB 4; Length 4079;
Best Local Similarity 65.7%; Pred. No. 2.5e-88;
Matches 634; Conservative 0; Mismatches 307; Indels 24; Gaps 3;
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Qy      505 TGCCAAGGACCCATCGAGATCAAGGAGACTTTCAAATACATCAACACGGTTGTGTCTGC 564
          |||| | | | | | | | | | | | | | | | | | | | |
Db      685 TGCCACAGCAGACTAAAATTACTTCAGCTTTCAAATACATTAACACTGTGATATCTTGT 744

Qy      565 CTTGTGTTCGTGCTGGGGATCATCGGGAACCCACACTTCTGAGAATTATCTACAAGAAC 624
          | | || | | |||| | | | | | | | | | | | | | |
Db      745 ACTATTTTCATCGTGGGAATGGTGGGGAATGCAACTCTGCTCAGGATCATTTACCAGAAC 804

Qy      625 AAGTGCATGCGAAACGGTCCCAATATCTTGATCGCCAGCTTGGCTCTGGGAGACCTGCTG 684
          || || || | | | | |||| | | | | | | | | | | |
Db      805 AAATGTATGAGGAATGGCCCCAACGCGCTGATAGCCAGTCTTGCCCTTGGGAGACCTTATC 864

Qy      685 CACATCGTCATTGACATCCCTATCAATGTCTACAAGCTGCTGGCAGAGGACTGGCC---- 740
          | | |||| || | | | | | | | | | | | | | |
Db      865 TATGTGGTCATTGATCTCCCTATCAATGTATTTAAGCTGCTGGCTGGGCGCTGGCCCTTTT 924

Qy      741 -----ATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTTCATACAGAAAGCCTCC 789
          |||| | | | | | | | | | | | | | | | | | |
Db      925 GATCACAATGACTTTGGCGTATTTCTTTGCAAGCTGTTCCCTTTTTGCAGAAGTCCTCG 984

Qy      790 GTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATATCGAGCTGTTGCT 849
          |||| |||| | | | | | | | | | | | | | | | |
Db      985 GTGGGGATCACCGTCCTCAACCTCTGCGCTCTTAGTGTTGACAGGTACAGAGCAGTTGCC 1044

Qy      850 TCTTGGAGTAGAATTAAAGGAATTGGGGTTCCAAAATGGACAGCAGTAGAAATTGTTTTG 909
          || |||| | | | | | | | | | | | | | | | |
Db      1045 TCCTGGAGTCGTGTTTCAGGGAATTGGGATTCTTTGGTAACTGCCATTGAAATTGTCTCC 1104

Qy      910 ATTTGGGTGGTCTCTGTGGTTCTGGCTGTCCCTGAAGCCATAGGTTTTGATATAATTACG 969
          || || | | | | | | | | | | | | | | | | | |
Db      1105 ATCTGGATCCTGTCCTTTATCCTGGCCATTCTCTGAAGCGATTGGCTTCGTATGGTACCC 1164

Qy      970 ATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTTCAGAAGACAGCT 1029
          | | || | | | | | | | | | | | | | | | | |
Db      1165 TTTGAATATAGGGGTGAACAGCATAAAACCTGTATGCTCAATGCC-----ACATCAAAA 1218

Qy      1030 TTCATGCAGTTTTACAAGACAGCAAAAGATTGGTGGCTGTTTCAGTTTCTATTTCTGCTTG 1089
          |||| |||| || | | | | | | | | | | | | | |
Db      1219 TTCATGGAGTTCTACCAAGATGTAAAGGACTGGTGGCTCTTCGGGTTCTATTTCTGTATG 1278

Qy      1090 CCATTGGCCATCACTGCATTTTTTTTATACACTAATGACCTGTGAAATGTTG---AGAAAG 1146
          || |||| | | | | | | | | | | | | | | | |
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Db 1279 CCCTTGGTGTGCACTGCGATCTTCTACACCCTCATGACTTGTGAGATGTTGAACAGAAGG 1338  
 Qy 1147 AAAAGTGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAAGTGGCCAAA 1206  
 || | ||| || |||| | | ||| || || ||||| | || ||||| |||  
 Db 1339 AATGGCAGCTTGAGAATTGCCCTCAGTGAACATCTTAAGCAGCGTCGAGAAGTGGCAAAA 1398  
 Qy 1207 ACCGTCTTTTGCTGGTCCCTTGTCTTTGCCCTCTGCTGGCTTCCCCCTTCACCTCAGCAGG 1266  
 || || || ||| |||| | | ||||| || ||||| | || ||||| | ||| |  
 Db 1399 ACAGTTTCTGCTTGGTTGTAATTTTGTCTTTGCTGGTTCCCTCTTCACTTAAGCCGT 1458  
 Qy 1267 ATTCTGAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGAACTTTGAGCTTT 1326  
 || ||||| ||| | ||||| | | || || ||||| | | || ||  
 Db 1459 ATATTGAAGAAAAGTGTGTATAACGAAATGGACAAGAACCGATGTGAATTACTTAGTTTC 1518  
 Qy 1327 CTGTTGGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCCTGCATTAACCCA 1386  
 | || | |||| || || |||| || |||| | ||||| || || |||||  
 Db 1519 TTACTGCTCATGGATTACATCGGTATTAACCTGGCAACCATGAATTCATGTATAAACCCC 1578  
 Qy 1387 ATTGCTCTGTATTTGGTGAGCAAAAGATTCAAAAAGTCTTTAAGTCATGCTTATGCTGC 1446  
 || ||||| ||||| ||||| || || ||||| || || ||||| || |||||  
 Db 1579 ATAGCTCTGTATTTTGTGAGCAAGAAATTTAAAAATGTTTCCAGTCATGCCTCTGCTGC 1638  
 Qy 1447 TGGTG 1451  
 || ||  
 Db 1639 TGCTG 1643

RESULT 6

US-08-121-446-1

; Sequence 1, Application US/08121446  
 ; Patent No. 6313276  
 ; GENERAL INFORMATION:  
 ; APPLICANT: IMURA, HIROO  
 ; APPLICANT: NAKAO, KAZUWA  
 ; APPLICANT: NAKANISHI, SHIGETADA  
 ; TITLE OF INVENTION: A HUMAN ENDOTHELIN RECEPTOR  
 ; NUMBER OF SEQUENCES: 4  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: MORRISON & FOERSTER  
 ; STREET: 755 Page Mill Road  
 ; CITY: Palo Alto  
 ; STATE: California  
 ; COUNTRY: USA  
 ; ZIP: 94304-1018  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/121,446  
 ; FILING DATE:  
 ; CLASSIFICATION: 435  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 07/911,684  
 ; FILING DATE: 10-JUL-1992  
 ; ATTORNEY/AGENT INFORMATION:

```

; NAME: CIOTTI, THOMAS E.
; REGISTRATION NUMBER: 21,013
; REFERENCE/DOCKET NUMBER: 29900-20324.00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4105 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 485..1768
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 545
US-08-121-446-1

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Query Match          9.2%; Score 395.8; DB 4; Length 4105;
Best Local Similarity 65.7%; Pred. No. 2.5e-88;
Matches 634; Conservative 0; Mismatches 307; Indels 24; Gaps 3;

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Qy      505 TGCCAAGGACCCATCGAGATCAAGGAGACTTTCAAATACATCAACACGGTTGTGTCCTGC 564
        |||| |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Db      689 TGCCACAGCAGACTAAAATTACTTCAGCTTTCAAATACATTAACACTGTGATATCTTGT 748

Qy      565 CTTGTGTTTCGTGCTGGGGATCATCGGGAACCTCCACACTTCTGAGAATTATCTACAAGAAC 624
        |  |  ||| |  |||| |  |  |||| |  |  |||| |  |  |||| |  |  |||| |
Db      749 ACTATTTTCATCGTGGGAATGGTGGGGAATGCAACTCTGCTCAGGATCATTTACCAGAAC 808

Qy      625 AAGTGCATGCGAAACGGTCCCAATATCTTGATCGCCAGCTTGGCTCTGGGAGACCTGCTG 684
        || || ||| |  || || |||| |  |||| |||| |  || || |||| || |
Db      809 AAATGTATGAGGAATGGCCCCAACGCGCTGATAGCCAGTCTTGCCCTTGGAGACCTTATC 868

Qy      685 CACATCGTCATTGACATCCCTATCAATGTCTACAAGCTGCTGGCAGAGGACTGGCC---- 740
        |  |  |||| |||  |||| |||| || |  |||| |||| |  |  |||| |
Db      869 TATGTGGTCATTGATCTCCCTATCAATGTATTTAAGCTGCTGGCTGGGCGCTGGCCTTTT 928

Qy      741 -----ATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTTCATACAGAAAGCCTCC 789
        |||| |  |  |  |||| |  |  || ||  |||| |  |||| |
Db      929 GATCACAATGACTTTGGCGTATTTCTTTGCAAGCTGTTCCCCTTTTGCAGAAGTCCTCG 988

Qy      790 GTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATATCGAGCTGTTGCT 849
        |||| |  |||| |  || || |  || || |||| |  || || |||| |  || || |||| |
Db      989 GTGGGGATCACCGTCCTCAACCTCTGCGCTCTTAGTGTTGACAGGTACAGAGCAGTTGCC 1048

Qy      850 TCTTGGAGTAGAATTAAAGGAATTGGGGTTCCAAAATGGACAGCAGTAGAAATTGTTTTG 909
        || |||| |  |  |  |||| |||| |||| |  || || |  |||| || |
Db      1049 TCCTGGAGTCGTGTTTCAGGGAATTGGGATTCCTTTGGTAAGTCCATTGAAATTGTCTCC 1108

Qy      910 ATTTGGGTGGTCTCTGTGGTTCTGGCTGTCCCTGAAGCCATAGGTTTTGATATAATTACG 969
        || ||| |  |  || |  |  |||| |  |||| |||| |  || || |  || || |
Db      1109 ATCTGGATCCTGTCCTTTATCCTGGCCATTCTGAAGCGATTGGCTTCGTCATGGTACCC 1168

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Qy 970 ATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTTCAGAAGACAGCT 1029  
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 Db 1169 TTTGAATATAGGGGTGAACAGCATAAAACCTGTATGCTCAATGCC-----ACATCAAAA 1222  
 Qy 1030 TTCATGCAGTTTACAAAGACAGCAAAAGATTGGTGGCTGTTCAAGTTTCTATTTCTGCTTG 1089  
 | | | | | | | | | | | | | | | | | | | | | |  
 Db 1223 TTCATGGAGTTCTACCAAGATGTAAAGGACTGGTGGCTCTTCGGGTCTATTTCTGTATG 1282  
 Qy 1090 CCATTGGCCATCACTGCATTTTTTTATACACTAATGACCTGTGAAATGTTG---AGAAAAG 1146  
 | | | | | | | | | | | | | | | | | | | | | |  
 Db 1283 CCCTTGGTGTGCACTGCGATCTTCTACACCCTCATGACTTGTGAGATGTTGAACAGAAGG 1342  
 Qy 1147 AAAAGTGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAAGTGGCCAAA 1206  
 | | | | | | | | | | | | | | | | | | | | | |  
 Db 1343 AATGGCAGCTTGAGAATTGCCCTCAGTGAACATCTTAAGCAGCGTCGAGAAGTGGCAAAA 1402  
 Qy 1207 ACCGTCTTTTGCCTGGTCTTGTCTTTGCCCTCTGCTGGCTTCCCTTCACCTCAGCAGG 1266  
 | | | | | | | | | | | | | | | | | | | | | |  
 Db 1403 ACAGTTTCTGCTTGGTTGTAATTTTGTCTTTGCTGGTTCCTCTTCACTTAAGCCGT 1462  
 Qy 1267 ATTCTGAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGAACTTTGAAGCTTT 1326  
 | | | | | | | | | | | | | | | | | | | | | |  
 Db 1463 ATATTGAAGAAAAGTGTGTATAACGAAATGGACAAGAACCGATGTGAATTACTTAGTTTC 1522  
 Qy 1327 CTGTTGGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCCTGCATTAACCCA 1386  
 | | | | | | | | | | | | | | | | | | | | | |  
 Db 1523 TTAAGTCTCATGGATTACATCGGTATTAAGTGGCAACCATGAATTCATGTATAAACCCC 1582  
 Qy 1387 ATTGCTCTGTATTTGGTGAGCAAAAGATTCAAAAAGTCTTTAAGTCATGCTTATGCTGC 1446  
 | | | | | | | | | | | | | | | | | | | | | |  
 Db 1583 ATAGCTCTGTATTTGTGAGCAAGAAATTTAAAATTTGTTTCCAGTCATGCCTCTGCTGC 1642  
 Qy 1447 TGGTG 1451  
 | | | |  
 Db 1643 TGCTG 1647

RESULT 7

PCT-US92-02091-1

; Sequence 1, Application PC/TUS9202091

; GENERAL INFORMATION:

; APPLICANT: Battey Jr., James F.

; APPLICANT: Corjay, Martha H.

; APPLICANT: Feldman, Richard I.

; APPLICANT: Harkins, Richard N.

; TITLE OF INVENTION: RECEPTORS FOR BOMBESIN-LIKE PEPTIDES

; NUMBER OF SEQUENCES: 8

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Edwin P. Ching

; STREET: 1501 Harbor Bay Parkway

; CITY: Alameda

; STATE: CA

; COUNTRY: USA

; ZIP: 94501

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible



```

;   OPERATING SYSTEM:  PC-DOS/MS-DOS
;   SOFTWARE:  PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER:  PCT/US92/02091
;   FILING DATE:  19920313
;   CLASSIFICATION:  435
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER:  US 07/426,150
;   FILING DATE:  24-OCT-1989
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER:  US 07/533,659
;   FILING DATE:  05-JUN-1990
;   ATTORNEY/AGENT INFORMATION:
;   NAME:  Ching, Edwin P.
;   REGISTRATION NUMBER:  34090
;   REFERENCE/DOCKET NUMBER:  A-0092C
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE:  415-266-7476
;   TELEFAX:  415-266-7400
;   INFORMATION FOR SEQ ID NO:  1:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH:  1700 base pairs
;   TYPE:  NUCLEIC ACID
;   STRANDEDNESS:  double
;   TOPOLOGY:  linear
;   MOLECULE TYPE:  cDNA to mRNA
;   HYPOTHETICAL:  NO
;   ORIGINAL SOURCE:
;   ORGANISM:  Mus musculus
;   CELL LINE:  Swiss 3T3
;   IMMEDIATE SOURCE:
;   LIBRARY:  Lambda GT10
;   FEATURE:
;   NAME/KEY:  CDS
;   LOCATION:  378..1532
PCT-US92-02091-1

```

```

Query Match          3.1%;  Score 132.2;  DB 5;  Length 1700;
Best Local Similarity 56.9%;  Pred. No. 6.4e-23;
Matches 242;  Conservative 0;  Mismatches 183;  Indels 0;  Gaps 0;

```

```

Qy      535 TTCAAATACATCAACACGGTTGTGTCCTGCCTTGTGTTTCGTGCTGGGGATCATCGGGAAC 594
        ||||  ||  |||  |  |  |  |  |  |  |  |||  |  ||||  |  ||  |  ||  ||  ||
Db      495 TTCATCTATGTCATCCCTGCAGTTTATGGGCTTATCATCGTGATAGGTCTTATTGGCAAC 554

Qy      595 TCCACACTTCTGAGAATTATCTACAAGAACAAGTGCATGCGAAACGGTCCCAATATCTTG 654
        |||  ||  |  |  ||  ||  |  |  ||||  ||||  ||||  ||  ||  |  ||
Db      555 ATCACGCTCATCAAGATCTTCTGCACGGTCAAGTCCATGCGAAACGTGCCAAACCTGTTC 614

Qy      655 ATCGCCAGCTTGGCTCTGGGAGACCTGCTGCACATCGTCATTGACATCCCTATCAATGTC 714
        |||  |  |||  ||||  ||||  ||||  ||||  ||||  ||  ||  |  ||||  |  |||  |
Db      615 ATCTCTAGCCTGGCTTTGGGAGACCTGCTGCTGCTGGTGACATGCGCCCCTGTGGATGCC 674

Qy      715 TACAAGCTGCTGGCAGAGGACTGGCCATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTC 774
        ||||  ||||  ||  ||||  ||||  ||||  ||||  ||  ||  |||  |  ||  ||
Db      675 AGCAAGTACCTGGCTGACAGGTGGCTATTTGGCAGAATTGGCTGCAAACCTGATCCCCTTT 734

```

Qy 775 ATACAGAAAGCCTCCGTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGA 834  
 ||||| | || ||||| | |||| | | || ||||| |||||  
 Db 735 ATACAACTTACTTCAGTGGGGGTGTCTGTCTTCACACTTACGGCACTGTCAGCTGACAGG 794  
 Qy 835 TATCGAGCTGTTGCTTCTTGGAGTAGAATTAAAGGAATTGGGGTTCCAAAATGGACAGCA 894  
 || ||| ||| | || | | | | | | ||  
 Db 795 TACAAAGCCATTGTACGGCCAATGGATATCCAGGCATCCCATGCCCTGATGAAGATCTGT 854  
 Qy 895 GTAGAAATTGTTTTGATTTGGGTGGTCTCTGTGGTTCTGGCTGTCCCTGAAGCCATAGGT 954  
 | || ||||| ||| | ||||| || | |||| ||||| || | |  
 Db 855 CTCAAAGCTGCTTTGATCTGGATTGTCTCTATGTTGTTGGCCATCCAGAGGCTGTGTTT 914  
 Qy 955 TTTGA 959  
 | |||  
 Db 915 TCTGA 919

RESULT 8

US-08-724-394A-20

; Sequence 20, Application US/08724394A

; Patent No. 5872237

; GENERAL INFORMATION:

; APPLICANT: Feder, John N.

; APPLICANT: Kronmal, Gregory S.

; APPLICANT: Lauer, Peter M.

; APPLICANT: Ruddy, David A.

; APPLICANT: Thomas, Winston

; APPLICANT: Tsuchihashi, Zenta

; APPLICANT: Wolff, Roger K.

; TITLE OF INVENTION: Megabase Transcript Map: No. 5872237e1

; TITLE OF INVENTION: Sequences and Antibodies Thereto

; NUMBER OF SEQUENCES: 31

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP

; STREET: Two Embarcadero Center, 8th Floor

; CITY: San Francisco

; STATE: CA

; COUNTRY: USA

; ZIP: 94111-3834

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/724,394A

; FILING DATE: 01-OCT-1996

; CLASSIFICATION: 536

; ATTORNEY/AGENT INFORMATION:

; NAME: Fitts, Renee A.

; REGISTRATION NUMBER: 35,136

; REFERENCE/DOCKET NUMBER: 017957-000100

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 415-576-0200

; TELEFAX: 415-576-0300

; INFORMATION FOR SEQ ID NO: 20:

; SEQUENCE CHARACTERISTICS:

```
;   LENGTH: 246240 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: not relevant
;   TOPOLOGY: not relevant
;   MOLECULE TYPE: cDNA
;   FEATURE:
;     NAME/KEY: misc_feature
;     LOCATION: 1..246240
;     OTHER INFORMATION: /note= "HLA-H.CONTIG"
US-08-724-394A-20
```

```
Query Match          2.7%;   Score 114.6;   DB 2;   Length 246240;
Best Local Similarity 82.0%;   Pred. No. 2.5e-17;
Matches 132;   Conservative 0;   Mismatches 29;   Indels 0;   Gaps 0;
```

```
Qy          5 CATTCCGGTGGGGGACTCTGGCCAGCCCAGCAACGTGGATCCTGAGAGCACTCCCAGGT 64
      ||| || |||| |||| |||| |||| || || |||| ||||| ||||| |||||
Db   180691 CATCCCTACGGGGAAGTCCAGCCAGTTTGAGCGACACAGATCTGGAGAGCGCTCCCAGGT
180750
```

```
Qy          65 AGGCATTTGCCCCGGTGGGACGCCTTGCCAGAGCAGTGTGTGGCAGGCCCCCGTGGAGGA 124
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db   180751 AGGCAATTGCCCCGGTGGGAACGCCTCACCAGAGCAGCACGTGGCAGGCCCTCGTGGAGGA
180810
```

```
Qy          125 TCAACACAGTGGCTGAACACTGGGAAGGAACTGGTACTTGG 165
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db   180811 TCAACGCAGTGGCTGAACACCGGGAAGGAACTGGCACTTTG 180851
```

# RESULT 9

US-08-724-394A-21

```
; Sequence 21, Application US/08724394A
; Patent No. 5872237
```

## GENERAL INFORMATION:

```
; APPLICANT: Feder, John N.
; APPLICANT: Kronmal, Gregory S.
; APPLICANT: Lauer, Peter M.
; APPLICANT: Ruddy, David A.
; APPLICANT: Thomas, Winston
; APPLICANT: Tsuchihashi, Zenta
; APPLICANT: Wolff, Roger K.
; TITLE OF INVENTION: Megabase Transcript Map: No. 5872237e1
; TITLE OF INVENTION: Sequences and Antibodies Thereto
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
```

```

; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/724,394A
; FILING DATE: 01-OCT-1996
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Fitts, Renee A.
; REGISTRATION NUMBER: 35,136
; REFERENCE/DOCKET NUMBER: 017957-000100
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-576-0200
; TELEFAX: 415-576-0300
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 246240 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1..246240
; OTHER INFORMATION: /note= "HLA-H.CONTIG"
US-08-724-394A-21

```

```

Query Match          2.7%; Score 114.6; DB 2; Length 246240;
Best Local Similarity 82.0%; Pred. No. 2.5e-17;
Matches 132; Conservative 0; Mismatches 29; Indels 0; Gaps 0;

```

```

Qy          5 CATTCCGGTGGGGGACTCTGGCCAGCCCGAGCAACGTGGATCCTGAGAGCACTCCCAGGT 64
             ||| ||   ||| ||| ||| ||| ||| ||   ||| ||| ||| ||| |||
Db    180691 CATCCCTACGGGGAAGTCCAGCCAGTTTGAGCGACACAGATCTGGAGAGCGCTCCCAGGT
180750

Qy          65 AGGCATTTGCCCCGGTGGGACGCCTTGCCAGAGCAGTGTGTGGCAGGCCCGTGGAGGA 124
             ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db    180751 AGGCAATTGCCCCGGTGGAAACGCCTCACCAGAGCAGCACGTGGCAGGCCCTCGTGGAGGA
180810

Qy          125 TCAACACAGTGGCTGAACACTGGGAAGGAAGTGGTACTTGG 165
             ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db    180811 TCAACGCAGTGGCTGAACACCGGGAAGGAAGTGGCACTTTG 180851

```

# RESULT 10

US-08-724-394A-22

; Sequence 22, Application US/08724394A

; Patent No. 5872237

## ; GENERAL INFORMATION:

; APPLICANT: Feder, John N.

; APPLICANT: Kronmal, Gregory S.

; APPLICANT: Lauer, Peter M.

; APPLICANT: Ruddy, David A.

; APPLICANT: Thomas, Winston

; APPLICANT: Tsuchihashi, Zenta

; APPLICANT: Wolff, Roger K.

; TITLE OF INVENTION: Megabase Transcript Map: No. 5872237e1

; TITLE OF INVENTION: Sequences and Antibodies Thereto

```

; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/724,394A
; FILING DATE: 01-OCT-1996
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Fitts, Renee A.
; REGISTRATION NUMBER: 35,136
; REFERENCE/DOCKET NUMBER: 017957-000100
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-576-0200
; TELEFAX: 415-576-0300
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 246240 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1..246240
; OTHER INFORMATION: /note= "HLA-H.CONTIG"
US-08-724-394A-22

```

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Query Match          2.7%; Score 114.6; DB 2; Length 246240;
Best Local Similarity 82.0%; Pred. No. 2.5e-17;
Matches 132; Conservative 0; Mismatches 29; Indels 0; Gaps 0;

```

```

Qy          5 CATTCCGGTGGGGGACTCTGGCCAGCCCGAGCAACGTGGATCCTGAGAGCACTCCCAGGT 64
             ||| ||  |||| ||||  ||||  ||||  ||  ||||  |||||  |||||
Db    180691 CATCCCTACGGGGAACCTCCAGCCAGTTTGTAGCGACACAGATCTGGAGAGCGCTCCCAGGT
180750

Qy          65 AGGCATTTGCCCCGGTGGGACGCCTTGCCAGAGCAGTGTGTGGCAGGCCCCCGTGGAGGA 124
             |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db    180751 AGGCAATTGCCCCGGTGGAAACGCCTCACCAGAGCAGCACGTGGCAGGCCCTCGTGGAGGA
180810

Qy          125 TCAACACAGTGGCTGAACACTGGGAAGGAACTGGTACTTGG 165
             |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db    180811 TCAACGCAGTGGCTGAACACCGGGAAGGAACTGGCACTTTG 180851

```

RESULT 11

PCT-US92-02091-5  
; Sequence 5, Application PC/TUS9202091  
; GENERAL INFORMATION:  
; APPLICANT: Battey Jr., James F.  
; APPLICANT: Corjay, Martha H.  
; APPLICANT: Feldman, Richard I.  
; APPLICANT: Harkins, Richard N.  
; TITLE OF INVENTION: RECEPTORS FOR BOMBESIN-LIKE PEPTIDES  
; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Edwin P. Ching  
; STREET: 1501 Harbor Bay Parkway  
; CITY: Alameda  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94501  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US92/02091  
; FILING DATE: 19920313  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/426,150  
; FILING DATE: 24-OCT-1989  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/533,659  
; FILING DATE: 05-JUN-1990  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Ching, Edwin P.  
; REGISTRATION NUMBER: 34090  
; REFERENCE/DOCKET NUMBER: A-0092C  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-266-7476  
; TELEFAX: 415-266-7400  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1584 base pairs  
; TYPE: NUCLEIC ACID  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA to mRNA  
; HYPOTHETICAL: NO  
; ORIGINAL SOURCE:  
; ORGANISM: Rattus rattus  
; TISSUE TYPE: Esophagus  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 132..1304  
PCT-US92-02091-5

Query Match 2.5%; Score 108.8; DB 5; Length 1584;  
Best Local Similarity 54.8%; Pred. No. 4.1e-17;  
Matches 215; Conservative 0; Mismatches 177; Indels 0; Gaps 0;

|    |     |   |     |
|----|-----|---|-----|
| Qy | 572 | TCGTGCTGGGGATCATCGGGAACCTCCACACTTCTGAGAATTATCTACAAGAACAAGTGCA | 631 |
|    |     |   |     |
| Db | 292 | TCTCGGTGGGCTTGCTGGGGCAACATCATGCTGGTGAAGATATTCCTCACCAACAGCACCA | 351 |
| Qy | 632 | TGCGAAACGGTCCCAATATCTTGATCGCCAGCTTGGCTCTGGGAGACCTGCTGCACATCG  | 691 |
|    |     |   |     |
| Db | 352 | TGCGGAGTGTCCCAACATCTTCATCTCTAACCTGGCTGCGGGAGACCTGCTGCTGCTGC   | 411 |
| Qy | 692 | TCATTGACATCCCTATCAATGTCTACAAGCTGCTGGCAGAGGACTGGCCATTTGGAGCTG  | 751 |
|    |     |   |     |
| Db | 412 | TGACCTGCGTCCCAGTGGATGCCTCCCGATACTTCTTTGATGAATGGGTGTTCTGGCAAGC | 471 |
| Qy | 752 | AGATGTGTAAGCTGGTGCCTTTCATACAGAAAGCCTCCGTGGGAATCACTGTGCTGAGTC  | 811 |
|    |     |   |     |
| Db | 472 | TGGGCTGCAAACCTCATCCCAGCCATCCAGCTCACCTCGGTGGGGGTTTCCGTGTTCACTC | 531 |
| Qy | 812 | TATGTGCTCTGAGTATTGACAGATATCGAGCTGTTGCTTCTTGAGTAGAATTAAAGGAA   | 871 |
|    |     |   |     |
| Db | 532 | TCACGGCCCTCAGCGTGACAGGTACAGAGCTATCGTGAACCCCATGGACATGCAGACGT   | 591 |
| Qy | 872 | TTGGGGTTCCAAAATGGACAGCAGTAGAAATTGTTTTGATTTGGGTGGTCTCTGTGGTTC  | 931 |
|    |     |   |     |
| Db | 592 | CTGGTGTGGTGTCTGTGGACCAGTTTGAAGGCCGTGGGCATCTGGGTGGTCTCTGTGCTGT | 651 |
| Qy | 932 | TGGCTGTCCCTGAAGCCATAGGTTTTGATATA                              | 963 |
|    |     |   |     |
| Db | 652 | TGGCTGTCCCTGAGGCTGTGTTTTCGGAAGTA                              | 683 |

## RESULT 12

US-09-175-658B-25/c

; Sequence 25, Application US/09175658B

; Patent No. 6372900

## ; GENERAL INFORMATION:

; APPLICANT: METALLINOS, DANIKA

; APPLICANT: RINE, JASPER

; APPLICANT: BOWLING, ANN

10 TITLE OF INVENTION: HORSE ENDOTHELIN-B RECEPTOR GENE AND GENE PRODUCTS

; FILE REFERENCE: GOBR-110

: CURRENT APPLICATION NUMBER: US/09/175,658B

: CURRENT FILING DATE: 1998-10-20

: PRIOR APPLICATION NUMBER: 60/062,562

; PRIOR FILING DATE: 1997-10-21

```

; NUMBER OF SEQ ID NOS: 25

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; SOFTWARE: PatentIn Ver. 2.1

```

; SEO ID NO 25

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; LENGTH: 801

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; TYPE: DNA

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: ORGANISM: Horse

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; FEATURE:

```

```

; OTHER INFORMATION: Uncertain of the nucleotide sequence at positions

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OTHER INFORMATION: 30, 54, 286, 436, 445, 542, 614, 617, 624, 641,

OTHER INFORMATION: 731, 746, 753, 770, 775 and 793.

US-09-175-658B-25

Query Match

2.5%; Score 107.2; DB 4; Length 801;

Best Local Similarity 86.8%; Pred. No. 7e-17;  
Matches 118; Conservative 0; Mismatches 18; Indels 0; Gaps 0;

```
Qy      1408 AAAAGATTCAAAAAGTCTTTAAGTCATGCTTATGCTGCTGGTGCCAGTCATTTGAAGAA 1467
          ||| || | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      223 AAACGAGTTATTTGTTTTGTACAGTCGTGCTTATGCTGCTGGTGCCAATCATTTGAAGAA 164

Qy      1468 AAACAGTCCTTGGAGGAAAAGCAGTCGTGCTTAAAGTTCAAAGCTAATGATCACGGATAT 1527
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      163 AAACAGTCCTTGAAGACAAGCAGTCATGCTTAAAGTTCAAAGCTAATGATCACGGATAT 104

Qy      1528 GACAACTTCCGTTCCA 1543
          ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      103 GACAACTTCCGTTCCA 88
```

RESULT 13

US-09-120-772-1

; Sequence 1, Application US/09120772

; Patent No. 6143521

; GENERAL INFORMATION:

; APPLICANT: LANE, PAMELA

; APPLICANT: TSUI, PING

; APPLICANT: ELSHOUBAGY, NABIL

; TITLE OF INVENTION: HUMAN BOMBESIN RECEPTOR SUBTYPE

; TITLE OF INVENTION: 3

; NUMBER OF SEQUENCES: 2

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Ratner & Prestia

; STREET: P.O. Box 980

; CITY: Valley Forge

; STATE: PA

; COUNTRY: USA

; ZIP: 19482

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSEQ for Windows Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/120,772

; FILING DATE: 22-JUL-1998

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER:

; FILING DATE:

; ATTORNEY/AGENT INFORMATION:

; NAME: Prestia, Paul F

; REGISTRATION NUMBER: 23,031

; REFERENCE/DOCKET NUMBER: GP-70505

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 610-407-0700

; TELEFAX: 610-407-0700

; TELEX: 846169

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1205 base pairs



; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
US-09-120-772-1

Query Match 2.5%; Score 106.6; DB 3; Length 1205;  
Best Local Similarity 48.5%; Pred. No. 1.2e-16;  
Matches 425; Conservative 0; Mismatches 434; Indels 18; Gaps 4;

```
Qy      578 TGGGGATCATCGGGAAGTCCACACTTCTGAGAATTATCTACAAGAACAAGTGCATGCGAA 637
      |||| ||| | || || | | | | | | | | | | | | | | | |
Db      181 TGGGCATCCTTGGAAATGCTATTCTCATCAAAGTCTTTTCAAGACCAAATCCATGCAAA 240

Qy      638 ACGGTCCCAATATCTTGATCGCCAGCTTGGCTCTGGGAGACCTGCTGCACATCGTCATTG 697
      | ||| |||| | || | |||| | |||| | | | | | | | | | |
Db      241 CAGTTCCAAATATTTTCATCACCAGCCTGGCTTTTGGAGATCTTTTACTTCTGCTAACTT 300

Qy      698 ACATCCCTATCAATGTCTACAAGCTGCTGGCAGAGGACTGGCCATTTGGAGCTGAGATGT 757
      | || | || | | | | | | | | | | | | | | | | |
Db      301 GTGTGCCAGTGGATGCAACTCACTACCTTGAGAAGGATGGCTGTTCGGAAGAATTGGTT 360

Qy      758 GTAAGCTGGTGCCTTTTCATACAGAAAGCCTCCGTGGGAATCACTGTGCTGAGTCTATGTG 817
      |||| | | | | |||| | | | | | | | | | | | | | |
Db      361 GTAAGGTGCTCTCTTTTCATCCGGCTCACTTCTGTTGGTGTGTGAGTGTTCACATTAGCAA 420

Qy      818 CTCTGAGTATTGACAGATATCGAGCTGTTGCTTCTTGGAGTAGAATTAAGGAATTGGGG 877
      ||| || | |||| | | | | | | | | | | | | | | |
Db      421 TTCTCAGCGCTGACAGATACAAGGCAGTTGTGAAGCCACTTGAGCGACAGCCCTCCAATG 480

Qy      878 TTCCAAATGGACAGCAGTAGAAATTGTTTTGATTTGGGTGGTCTCTGTGGTTCTGGCTG 937
      ||| | | | | | | | | | | | | | | | | | | | | |
Db      481 CCATCCTGAAGACTTGTGTAAAAGCTGGCTGCGTCTGGATCGTGTCTATGATATTTGCTC 540

Qy      938 TCCCTGAAGCCATAGGTTTTGATATA-----ATTACGATGGACTACAAAGGAAGTTATCT 992
      | |||| | | || | | | | | | | | | | | | | | | |
Db      541 TACCTGAGGCTATATTTTCAAATGTATACACTTTTCGAGATCCCAATAAAATATGACAT 600

Qy      993 GCGAATCTGCTTGCT-TCATCCCGTTTCAAGACAGCTTTTCATGCAGTTTTACAAGACAG 1051
      |||| | | | | || | | | | | | | | | | | | | |
Db      601 TTGAATCATGTACCTCTTATCCTGTCTCTAAGAAGCTCTTGCAAGAAATACATTCTCTGC 660

Qy      1052 CAAAAGATTGGTGGCTGTTTCAGTTTCTATTTCTGCTTGCCATTGGCCATCACTGCATTTT 1111
      | | | | | | | | | | | | | | | | | | | | | |
Db      661 TGTGCTTCTTAGTGTTCTACATTATTCACCTCTCTATTATCTCTGTCTACTATTCTTGA 720

Qy      1112 TTTATACACTAATGACCTGTGAAATGTTGAGAAAGAAAAGTGGCATGCAGATTGCTTTAA 1171
      || || | | | | | | | | | | | | | | | | | |
Db      721 TTGCTAGGACCCTTTACAAAAGCACCTGAACATACCTACTGAGGAACAAAGCCATGCCC 780

Qy      1172 ATGATCACCTAAAGCAGAGACGGGAAGTGGCCAAAACCGTCTTTTGCTGGTCTTGTCT 1231
      | | || | | | | | | | | | | | | | | | | | |
Db      781 GTAAGCAGATTGAATCCCGAAAGAGAATTGCCAGAACGGTATTGGTGTGGTGGCTCTGT 840

Qy      1232 TTGCCCTCTGCTGGCTTCCCTTCACCTCAGCAGGATTCTGAAGCTCACTCTTTATAATC 1291
      |||| | | | | | | | | | | | | | | | | | |
Db      841 TTGCCCTCTGCTGGTTGCCAAATCACCTC-----CTGTACCTCTACCATTCATTCA 891
```

Qy 1292 AGAATGATCCCAATAGATGTGAACTTTTGAGCTTTCTGTTGGTATTGGACTATATTGGTA 1351  
 | | | | | | | | | | | | | | | | | | |  
 Db 892 CTTCTCAAACCTATGTA---GACCCCTCTGCCATGCATTTTCATTTTCACCATTTTCTCTC 948  
 Qy 1352 TCAACATGGCTTCACTGAATTCCTGCATTAACCCAATTGCTCTGTATTTGGTGAGCAAAA 1411  
 | | | | | | | | | | | | | | | | | | | | | | |  
 Db 949 GGGTTTGGCTTTTCAGCAATTCTTGCGTAAACCCCTTTGCTCTCTACTGGCTGAGCAAAA 1008  
 Qy 1412 GATTCAAAAAGCTGCTTTAAGTCATGCTTATGCTGCTG 1448  
 | | | | | | | | | | | | | | | | | | |  
 Db 1009 GCTTCCAGAAGCATTTTAAAGCTCAGTTGTTCTGTTG 1045

RESULT 14

US-09-016-434-1275

; Sequence 1275, Application US/09016434

; Patent No. 6500938

; GENERAL INFORMATION:

; APPLICANT: Janice Au-Young

; APPLICANT: Jeffrey J. Seilhamer

; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING

; TITLE OF INVENTION: PATHWAY GENE EXPRESSION

; NUMBER OF SEQUENCES: 1490

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.

; STREET: 3174 PORTER DRIVE

; CITY: PALO ALTO

; STATE: CALIFORNIA

; COUNTRY: USA

; ZIP: 94304

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/016,434

; FILING DATE: HERewith

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER:

; FILING DATE:

; CLASSIFICATION:

; ATTORNEY/AGENT INFORMATION:

; NAME: Zeller, Karen J.

; REGISTRATION NUMBER: 37,071

; REFERENCE/DOCKET NUMBER: PA-0002 US

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (650) 855-0555

; TELEFAX: (650) 845-4166

; INFORMATION FOR SEQ ID NO: 1275:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1413 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; IMMEDIATE SOURCE:  
; LIBRARY: GENBANK  
; CLONE: g291876  
US-09-016-434-1275

Query Match 2.5%; Score 106.6; DB 4; Length 1413;  
Best Local Similarity 48.5%; Pred. No. 1.4e-16;  
Matches 425; Conservative 0; Mismatches 434; Indels 18; Gaps 4;

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Qy      638 ACGGTCCCAATATCTTGATCGCCAGCTTGGCTCTGGGAGACCTGCTGCACATCGTCATTG 697
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Db      388 CAGTTCCAAATATTTTCATCACCAGCCTGGCTTTTGGAGATCTTTTACTTCTGCTAACTT 447

Qy      698 ACATCCCTATCAATGTCTACAAGCTGCTGGCAGAGGACTGGCCATTTGGAGCTGAGATGT 757
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Db      448 GTGTGCCAGTGGATGCAACTCACTACCTTGCAAGGATGGCTGTTTCGGAAGAATTGGTT 507

Qy      758 GTAAGCTGGTGCCTTTCATACAGAAAGCCTCCGTGGGAATCACTGTGCTGAGTCTATGTG 817
      ||||| || | ||||| | | | | | | | | | | | | |
Db      508 GTAAGGTGCTCTCTTTCATCCGGCTCACTTCTGTTGGTGTGTGTCAGTGTTCACATTAACAA 567

Qy      818 CTCTGAGTATTGACAGATATCGAGCTGTTGCTTCTTGGAGTAGAATTAAAGGAATTGGGG 877
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Db      568 TTCTCAGCGCTGACAGATACAAGGCAGTTGTGAAGCCACTTGAGCGACAGCCCTCCAATG 627

Qy      878 TTCCAAATGGACAGCAGTAGAAATTGTTTTGATTGGGTGGTCTCTGTGGTTCTGGCTG 937
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Qy      938 TCCCTGAAGCCATAGGTTTTGATATA-----ATTACGATGGACTACAAAGGAAGTTATCT 992
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RESULT 15

US-09-016-434-1215

; Sequence 1215, Application US/09016434

; Patent No. 6500938

; GENERAL INFORMATION:

; APPLICANT: Janice Au-Young

; APPLICANT: Jeffrey J. Seilhamer

; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING

; TITLE OF INVENTION: PATHWAY GENE EXPRESSION

; NUMBER OF SEQUENCES: 1490

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.

; STREET: 3174 PORTER DRIVE

; CITY: PALO ALTO

; STATE: CALIFORNIA

; COUNTRY: USA

; ZIP: 94304

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/016,434

; FILING DATE: HERewith

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER:

; FILING DATE:

; CLASSIFICATION:

; ATTORNEY/AGENT INFORMATION:

; NAME: Zeller, Karen J.

; REGISTRATION NUMBER: 37,071

; REFERENCE/DOCKET NUMBER: PA-0002 US

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (650) 855-0555

; TELEFAX: (650) 845-4166

; INFORMATION FOR SEQ ID NO: 1215:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1726 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; IMMEDIATE SOURCE:

; LIBRARY: GENBANK  
; CLONE: g183649  
US-09-016-434-1215

Query Match 2.5%; Score 106; DB 4; Length 1726;  
Best Local Similarity 52.0%; Pred. No. 2.1e-16;  
Matches 238; Conservative 0; Mismatches 220; Indels 0; Gaps 0;

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Job time : 274.574 secs

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: May 14, 2004, 10:14:36 ; Search time 1634.24 Seconds  
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Perfect score: 4301  
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Searched: 2947324 seqs, 2269024515 residues

Total number of hits satisfying chosen parameters: 5894648

Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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19: /cgn2\_6/ptodata/2/pubpna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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| 2    | 4284.4 | 99.6  | 4286   | 10 | US-09-921-406C-13   | Sequence 13, Appl |
| 3    | 4284.4 | 99.6  | 4286   | 15 | US-10-225-567A-113  | Sequence 113, App |
| 4    | 4284.4 | 99.6  | 4286   | 15 | US-10-007-926A-177  | Sequence 177, App |
| 5    | 4284.4 | 99.6  | 4286   | 15 | US-10-210-120-15    | Sequence 15, Appl |
| 6    | 4284.4 | 99.6  | 4286   | 16 | US-10-372-683-48    | Sequence 48, Appl |
| 7    | 4202.4 | 97.7  | 4305   | 13 | US-10-116-802-116   | Sequence 116, App |
| c 8  | 2841.8 | 66.1  | 183337 | 15 | US-10-020-141-5     | Sequence 5, Appli |
| 9    | 1684.6 | 39.2  | 1892   | 13 | US-10-116-802-117   | Sequence 117, App |
| 10   | 1676.6 | 39.0  | 1877   | 13 | US-10-116-802-118   | Sequence 118, App |
| 11   | 1466.8 | 34.1  | 1470   | 16 | US-10-305-720-1203  | Sequence 1203, Ap |
| 12   | 1389   | 32.3  | 1632   | 12 | US-10-311-671-28    | Sequence 28, Appl |
| 13   | 1322.6 | 30.8  | 1329   | 11 | US-09-826-509-496   | Sequence 496, App |
| 14   | 1220.4 | 28.4  | 1578   | 13 | US-10-235-192A-32   | Sequence 32, Appl |
| 15   | 763.2  | 17.7  | 800    | 9  | US-09-778-927A-27   | Sequence 27, Appl |
| c 16 | 440.6  | 10.2  | 592    | 9  | US-09-962-436-531   | Sequence 531, App |
| c 17 | 440.6  | 10.2  | 592    | 9  | US-09-880-107-2060  | Sequence 2060, Ap |
| c 18 | 440.6  | 10.2  | 592    | 9  | US-09-954-531-917   | Sequence 917, App |
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| 20   | 395.8  | 9.2   | 4079   | 16 | US-10-305-720-1257  | Sequence 1257, Ap |
| 21   | 395.8  | 9.2   | 4105   | 9  | US-09-931-157-1     | Sequence 1, Appli |
| 22   | 395.8  | 9.2   | 4105   | 15 | US-10-225-567A-115  | Sequence 115, App |
| 23   | 395.8  | 9.2   | 4105   | 15 | US-10-007-926A-229  | Sequence 229, App |
| 24   | 395.8  | 9.2   | 4105   | 15 | US-10-101-510-370   | Sequence 370, App |
| 25   | 395.8  | 9.2   | 4105   | 16 | US-10-372-683-46    | Sequence 46, Appl |
| 26   | 392.6  | 9.1   | 1284   | 11 | US-09-826-509-494   | Sequence 494, App |
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| c 29 | 302    | 7.0   | 363    | 9  | US-09-954-456-209   | Sequence 209, App |
| c 30 | 302    | 7.0   | 363    | 9  | US-09-954-456-467   | Sequence 467, App |
| c 31 | 302    | 7.0   | 363    | 9  | US-09-954-456-925   | Sequence 925, App |
| c 32 | 302    | 7.0   | 363    | 9  | US-09-954-456-1550  | Sequence 1550, Ap |
| c 33 | 302    | 7.0   | 363    | 9  | US-09-880-107-2076  | Sequence 2076, Ap |
| c 34 | 302    | 7.0   | 363    | 10 | US-09-873-367C-129  | Sequence 129, App |
| c 35 | 275    | 6.4   | 307    | 10 | US-09-921-406C-12   | Sequence 12, Appl |
| 36   | 152.2  | 3.5   | 6896   | 13 | US-09-854-867-422   | Sequence 422, App |
| 37   | 148.8  | 3.5   | 1889   | 9  | US-09-867-701-10875 | Sequence 10875, A |
| 38   | 147.6  | 3.4   | 3697   | 13 | US-10-363-616-178   | Sequence 178, App |
| c 39 | 144    | 3.3   | 60381  | 13 | US-10-087-192-970   | Sequence 970, App |
| 40   | 131.6  | 3.1   | 1330   | 10 | US-09-374-046A-151  | Sequence 151, App |
| 41   | 131.6  | 3.1   | 1330   | 13 | US-10-616-263-151   | Sequence 151, App |
| 42   | 131    | 3.0   | 7813   | 13 | US-09-854-867-27    | Sequence 27, Appl |
| c 43 | 128.4  | 3.0   | 503    | 15 | US-10-264-283-84    | Sequence 84, Appl |
| c 44 | 128.4  | 3.0   | 738    | 13 | US-10-276-774-868   | Sequence 868, App |
| 45   | 128.4  | 3.0   | 858    | 15 | US-10-198-846-12892 | Sequence 12892, A |

#### ALIGNMENTS

##### RESULT 1

US-09-931-157-2

; Sequence 2, Application US/09931157

; Patent No. US20020082414A1

; GENERAL INFORMATION:

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; APPLICANT: Imura, Hiroo
; APPLICANT: Nakao, Kazuwa
; APPLICANT: Nakanishi, Shigetada
; TITLE OF INVENTION: Human Endothelin Receptor
; FILE REFERENCE: 299002032411
; CURRENT APPLICATION NUMBER: US/09/931,157
; CURRENT FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 08/121,446
; PRIOR FILING DATE: 1993-09-14
; PRIOR APPLICATION NUMBER: 07/911,684
; PRIOR FILING DATE: 1992-07-10
; PRIOR APPLICATION NUMBER: JP 3-172828
; PRIOR FILING DATE: 1991-07-12
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 4301
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (238)...(1566)
US-09-931-157-2

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Query Match          100.0%; Score 4301; DB 9; Length 4301;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4301; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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| Db | 481  | <br>CCACGCACCATCTCCCCCTCCCCCGTGCCAAGGACCCATCGAGATCAAGGAGACTTTCAAA  | 540  |
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| Db | 541  | <br>TACATCAACACGGTTGTGTCCTGCCTTGTGTTTCGTGCTGGGGATCATCGGGAACCTCCACA | 600  |
| Qy | 601  | CTTCTGAGAATTATCTACAAGAACAAGTGCATGCGAAACGGTCCCAATATCTTGATCGCC       | 660  |
| Db | 601  | <br>CTTCTGAGAATTATCTACAAGAACAAGTGCATGCGAAACGGTCCCAATATCTTGATCGCC   | 660  |
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| Db | 721  | <br>CTGCTGGCAGAGGACTGGCCATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTCATACAG   | 780  |
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| Db | 841  | <br>GCTGTTGCTTCTTGGAGTAGAATTAAAGGAATTGGGGTTCCAAAATGGACAGCAGTAGAA   | 900  |
| Qy | 901  | ATTGTTTTGATTTGGGTGGTCTCTGTGGTTCTGGCTGTCCCTGAAGCCATAGGTTTTGAT       | 960  |
| Db | 901  | <br>ATTGTTTTGATTTGGGTGGTCTCTGTGGTTCTGGCTGTCCCTGAAGCCATAGGTTTTGAT   | 960  |
| Qy | 961  | ATAATTACGATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTTCAG       | 1020 |
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| Qy | 1021 | AAGACAGCTTTCATGCAGTTTTTACAAGACAGCAAAAGATTGGTGGCTGTTTCAGTTTCTAT     | 1080 |
| Db | 1021 | <br>AAGACAGCTTTCATGCAGTTTTTACAAGACAGCAAAAGATTGGTGGCTGTTTCAGTTTCTAT | 1080 |
| Qy | 1081 | TTCTGCTTGCCATTGGCCATCACTGCATTTTTTTTATACACTAATGACCTGTGAAATGTTG      | 1140 |
| Db | 1081 | <br>TTCTGCTTGCCATTGGCCATCACTGCATTTTTTTTATACACTAATGACCTGTGAAATGTTG  | 1140 |
| Qy | 1141 | AGAAAGAAAAGTGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAAGTG       | 1200 |
| Db | 1141 | <br>AGAAAGAAAAGTGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAAGTG   | 1200 |
| Qy | 1201 | GCCAAAACCGTCTTTTGCCTGGTCCTTGTCTTTGCCCTCTGCTGGCTTCCCCTTCACCTC       | 1260 |
| Db | 1201 | <br>GCCAAAACCGTCTTTTGCCTGGTCCTTGTCTTTGCCCTCTGCTGGCTTCCCCTTCACCTC   | 1260 |
| Qy | 1261 | AGCAGGATTCTGAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGAACTTTTG       | 1320 |
|    |      |  |      |

|    |      |  |      |
|----|------|--|------|
| Db | 1261 | AGCAGGATTCTGAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGAACTTTTG   | 1320 |
| Qy | 1321 | AGCTTTCTGTTGGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCCTGCATT   | 1380 |
|    |      |  |      |
| Db | 1321 | AGCTTTCTGTTGGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCCTGCATT   | 1380 |
| Qy | 1381 | AACCCAATTGCTCTGTATTTGGTGAGCAAAAAGATTCAAAAAGCTGCTTTAAGTCATGCTTA | 1440 |
|    |      |  |      |
| Db | 1381 | AACCCAATTGCTCTGTATTTGGTGAGCAAAAAGATTCAAAAAGCTGCTTTAAGTCATGCTTA | 1440 |
| Qy | 1441 | TGCTGCTGGTGCCAGTCATTTGAAGAAAAACAGTCCTTGAGGAAAAGCAGTCGTGCTTA    | 1500 |
|    |      |  |      |
| Db | 1441 | TGCTGCTGGTGCCAGTCATTTGAAGAAAAACAGTCCTTGAGGAAAAGCAGTCGTGCTTA    | 1500 |
| Qy | 1501 | AAGTTCAAAGCTAATGATCACGGATATGACAACTTCCGTTCCAGTAATAAAATACAGCTCA  | 1560 |
|    |      |  |      |
| Db | 1501 | AAGTTCAAAGCTAATGATCACGGATATGACAACTTCCGTTCCAGTAATAAAATACAGCTCA  | 1560 |
| Qy | 1561 | TCTTGAAAGAAGAAGCTATTCACTGTATTTTCAATTTCTTTATATTGGACCGAAGTCATTAA | 1620 |
|    |      |  |      |
| Db | 1561 | TCTTGAAAGAAGAAGCTATTCACTGTATTTTCAATTTCTTTATATTGGACCGAAGTCATTAA | 1620 |
| Qy | 1621 | AACAAAATGAAACATTTGCCAAAACAAAACAAAAGCTATGTATTTGCACAGCACACTAT    | 1680 |
|    |      |  |      |
| Db | 1621 | AACAAAATGAAACATTTGCCAAAACAAAACAAAAGCTATGTATTTGCACAGCACACTAT    | 1680 |
| Qy | 1681 | TAAAATATTAAGTGTAATTATTTTAACACTCACAGCTACATATGACATTTTATGAGCTGT   | 1740 |
|    |      |  |      |
| Db | 1681 | TAAAATATTAAGTGTAATTATTTTAACACTCACAGCTACATATGACATTTTATGAGCTGT   | 1740 |
| Qy | 1741 | TTACGGCATGGAAAGAAAATCAGTGGGAATTAAGAAAGCCTCGTCGTGAAAGCACTTAAT   | 1800 |
|    |      |  |      |
| Db | 1741 | TTACGGCATGGAAAGAAAATCAGTGGGAATTAAGAAAGCCTCGTCGTGAAAGCACTTAAT   | 1800 |
| Qy | 1801 | TTTTTACAGTTAGCACTTCAACATAGCTCTTAACAACCTCCAGGATATTCACACAACACT   | 1860 |
|    |      |  |      |
| Db | 1801 | TTTTTACAGTTAGCACTTCAACATAGCTCTTAACAACCTCCAGGATATTCACACAACACT   | 1860 |
| Qy | 1861 | TAGGCTTAAAAATGAGCTCACTCAGAATTTCTATTCTTTCTAAAAGAGATTTATTTTTTA   | 1920 |
|    |      |  |      |
| Db | 1861 | TAGGCTTAAAAATGAGCTCACTCAGAATTTCTATTCTTTCTAAAAGAGATTTATTTTTTA   | 1920 |
| Qy | 1921 | AATCAATGGGACTCTGATATAAAGGAAGAATAAGTCACTGTAAAACAGAACTTTTAAATG   | 1980 |
|    |      |  |      |
| Db | 1921 | AATCAATGGGACTCTGATATAAAGGAAGAATAAGTCACTGTAAAACAGAACTTTTAAATG   | 1980 |
| Qy | 1981 | AAGCTTAAATTACTCAATTTAAATTTTAAATCCTTTAAACAACCTTTTCAATTAATAT     | 2040 |
|    |      |  |      |
| Db | 1981 | AAGCTTAAATTACTCAATTTAAATTTTAAATCCTTTAAACAACCTTTTCAATTAATAT     | 2040 |
| Qy | 2041 | TATCACACTATTATCAGATTGTAATTAGATGCAAATGAGAGAGCAGTTTAGTTGTTGCAT   | 2100 |
|    |      |  |      |
| Db | 2041 | TATCACACTATTATCAGATTGTAATTAGATGCAAATGAGAGAGCAGTTTAGTTGTTGCAT   | 2100 |
| Qy | 2101 | TTTTCGGACACTGGAAACATTTAAATGATCAGGAGGGAGTAACAGAAAGAGCAAGGCTGT   | 2160 |
|    |      |  |      |
| Db | 2101 | TTTTCGGACACTGGAAACATTTAAATGATCAGGAGGGAGTAACAGAAAGAGCAAGGCTGT   | 2160 |

|    |      |  |      |
|----|------|--|------|
| Qy | 2161 | TTTTGAAAATCATTACACTTTTCTACTAGAAGCCCAAACCTCAGCATTCTGCAATATGTAAC | 2220 |
|    |      |  |      |
| Db | 2161 | TTTTGAAAATCATTACACTTTTCTACTAGAAGCCCAAACCTCAGCATTCTGCAATATGTAAC | 2220 |
| Qy | 2221 | CAACATGTCACAAACAAGCAGCATGTAACAGACTGGCACATGTGCCAGCTGAATTTAAAA   | 2280 |
|    |      |  |      |
| Db | 2221 | CAACATGTCACAAACAAGCAGCATGTAACAGACTGGCACATGTGCCAGCTGAATTTAAAA   | 2280 |
| Qy | 2281 | TATAATACTTTTAAAAAGAAAATTATTACATCCTTTACATTAGTTAAGATCAAACCTCA    | 2340 |
|    |      |  |      |
| Db | 2281 | TATAATACTTTTAAAAAGAAAATTATTACATCCTTTACATTAGTTAAGATCAAACCTCA    | 2340 |
| Qy | 2341 | CAAAGAGAAATAGAATGTTTGAAAGGCTATCCCAAAGACTTTTTTGAATCTGTCATTCA    | 2400 |
|    |      |  |      |
| Db | 2341 | CAAAGAGAAATAGAATGTTTGAAAGGCTATCCCAAAGACTTTTTTGAATCTGTCATTCA    | 2400 |
| Qy | 2401 | CATACCCTGTGAAGACAATACTATCTACAATTTTTTCAGGATTATTTAAATCTTCTTTT    | 2460 |
|    |      |  |      |
| Db | 2401 | CATACCCTGTGAAGACAATACTATCTACAATTTTTTCAGGATTATTTAAATCTTCTTTT    | 2460 |
| Qy | 2461 | TCCTATCGTAGCTTAAACTCTGTTTGGTTTTGTCATCTGTAAATACTTACCTACATACA    | 2520 |
|    |      |  |      |
| Db | 2461 | TCCTATCGTAGCTTAAACTCTGTTTGGTTTTGTCATCTGTAAATACTTACCTACATACA    | 2520 |
| Qy | 2521 | CTGCATGTAGATGATTAAATGAGGGCAGGCCCTGTGCTCATAGCTTTACGATGGAGAGAT   | 2580 |
|    |      |  |      |
| Db | 2521 | CTGCATGTAGATGATTAAATGAGGGCAGGCCCTGTGCTCATAGCTTTACGATGGAGAGAT   | 2580 |
| Qy | 2581 | GCCAGTGACCTCATAATAAAGACTGTGAAGTGCCTGGTGCAGTGTCCACATGACAAAGGG   | 2640 |
|    |      |  |      |
| Db | 2581 | GCCAGTGACCTCATAATAAAGACTGTGAAGTGCCTGGTGCAGTGTCCACATGACAAAGGG   | 2640 |
| Qy | 2641 | GCAGGTAGCACCCCTCTCTCACCCATGCTGTGGTTAAATGGTTTCTAGCATATGTATAAT   | 2700 |
|    |      |  |      |
| Db | 2641 | GCAGGTAGCACCCCTCTCTCACCCATGCTGTGGTTAAATGGTTTCTAGCATATGTATAAT   | 2700 |
| Qy | 2701 | GCTATAGTTAAAATACTATTTTTCAAATCATACAGATTAGTACATTTAACAGCTACCTG    | 2760 |
|    |      |  |      |
| Db | 2701 | GCTATAGTTAAAATACTATTTTTCAAATCATACAGATTAGTACATTTAACAGCTACCTG    | 2760 |
| Qy | 2761 | TAAAGCTTATTACTAATTTTTGTATTATTTTTGTAAATAGCCAATAGAAAAGTTTGCTTG   | 2820 |
|    |      |  |      |
| Db | 2761 | TAAAGCTTATTACTAATTTTTGTATTATTTTTGTAAATAGCCAATAGAAAAGTTTGCTTG   | 2820 |
| Qy | 2821 | ACATGGTGCTTTTCTTTCATCTAGAGGCAAACTGCTTTTTGAGACCGTAAGAACCTCTT    | 2880 |
|    |      |  |      |
| Db | 2821 | ACATGGTGCTTTTCTTTCATCTAGAGGCAAACTGCTTTTTGAGACCGTAAGAACCTCTT    | 2880 |
| Qy | 2881 | AGCTTTGTGCGTTCCTGCCTAATTTTTATATCTTCTAAGCAAAGTGCCTTAGGATAGCTT   | 2940 |
|    |      |  |      |
| Db | 2881 | AGCTTTGTGCGTTCCTGCCTAATTTTTATATCTTCTAAGCAAAGTGCCTTAGGATAGCTT   | 2940 |
| Qy | 2941 | GGGATGAGATGTGTGTGAAAGTATGTACAAGAGAAAACGGAAGAGAGAGGAAATGAGGTG   | 3000 |
|    |      |  |      |
| Db | 2941 | GGGATGAGATGTGTGTGAAAGTATGTACAAGAGAAAACGGAAGAGAGAGGAAATGAGGTG   | 3000 |

|    |      |  |      |
|----|------|--|------|
| Qy | 3001 | GGGTTGGAGGAAACCCATGGGGACAGATTCCCATTTCTTAGCCTAACGTTGTCATTGCCT   | 3060 |
|    |      |  |      |
| Db | 3001 | GGGTTGGAGGAAACCCATGGGGACAGATTCCCATTTCTTAGCCTAACGTTGTCATTGCCT   | 3060 |
| Qy | 3061 | CGTCACATCAATGCAAAAGGTCTGATTTTGTTCAGCAAAACACAGTGCAATGTTCTCA     | 3120 |
|    |      |  |      |
| Db | 3061 | CGTCACATCAATGCAAAAGGTCTGATTTTGTTCAGCAAAACACAGTGCAATGTTCTCA     | 3120 |
| Qy | 3121 | GAGTGACTTTCGAAATAAATTGGGCCCAAGAGCTTTAACTCGGTCTTAAAAATATGCCCAA  | 3180 |
|    |      |  |      |
| Db | 3121 | GAGTGACTTTCGAAATAAATTGGGCCCAAGAGCTTTAACTCGGTCTTAAAAATATGCCCAA  | 3180 |
| Qy | 3181 | ATTTTTACTTTGTTTTTCTTTTAATAGGCTGGGCCACATGTTGGAAATAAGCTAGTAATG   | 3240 |
|    |      |  |      |
| Db | 3181 | ATTTTTACTTTGTTTTTCTTTTAATAGGCTGGGCCACATGTTGGAAATAAGCTAGTAATG   | 3240 |
| Qy | 3241 | TTGTTTTCTGTCAATATTGAATGTGATGGTACAGTAAACCAAAACCAACAATGTGGCCA    | 3300 |
|    |      |  |      |
| Db | 3241 | TTGTTTTCTGTCAATATTGAATGTGATGGTACAGTAAACCAAAACCAACAATGTGGCCA    | 3300 |
| Qy | 3301 | GAAAGAAAGAGCAATAATAATTAATTCACACACCATATGGATTCTATTTATAAATCACCC   | 3360 |
|    |      |  |      |
| Db | 3301 | GAAAGAAAGAGCAATAATAATTAATTCACACACCATATGGATTCTATTTATAAATCACCC   | 3360 |
| Qy | 3361 | ACAAACTTGTTCTTTAATTTTCATCCCAATCACTTTTTTCAGAGGCCTGTTATCATAGAAGT | 3420 |
|    |      |  |      |
| Db | 3361 | ACAAACTTGTTCTTTAATTTTCATCCCAATCACTTTTTTCAGAGGCCTGTTATCATAGAAGT | 3420 |
| Qy | 3421 | CATTTTAGACTCTCAATTTTAAATTAATTTGAATCACTAATATTTTCACAGTTTATTAA    | 3480 |
|    |      |  |      |
| Db | 3421 | CATTTTAGACTCTCAATTTTAAATTAATTTGAATCACTAATATTTTCACAGTTTATTAA    | 3480 |
| Qy | 3481 | TATATTTAATTTCTATTTAAATTTTAGATTATTTTATTACCATGTACTGAATTTTTACA    | 3540 |
|    |      |  |      |
| Db | 3481 | TATATTTAATTTCTATTTAAATTTTAGATTATTTTATTACCATGTACTGAATTTTTACA    | 3540 |
| Qy | 3541 | TCCTGATACCCTTTCCTTCTCCATGTGAGTATCATGTTCTCTAATTATCTTGCCAAATTT   | 3600 |
|    |      |  |      |
| Db | 3541 | TCCTGATACCCTTTCCTTCTCCATGTGAGTATCATGTTCTCTAATTATCTTGCCAAATTT   | 3600 |
| Qy | 3601 | TGAAACTACACACAAAAAGCATACTTGCATTATTTATAATAAAATTGCATTTCAGTGGCTT  | 3660 |
|    |      |  |      |
| Db | 3601 | TGAAACTACACACAAAAAGCATACTTGCATTATTTATAATAAAATTGCATTTCAGTGGCTT  | 3660 |
| Qy | 3661 | TTTAAAAAAATGTTTGATTCAAACTTTAACATACTGATAAGTAAGAAACAATTATAAT     | 3720 |
|    |      |  |      |
| Db | 3661 | TTTAAAAAAATGTTTGATTCAAACTTTAACATACTGATAAGTAAGAAACAATTATAAT     | 3720 |
| Qy | 3721 | TTCTTTACATACTCAAAACCAAGATAGAAAAAGGTGCTATCGTTCAACTTCAAAACATGT   | 3780 |
|    |      |  |      |
| Db | 3721 | TTCTTTACATACTCAAAACCAAGATAGAAAAAGGTGCTATCGTTCAACTTCAAAACATGT   | 3780 |
| Qy | 3781 | TTCTTAGTATTAAGGACTTTAATATAGCAACAGACAAAATTATTGTTAACATGGATGTTA   | 3840 |
|    |      |  |      |
| Db | 3781 | TTCTTAGTATTAAGGACTTTAATATAGCAACAGACAAAATTATTGTTAACATGGATGTTA   | 3840 |
| Qy | 3841 | CAGCTCAAAAGATTTATAAAAGATTTTAACCTATTTTCTCCCTTATTATCCACTGCTAAT   | 3900 |

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Db      3841  |||||CAGCTCAAAAAGATTTATAAAAAGATTTTAACCTATTTTCTCCCTTATTATCCACTGCTAAT 3900
Qy      3901  GTGGATGTATGTTCAAACACCTTTTAGTATTGATAGCTTACATATGGCCAAAGGAATACA 3960
Db      3901  |||||GTGGATGTATGTTCAAACACCTTTTAGTATTGATAGCTTACATATGGCCAAAGGAATACA 3960
Qy      3961  GTTTATAGCAAAACATGGGTATGCTGTAGCTAACTTTATAAAAAGTGTAATATAACAATGT 4020
Db      3961  |||||GTTTATAGCAAAACATGGGTATGCTGTAGCTAACTTTATAAAAAGTGTAATATAACAATGT 4020
Qy      4021  AAAAAATTATATATCTGGGAGGATTTTTTGGTTGCCTAAAGTGGCTATAGTTACTGATTT 4080
Db      4021  |||||AAAAAATTATATATCTGGGAGGATTTTTTGGTTGCCTAAAGTGGCTATAGTTACTGATTT 4080
Qy      4081  TTTATTATGTAAGCAAAACCAATAAAAAATTTAAGTTTTTTTAAACAACCTACCTATTTTTTC 4140
Db      4081  |||||TTTATTATGTAAGCAAAACCAATAAAAAATTTAAGTTTTTTTAAACAACCTACCTATTTTTTC 4140
Qy      4141  ACTGTACAGACACTAATTCATTAAATACTAATTGATTGTTTAAAAGAAATATAAATGTGA 4200
Db      4141  |||||ACTGTACAGACACTAATTCATTAAATACTAATTGATTGTTTAAAAGAAATATAAATGTGA 4200
Qy      4201  CAAGTGGACATTATTTATGTTAAATATACAATTATCAAGCAAGTATGAAGTTATTCAATT 4260
Db      4201  |||||CAAGTGGACATTATTTATGTTAAATATACAATTATCAAGCAAGTATGAAGTTATTCAATT 4260
Qy      4261  AAAATGCCACATTTCTGGTCTCTGGGAAAAAAAAAAAAAAAAA 4301
Db      4261  |||||AAAATGCCACATTTCTGGTCTCTGGGAAAAAAAAAAAAAAAAA 4301

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RESULT 2

US-09-921-406C-13

; Sequence 13, Application US/09921406C

; Publication No. US20030152923A1

; GENERAL INFORMATION:

; APPLICANT: Yakhini, Zohar

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; APPLICANT: Jiang, Yuan

; APPLICANT: Bittner, Michael

; TITLE OF INVENTION: Classifying Cancers

; FILE REFERENCE: 10010313-1

; CURRENT APPLICATION NUMBER: US/09/921,406C

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; NUMBER OF SEQ ID NOS: 41

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 13

; LENGTH: 4286

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-921-406C-13

Query Match 99.6%; Score 4284.4; DB 10; Length 4286;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 4285; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy      1 GAGACATTCCGGTGGGGGACTCTGGCCAGCCCAGCAACGTGGATCCTGAGAGCACTCCC 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 GAGACATTCCGGTGGGGGACTCTGGCCAGCCCAGCAACGTGGATCCTGAGAGCACTCCC 60

Qy     61 AGGTAGGCATTTGCCCCGGTGGGACGCCTTGCCAGAGCAGTGTGTGGCAGGCCCCCGTGG 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 AGGTAGGCATTTGCCCCGGTGGGACGCCTTGCCAGAGCAGTGTGTGGCAGGCCCCCGTGG 120

Qy    121 AGGATCAACACAGTGGCTGAACACTGGGAAGGAACTGGTACTTGAGTCTGGACATCTGA 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 AGGATCAACACAGTGGCTGAACACTGGGAAGGAACTGGTACTTGAGTCTGGACATCTGA 180

Qy    181 AACTTGGCTCTGAAACTGCGGAGCGGCCACCGGACGCCTTCTGGAGCAGGTAGCAGCATG 240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 AACTTGGCTCTGAAACTGCGCAGCGGCCACCGGACGCCTTCTGGAGCAGGTAGCAGCATG 240

Qy    241 CAGCCGCCTCCAAGTCTGTGCGGACGCGCCCTGGTTGCGCTGGTTCTTGCCTGCGGCCTG 300
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 CAGCCGCCTCCAAGTCTGTGCGGACGCGCCCTGGTTGCGCTGGTTCTTGCCTGCGGCCTG 300

Qy    301 TCGCGGATCTGGGGAGAGGAGAGAGGCTTCCCGCCTGACAGGGCCACTCCGCTTTTGCAA 360
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 TCGCGGATCTGGGGAGAGGAGAGAGGCTTCCCGCCTGACAGGGCCACTCCGCTTTTGCAA 360

Qy    361 ACCGCAGAGATAATGACGCCACCCACTAAGACCTTATGGCCCAAGGGTTCCAACGCCAGT 420
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 ACCGCAGAGATAATGACGCCACCCACTAAGACCTTATGGCCCAAGGGTTCCAACGCCAGT 420

Qy    421 CTGGCGCGGTCGTTGGCACCTGCGGAGGTGCCTAAAGGAGACAGGACGGCAGGATCTCCG 480
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 CTGGCGCGGTCGTTGGCACCTGCGGAGGTGCCTAAAGGAGACAGGACGGCAGGATCTCCG 480

Qy    481 CCACGCACCATCTCCCCTCCCCCGTGCCAAGGACCCATCGAGATCAAGGAGACTTTCAA 540
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 CCACGCACCATCTCCCCTCCCCCGTGCCAAGGACCCATCGAGATCAAGGAGACTTTCAA 540

Qy    541 TACATCAACACGGTTGTGTCCTGCCTTGTGTTGCTGCTGGGGATCATCGGGAACCTCACA 600
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 TACATCAACACGGTTGTGTCCTGCCTTGTGTTGCTGCTGGGGATCATCGGGAACCTCACA 600

Qy    601 CTTCTGAGAATTATCTACAAGAACAAGTGCATGCGAAACGGTCCCAATATCTTGATCGCC 660
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 CTTCTGAGAATTATCTACAAGAACAAGTGCATGCGAAACGGTCCCAATATCTTGATCGCC 660

Qy    661 AGCTTGGCTCTGGGAGACCTGCTGCACATCGTCATTGACATCCCTATCAATGTCTACAAG 720
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 AGCTTGGCTCTGGGAGACCTGCTGCACATCGTCATTGACATCCCTATCAATGTCTACAAG 720

Qy    721 CTGCTGGCAGAGGACTGGCCATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTCATACAG 780
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    721 CTGCTGGCAGAGGACTGGCCATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTCATACAG 780
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|    |      |   |      |
|----|------|---|------|
| Qy | 781  | AAAGCCTCCGTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATATCGA  | 840  |
|    |      |   |      |
| Db | 781  | AAAGCCTCCGTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATATCGA  | 840  |
| Qy | 841  | GCTGTTGCTTCTTGGAGTAGAATTAAAGGAATTGGGGTTCCAAAATGGACAGCAGTAGAA  | 900  |
|    |      |   |      |
| Db | 841  | GCTGTTGCTTCTTGGAGTAGAATTAAAGGAATTGGGGTTCCAAAATGGACAGCAGTAGAA  | 900  |
| Qy | 901  | ATTGTTTTGATTTGGGTGGTCTCTGTGGTTCTGGCTGTCCCTGAAGCCATAGGTTTTGAT  | 960  |
|    |      |   |      |
| Db | 901  | ATTGTTTTGATTTGGGTGGTCTCTGTGGTTCTGGCTGTCCCTGAAGCCATAGGTTTTGAT  | 960  |
| Qy | 961  | ATAATTACGATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTTCAG  | 1020 |
|    |      |   |      |
| Db | 961  | ATAATTACGATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTTCAG  | 1020 |
| Qy | 1021 | AAGACAGCTTTCATGCAGTTTTACAAGACAGCAAAAGATTGGTGGCTGTTGAGTTTCTAT  | 1080 |
|    |      |   |      |
| Db | 1021 | AAGACAGCTTTCATGCAGTTTTACAAGACAGCAAAAGATTGGTGGCTGTTGAGTTTCTAT  | 1080 |
| Qy | 1081 | TTCTGCTTGCCATTGGCCATCACTGCATTTTTTTTATACACTAATGACCTGTGAAATGTTG | 1140 |
|    |      |   |      |
| Db | 1081 | TTCTGCTTGCCATTGGCCATCACTGCATTTTTTTTATACACTAATGACCTGTGAAATGTTG | 1140 |
| Qy | 1141 | AGAAAGAAAAGTGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAAGTG  | 1200 |
|    |      |   |      |
| Db | 1141 | AGAAAGAAAAGTGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAAGTG  | 1200 |
| Qy | 1201 | GCCAAAACCGTCTTTTGCCTGGTCCTTGTCTTTGCCCTCTGCTGGCTTCCCCTTCACCTC  | 1260 |
|    |      |   |      |
| Db | 1201 | GCCAAAACCGTCTTTTGCCTGGTCCTTGTCTTTGCCCTCTGCTGGCTTCCCCTTCACCTC  | 1260 |
| Qy | 1261 | AGCAGGATTCTGAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGAACTTTTG  | 1320 |
|    |      |   |      |
| Db | 1261 | AGCAGGATTCTGAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGAACTTTTG  | 1320 |
| Qy | 1321 | AGCTTTCTGTTGGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCCTGCATT  | 1380 |
|    |      |   |      |
| Db | 1321 | AGCTTTCTGTTGGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCCTGCATT  | 1380 |
| Qy | 1381 | AACCCAATTGCTCTGTATTTGGTGAGCAAAAGATTCAAAAAGTCTTTAAGTCATGCTTA   | 1440 |
|    |      |   |      |
| Db | 1381 | AACCCAATTGCTCTGTATTTGGTGAGCAAAAGATTCAAAAAGTCTTTAAGTCATGCTTA   | 1440 |
| Qy | 1441 | TGCTGCTGGTGCCAGTCATTTGAAGAAAAACAGTCCTTGGAGGAAAAGCAGTCGTGCTTA  | 1500 |
|    |      |   |      |
| Db | 1441 | TGCTGCTGGTGCCAGTCATTTGAAGAAAAACAGTCCTTGGAGGAAAAGCAGTCGTGCTTA  | 1500 |
| Qy | 1501 | AAGTTCAAAGCTAATGATCACGGATATGACAACTCCGTTCCAGTAATAAATACAGCTCA   | 1560 |
|    |      |   |      |
| Db | 1501 | AAGTTCAAAGCTAATGATCACGGATATGACAACTCCGTTCCAGTAATAAATACAGCTCA   | 1560 |
| Qy | 1561 | TCTTGAAAGAAGAACTATTCACTGTATTTTCTTTTATATTGGACCGAAGTCATTAA      | 1620 |
|    |      |   |      |
| Db | 1561 | TCTTGAAAGAAGAACTATTCACTGTATTTTCTTTTATATTGGACCGAAGTCATTAA      | 1620 |

|    |      |   |      |
|----|------|---|------|
| Qy | 1621 | AACAAAATGAAACATTTGCCAAAACAAAACAAAAAACTATGTATTTGCACAGCACACTAT  | 1680 |
|    |      |   |      |
| Db | 1621 | AACAAAATGAAACATTTGCCAAAACAAAACAAAAAACTATGTATTTGCACAGCACACTAT  | 1680 |
| Qy | 1681 | TAAAATATTAAGTGTAAATTATTTTAACACTCACAGCTACATATGACATTTTATGAGCTGT | 1740 |
|    |      |   |      |
| Db | 1681 | TAAAATATTAAGTGTAAATTATTTTAACACTCACAGCTACATATGACATTTTATGAGCTGT | 1740 |
| Qy | 1741 | TTACGGCATGGAAAGAAAATCAGTGGGAATTAAGAAAGCCTCGTCGTGAAAGCACTTAAT  | 1800 |
|    |      |   |      |
| Db | 1741 | TTACGGCATGGAAAGAAAATCAGTGGGAATTAAGAAAGCCTCGTCGTGAAAGCACTTAAT  | 1800 |
| Qy | 1801 | TTTTTACAGTTAGCACTTCAACATAGCTCTTAACAACCTCCAGGATATTCACACAACACT  | 1860 |
|    |      |   |      |
| Db | 1801 | TTTTTACAGTTAGCACTTCAACATAGCTCTTAACAACCTCCAGGATATTCACACAACACT  | 1860 |
| Qy | 1861 | TAGGCTTAAAAATGAGCTCACTCAGAATTTCTATTCTTTCTAAAAAGAGATTTATTTTTTA | 1920 |
|    |      |   |      |
| Db | 1861 | TAGGCTTAAAAATGAGCTCACTCAGAATTTCTATTCTTTCTAAAAAGAGATTTATTTTTTA | 1920 |
| Qy | 1921 | AATCAATGGGACTCTGATATAAAGGAAGAATAAGTCACTGTAAACAGAACTTTTAAATG   | 1980 |
|    |      |   |      |
| Db | 1921 | AATCAATGGGACTCTGATATAAAGGAAGAATAAGTCACTGTAAACAGAACTTTTAAATG   | 1980 |
| Qy | 1981 | AAGCTTAAATTACTCAATTTAAATTTTAAATCCTTTAAACAACCTTTTCAATTAATAT    | 2040 |
|    |      |   |      |
| Db | 1981 | AAGCTTAAATTACTCAATTTAAATTTTAAATCCTTTAAACAACCTTTTCAATTAATAT    | 2040 |
| Qy | 2041 | TATCACACTATTATCAGATTGTAATTAGATGCAAATGAGAGAGCAGTTTAGTTGTTGCAT  | 2100 |
|    |      |   |      |
| Db | 2041 | TATCACACTATTATCAGATTGTAATTAGATGCAAATGAGAGAGCAGTTTAGTTGTTGCAT  | 2100 |
| Qy | 2101 | TTTTCGGACACTGGAAACATTTAAATGATCAGGAGGGAGTAACAGAAAGAGCAAGGCTGT  | 2160 |
|    |      |   |      |
| Db | 2101 | TTTTCGGACACTGGAAACATTTAAATGATCAGGAGGGAGTAACAGAAAGAGCAAGGCTGT  | 2160 |
| Qy | 2161 | TTTTGAAAATCATTACACTTTTACTAGAGCCCAAACCTCAGCATTCTGCAATATGTAAC   | 2220 |
|    |      |   |      |
| Db | 2161 | TTTTGAAAATCATTACACTTTTACTAGAGCCCAAACCTCAGCATTCTGCAATATGTAAC   | 2220 |
| Qy | 2221 | CAACATGTCACAAACAAGCAGCATGTAACAGACTGGCACATGTGCCAGCTGAATTTAAAA  | 2280 |
|    |      |   |      |
| Db | 2221 | CAACATGTCACAAACAAGCAGCATGTAACAGACTGGCACATGTGCCAGCTGAATTTAAAA  | 2280 |
| Qy | 2281 | TATAATACTTTTAAAAAGAAAATTATTACATCCTTTACATTAGTTAAGATCAAACCTCA   | 2340 |
|    |      |   |      |
| Db | 2281 | TATAATACTTTTAAAAAGAAAATTATTACATCCTTTACATTAGTTAAGATCAAACCTCA   | 2340 |
| Qy | 2341 | CAAAGAGAAATAGAATGTTTGAAAGGCTATCCCAAAGACTTTTTTGAATCTGTCATTCA   | 2400 |
|    |      |   |      |
| Db | 2341 | CAAAGAGAAATAGAATGTTTGAAAGGCTATCCCAAAGACTTTTTTGAATCTGTCATTCA   | 2400 |
| Qy | 2401 | CATACCCTGTGAAGACAATACTATCTACAATTTTTTCAGGATTATTAAATCTTCTTTTT   | 2460 |
|    |      |   |      |
| Db | 2401 | CATACCCTGTGAAGACAATACTATCTACAATTTTTTCAGGATTATTAAATCTTCTTTTT   | 2460 |
| Qy | 2461 | TCACTATCGTAGCTTAAACTCTGTTTGGTTTTGTCATCTGTAAATACTTACCTACATACA  | 2520 |



|    |      |   |      |
|----|------|---|------|
| Db | 2461 | <br>TCACTATCGTAGCTTAAACTCTGTTTGGTTTTGTTCATCTGTAAATACTTACCTACATACA | 2520 |
| Qy | 2521 | CTGCATGTAGATGATTAAATGAGGGCAGGCCCTGTGCTCATAGCTTTACGATGGAGAGAT      | 2580 |
| Db | 2521 | <br>CTGCATGTAGATGATTAAATGAGGGCAGGCCCTGTGCTCATAGCTTTACGATGGAGAGAT  | 2580 |
| Qy | 2581 | GCCAGTGACCTCATAATAAAGACTGTGAACTGCCTGGTGCAGTGTCCACATGACAAAGGG      | 2640 |
| Db | 2581 | <br>GCCAGTGACCTCATAATAAAGACTGTGAACTGCCTGGTGCAGTGTCCACATGACAAAGGG  | 2640 |
| Qy | 2641 | GCAGGTAGCACCCCTCTCTCACCCATGCTGTGGTTAAATGGTTTCTAGCATATGTATAAT      | 2700 |
| Db | 2641 | <br>GCAGGTAGCACCCCTCTCTCACCCATGCTGTGGTTAAATGGTTTCTAGCATATGTATAAT  | 2700 |
| Qy | 2701 | GCTATAGTTAAAATACTATTTTTCAAATCATACAGATTAGTACATTTAACAGCTACCTG       | 2760 |
| Db | 2701 | <br>GCTATAGTTAAAATACTATTTTTCAAATCATACAGATTAGTACATTTAACAGCTACCTG   | 2760 |
| Qy | 2761 | TAAAGCTTATTACTAATTTTTGTATTATTTTTGTAAATAGCCAATAGAAAAGTTTGCTTG      | 2820 |
| Db | 2761 | <br>TAAAGCTTATTACTAATTTTTGTATTATTTTTGTAAATAGCCAATAGAAAAGTTTGCTTG  | 2820 |
| Qy | 2821 | ACATGGTGCTTTTCTTTCATCTAGAGGCAAACTGCTTTTTGAGACCGTAAGAACCTCTT       | 2880 |
| Db | 2821 | <br>ACATGGTGCTTTTCTTTCATCTAGAGGCAAACTGCTTTTTGAGACCGTAAGAACCTCTT   | 2880 |
| Qy | 2881 | AGCTTTGTGCGTTCCTGCCTAATTTTTATATCTTCTAAGCAAAGTGCCTTAGGATAGCTT      | 2940 |
| Db | 2881 | <br>AGCTTTGTGCGTTCCTGCCTAATTTTTATATCTTCTAAGCAAAGTGCCTTAGGATAGCTT  | 2940 |
| Qy | 2941 | GGGATGAGATGTGTGTGAAAGTATGTACAAGAGAAAACGGAAGAGAGAGGAAATGAGGTG      | 3000 |
| Db | 2941 | <br>GGGATGAGATGTGTGTGAAAGTATGTACAAGAGAAAACGGAAGAGAGAGGAAATGAGGTG  | 3000 |
| Qy | 3001 | GGGTTGGAGGAAACCCATGGGGACAGATTCCCATTCTTAGCCTAACGTTTCGTATTGCCT      | 3060 |
| Db | 3001 | <br>GGGTTGGAGGAAACCCATGGGGACAGATTCCCATTCTTAGCCTAACGTTTCGTATTGCCT  | 3060 |
| Qy | 3061 | CGTCACATCAATGCAAAGGTCCTGATTTTGTTCAGCAAAACACAGTGCAATGTTCTCA        | 3120 |
| Db | 3061 | <br>CGTCACATCAATGCAAAGGTCCTGATTTTGTTCAGCAAAACACAGTGCAATGTTCTCA    | 3120 |
| Qy | 3121 | GAGTGACTTTCGAAATAAATTGGGCCCAAGAGCTTTAACTCGGTCTTAAATATGCCCAA       | 3180 |
| Db | 3121 | <br>GAGTGACTTTCGAAATAAATTGGGCCCAAGAGCTTTAACTCGGTCTTAAATATGCCCAA   | 3180 |
| Qy | 3181 | ATTTTTACTTTGTTTTTCTTTTAATAGGCTGGGCCACATGTTGGAAATAAGCTAGTAATG      | 3240 |
| Db | 3181 | <br>ATTTTTACTTTGTTTTTCTTTTAATAGGCTGGGCCACATGTTGGAAATAAGCTAGTAATG  | 3240 |
| Qy | 3241 | TTGTTTTCTGTCAATATTGAATGTGATGGTACAGTAAACCAAACCAACAATGTGGCCA        | 3300 |
| Db | 3241 | <br>TTGTTTTCTGTCAATATTGAATGTGATGGTACAGTAAACCAAACCAACAATGTGGCCA    | 3300 |
| Qy | 3301 | GAAAGAAAGAGCAATAATAATTAATTCACACACCATATGGATTCTATTTATAAATCACCC      | 3360 |
|    |      |   |      |

|    |      |  |      |
|----|------|--|------|
| Db | 3301 | GAAAGAAAGAGCAATAATAATTAATTCACACACCATATGGATTCTATTTATAAATCACCC   | 3360 |
| Qy | 3361 | ACAAACTTGTTCTTTAATTTTCATCCCAATCACTTTTTTCAGAGGCCTGTTATCATAGAAGT | 3420 |
|    |      |  |      |
| Db | 3361 | ACAAACTTGTTCTTTAATTTTCATCCCAATCACTTTTTTCAGAGGCCTGTTATCATAGAAGT | 3420 |
| Qy | 3421 | CATTTTAGACTCTCAATTTTAAATTAATTTTGAATCACTAATATTTTCACAGTTTATTAA   | 3480 |
|    |      |  |      |
| Db | 3421 | CATTTTAGACTCTCAATTTTAAATTAATTTTGAATCACTAATATTTTCACAGTTTATTAA   | 3480 |
| Qy | 3481 | TATATTTAATTTCTATTTAAATTTTAGATTATTTTTATTACCATGTACTGAATTTTTACA   | 3540 |
|    |      |  |      |
| Db | 3481 | TATATTTAATTTCTATTTAAATTTTAGATTATTTTTATTACCATGTACTGAATTTTTACA   | 3540 |
| Qy | 3541 | TCCTGATACCCTTTCCTTCTCCATGTCAGTATCATGTTCTCTAATTATCTTGCCAAATTT   | 3600 |
|    |      |  |      |
| Db | 3541 | TCCTGATACCCTTTCCTTCTCCATGTCAGTATCATGTTCTCTAATTATCTTGCCAAATTT   | 3600 |
| Qy | 3601 | TGAAACTACACACAAAAAGCATACTTGCATTATTTATAATAAAATTGCATTCACTGGCTT   | 3660 |
|    |      |  |      |
| Db | 3601 | TGAAACTACACACAAAAAGCATACTTGCATTATTTATAATAAAATTGCATTCACTGGCTT   | 3660 |
| Qy | 3661 | TTTAAAAAAATGTTTGATTCAAACTTTAACATACTGATAAGTAAGAAACAATTATAAT     | 3720 |
|    |      |  |      |
| Db | 3661 | TTTAAAAAAATGTTTGATTCAAACTTTAACATACTGATAAGTAAGAAACAATTATAAT     | 3720 |
| Qy | 3721 | TTCTTTACATACTCAAACCAAGATAGAAAAAGGTGCTATCGTTCAACTTCAAACATGT     | 3780 |
|    |      |  |      |
| Db | 3721 | TTCTTTACATACTCAAACCAAGATAGAAAAAGGTGCTATCGTTCAACTTCAAACATGT     | 3780 |
| Qy | 3781 | TTCTAGTATTAAGGACTTTAATATAGCAACAGACAAAATTATTGTTAACATGGATGTTA    | 3840 |
|    |      |  |      |
| Db | 3781 | TTCTAGTATTAAGGACTTTAATATAGCAACAGACAAAATTATTGTTAACATGGATGTTA    | 3840 |
| Qy | 3841 | CAGCTCAAAAGATTTATAAAAGATTTTAACCTATTTTCTCCCTTATTATCCACTGCTAAT   | 3900 |
|    |      |  |      |
| Db | 3841 | CAGCTCAAAAGATTTATAAAAGATTTTAACCTATTTTCTCCCTTATTATCCACTGCTAAT   | 3900 |
| Qy | 3901 | GTGGATGTATGTTCAAACACCTTTTAGTATTGATAGCTTACATATGGCCAAAGGAATACA   | 3960 |
|    |      |  |      |
| Db | 3901 | GTGGATGTATGTTCAAACACCTTTTAGTATTGATAGCTTACATATGGCCAAAGGAATACA   | 3960 |
| Qy | 3961 | GTTTATAGCAAAACATGGGTATGCTGTAGCTAACTTTATAAAAGTGTAATATAACAATGT   | 4020 |
|    |      |  |      |
| Db | 3961 | GTTTATAGCAAAACATGGGTATGCTGTAGCTAACTTTATAAAAGTGTAATATAACAATGT   | 4020 |
| Qy | 4021 | AAAAAATTATATATCTGGGAGGATTTTTTGGTTGCCTAAAGTGGCTATAGTTACTGATTT   | 4080 |
|    |      |  |      |
| Db | 4021 | AAAAAATTATATATCTGGGAGGATTTTTTGGTTGCCTAAAGTGGCTATAGTTACTGATTT   | 4080 |
| Qy | 4081 | TTTATTATGTAAGCAAAACCAATAAAATTTAAGTTTTTTTAACTACCTTATTTTTTC      | 4140 |
|    |      |  |      |
| Db | 4081 | TTTATTATGTAAGCAAAACCAATAAAATTTAAGTTTTTTTAACTACCTTATTTTTTC      | 4140 |
| Qy | 4141 | ACTGTACAGACACTAATTCATTAAATACTAATTGATTGTTTAAAAGAAATATAAATGTGA   | 4200 |
|    |      |  |      |
| Db | 4141 | ACTGTACAGACACTAATTCATTAAATACTAATTGATTGTTTAAAAGAAATATAAATGTGA   | 4200 |

Qy 4201 CAAAGTGGACATTATTTATGTTAAATATACAATTATCAAGCAAGTATGAAGTTATTCAATT 4260  
 |||  
 Db 4201 CAAAGTGGACATTATTTATGTTAAATATACAATTATCAAGCAAGTATGAAGTTATTCAATT 4260  
 Qy 4261 AAAATGCCACATTTCTGGTCTCTGGG 4286  
 |||  
 Db 4261 AAAATGCCACATTTCTGGTCTCTGGG 4286

RESULT 3

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; GENERAL INFORMATION:

; APPLICANT: LifeSpan Biosciences

; APPLICANT: Brown, Joseph P.

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; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS (GPCRS)

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; LENGTH: 4286

; TYPE: DNA

; ORGANISM: Homo sapiens

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Query Match 99.6%; Score 4284.4; DB 15; Length 4286;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 4285; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GAGACATTCCGGTGGGGGACTCTGGCCAGCCCAGCAACGTGGATCCTGAGAGCACTCCC 60  
 |||  
 Db 1 GAGACATTCCGGTGGGGGACTCTGGCCAGCCCAGCAACGTGGATCCTGAGAGCACTCCC 60  
 Qy 61 AGGTAGGCATTTGCCCCGGTGGGACGCCTTGCCAGAGCAGTGTGTGGCAGGCCCCCGTGG 120  
 |||  
 Db 61 AGGTAGGCATTTGCCCCGGTGGGACGCCTTGCCAGAGCAGTGTGTGGCAGGCCCCCGTGG 120  
 Qy 121 AGGATCAACACAGTGGCTGAACACTGGGAAGGAACTGGTACTTGGAGTCTGGACATCTGA 180  
 |||  
 Db 121 AGGATCAACACAGTGGCTGAACACTGGGAAGGAACTGGTACTTGGAGTCTGGACATCTGA 180  
 Qy 181 AACTTGGCTCTGAAACTGCGGAGCGGCCACCGGACGCCTTCTGGAGCAGGTAGCAGCATG 240  
 |||  
 Db 181 AACTTGGCTCTGAAACTGCGCAGCGGCCACCGGACGCCTTCTGGAGCAGGTAGCAGCATG 240  
 Qy 241 CAGCCGCCTCCAAGTCTGTGCGGACGCGCCCTGGTTGCGCTGGTTCTTGCCTGCGGCCTG 300  
 |||  
 Db 241 CAGCCGCCTCCAAGTCTGTGCGGACGCGCCCTGGTTGCGCTGGTTCTTGCCTGCGGCCTG 300

|    |      |  |      |
|----|------|--|------|
| Qy | 301  | TCGCGGATCTGGGGAGAGGAGAGAGGGCTTCCCGCCTGACAGGGCCACTCCGCTTTTGCAA  | 360  |
|    |      |  |      |
| Db | 301  | TCGCGGATCTGGGGAGAGGAGAGAGGGCTTCCCGCCTGACAGGGCCACTCCGCTTTTGCAA  | 360  |
| Qy | 361  | ACCGCAGAGATAATGACGCCACCCACTAAGACCTTATGGCCCAAGGGTTCCAACGCCAGT   | 420  |
|    |      |  |      |
| Db | 361  | ACCGCAGAGATAATGACGCCACCCACTAAGACCTTATGGCCCAAGGGTTCCAACGCCAGT   | 420  |
| Qy | 421  | CTGGCGCGGTCGTTGGCACCTGCGGAGGTGCCTAAAGGAGACAGGACGGCAGGATCTCCG   | 480  |
|    |      |  |      |
| Db | 421  | CTGGCGCGGTCGTTGGCACCTGCGGAGGTGCCTAAAGGAGACAGGACGGCAGGATCTCCG   | 480  |
| Qy | 481  | CCACGCACCATCTCCCCCTCCCCCGTGCCAAGGACCCATCGAGATCAAGGAGACTTTCAA   | 540  |
|    |      |  |      |
| Db | 481  | CCACGCACCATCTCCCCCTCCCCCGTGCCAAGGACCCATCGAGATCAAGGAGACTTTCAA   | 540  |
| Qy | 541  | TACATCAACACGGTTGTGTCTGCTTGTGTTTCGTGCTGGGGATCATCGGGAACCTCCACA   | 600  |
|    |      |  |      |
| Db | 541  | TACATCAACACGGTTGTGTCTGCTTGTGTTTCGTGCTGGGGATCATCGGGAACCTCCACA   | 600  |
| Qy | 601  | CTTCTGAGAATTATCTACAAGAACAAGTGCATGCGAAACGGTCCCAATATCTTGATCGCC   | 660  |
|    |      |  |      |
| Db | 601  | CTTCTGAGAATTATCTACAAGAACAAGTGCATGCGAAACGGTCCCAATATCTTGATCGCC   | 660  |
| Qy | 661  | AGCTTGGCTCTGGGAGACCTGCTGCACATCGTCATTGACATCCCTATCAATGTCTACAAG   | 720  |
|    |      |  |      |
| Db | 661  | AGCTTGGCTCTGGGAGACCTGCTGCACATCGTCATTGACATCCCTATCAATGTCTACAAG   | 720  |
| Qy | 721  | CTGCTGGCAGAGGACTGGCCATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTCATACAG   | 780  |
|    |      |  |      |
| Db | 721  | CTGCTGGCAGAGGACTGGCCATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTCATACAG   | 780  |
| Qy | 781  | AAAGCCTCCGTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATATCGA   | 840  |
|    |      |  |      |
| Db | 781  | AAAGCCTCCGTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATATCGA   | 840  |
| Qy | 841  | GCTGTTGCTTCTTGGAGTAGAATTAAAGGAATTGGGGTTCCAAAATGGACAGCAGTAGAA   | 900  |
|    |      |  |      |
| Db | 841  | GCTGTTGCTTCTTGGAGTAGAATTAAAGGAATTGGGGTTCCAAAATGGACAGCAGTAGAA   | 900  |
| Qy | 901  | ATTGTTTTGATTTGGGTGGTCTCTGTGGTTCCTGGCTGTCCCTGAAGCCATAGGTTTTGAT  | 960  |
|    |      |  |      |
| Db | 901  | ATTGTTTTGATTTGGGTGGTCTCTGTGGTTCCTGGCTGTCCCTGAAGCCATAGGTTTTGAT  | 960  |
| Qy | 961  | ATAATTACGATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTTCAG   | 1020 |
|    |      |  |      |
| Db | 961  | ATAATTACGATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTTCAG   | 1020 |
| Qy | 1021 | AAGACAGCTTTCATGCAGTTTTTACAAGACAGCAAAAGATTGGTGGCTGTTTCAATTTCTAT | 1080 |
|    |      |  |      |
| Db | 1021 | AAGACAGCTTTCATGCAGTTTTTACAAGACAGCAAAAGATTGGTGGCTGTTTCAATTTCTAT | 1080 |
| Qy | 1081 | TTCTGCTTGCCATTGGCCATCACTGCATTTTTTTTATACACTAATGACCTGTGAAATGTTG  | 1140 |
|    |      |  |      |
| Db | 1081 | TTCTGCTTGCCATTGGCCATCACTGCATTTTTTTTATACACTAATGACCTGTGAAATGTTG  | 1140 |

|    |      |  |      |
|----|------|--|------|
| Qy | 1141 | AGAAAGAAAAGTGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAAGTG | 1200 |
|    |      |  |      |
| Db | 1141 | AGAAAGAAAAGTGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAAGTG | 1200 |
| Qy | 1201 | GCCAAAACCGTCTTTTGCCTGGTCCTTGTCTTTGCCCTCTGCTGGCTTCCCCTTCACCTC | 1260 |
|    |      |  |      |
| Db | 1201 | GCCAAAACCGTCTTTTGCCTGGTCCTTGTCTTTGCCCTCTGCTGGCTTCCCCTTCACCTC | 1260 |
| Qy | 1261 | AGCAGGATTCTGAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGAACTTTTG | 1320 |
|    |      |  |      |
| Db | 1261 | AGCAGGATTCTGAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGAACTTTTG | 1320 |
| Qy | 1321 | AGCTTCTGTTGGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCCTGCATT  | 1380 |
|    |      |  |      |
| Db | 1321 | AGCTTCTGTTGGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCCTGCATT  | 1380 |
| Qy | 1381 | AACCCAATTGCTCTGTATTTGGTGAGCAAAAGATTCAAAAAGTCTTAAAGTCATGCTTA  | 1440 |
|    |      |  |      |
| Db | 1381 | AACCCAATTGCTCTGTATTTGGTGAGCAAAAGATTCAAAAAGTCTTAAAGTCATGCTTA  | 1440 |
| Qy | 1441 | TGCTGCTGGTGCCAGTCATTTGAAGAAAAACAGTCCTTGGAGGAAAAGCAGTCGTGCTTA | 1500 |
|    |      |  |      |
| Db | 1441 | TGCTGCTGGTGCCAGTCATTTGAAGAAAAACAGTCCTTGGAGGAAAAGCAGTCGTGCTTA | 1500 |
| Qy | 1501 | AAGTTCAAAGCTAATGATCACGGATATGACAACTTCCGTTCCAGTAATAAATACAGCTCA | 1560 |
|    |      |  |      |
| Db | 1501 | AAGTTCAAAGCTAATGATCACGGATATGACAACTTCCGTTCCAGTAATAAATACAGCTCA | 1560 |
| Qy | 1561 | TCTTGAAAGAAGAACTATTCAGTGTATTTCAATTTCTTTATATTGGACCGAAGTCATTAA | 1620 |
|    |      |  |      |
| Db | 1561 | TCTTGAAAGAAGAACTATTCAGTGTATTTCAATTTCTTTATATTGGACCGAAGTCATTAA | 1620 |
| Qy | 1621 | AACAAAATGAAACATTTGCCAAAACAAAACAAAAACTATGTATTTGCACAGCACACTAT  | 1680 |
|    |      |  |      |
| Db | 1621 | AACAAAATGAAACATTTGCCAAAACAAAACAAAAACTATGTATTTGCACAGCACACTAT  | 1680 |
| Qy | 1681 | TAAAATATTAAGTGTAATTATTTTAACTCACAGCTACATATGACATTTTATGAGCTGT   | 1740 |
|    |      |  |      |
| Db | 1681 | TAAAATATTAAGTGTAATTATTTTAACTCACAGCTACATATGACATTTTATGAGCTGT   | 1740 |
| Qy | 1741 | TTACGGCATGGAAAGAAAATCAGTGGGAATTAAGAAAGCCTCGTCGTGAAAGCACTTAAT | 1800 |
|    |      |  |      |
| Db | 1741 | TTACGGCATGGAAAGAAAATCAGTGGGAATTAAGAAAGCCTCGTCGTGAAAGCACTTAAT | 1800 |
| Qy | 1801 | TTTTTACAGTTAGCACTTCAACATAGCTCTTAACAACTTCCAGGATATTCACACAACACT | 1860 |
|    |      |  |      |
| Db | 1801 | TTTTTACAGTTAGCACTTCAACATAGCTCTTAACAACTTCCAGGATATTCACACAACACT | 1860 |
| Qy | 1861 | TAGGCTTAAAAATGAGCTCACTCAGAATTTCTATTCTTTCTAAAAAGAGATTTATTTT   | 1920 |
|    |      |  |      |
| Db | 1861 | TAGGCTTAAAAATGAGCTCACTCAGAATTTCTATTCTTTCTAAAAAGAGATTTATTTT   | 1920 |
| Qy | 1921 | AATCAATGGGACTCTGATATAAAGGAAGAATAAGTCACTGTAAAACAGAACTTTTAAATG | 1980 |
|    |      |  |      |
| Db | 1921 | AATCAATGGGACTCTGATATAAAGGAAGAATAAGTCACTGTAAAACAGAACTTTTAAATG | 1980 |
| Qy | 1981 | AAGCTTAAATTACTCAATTTAAATTTTAAATCCTTTAAACAACCTTTTCAATTAATAT   | 2040 |

|    |      |   |      |
|----|------|---|------|
| Db | 1981 | <br>AAGCTTAAATTACTCAATTTAAAATTTTAAAATCCTTTAAAACAACCTTTTCAATTAATAT | 2040 |
| Qy | 2041 | TATCACACTATTATCAGATTGTAATTAGATGCAAATGAGAGAGCAGTTTAGTTGTTGCAT      | 2100 |
| Db | 2041 | <br>TATCACACTATTATCAGATTGTAATTAGATGCAAATGAGAGAGCAGTTTAGTTGTTGCAT  | 2100 |
| Qy | 2101 | TTTTCGGACACTGGAAACATTTAAATGATCAGGAGGGAGTAACAGAAAGAGCAAGGCTGT      | 2160 |
| Db | 2101 | <br>TTTTCGGACACTGGAAACATTTAAATGATCAGGAGGGAGTAACAGAAAGAGCAAGGCTGT  | 2160 |
| Qy | 2161 | TTTTGAAAATCATTACACTTTCACTAGAAGCCCAAACCTCAGCATTCTGCAATATGTAAC      | 2220 |
| Db | 2161 | <br>TTTTGAAAATCATTACACTTTCACTAGAAGCCCAAACCTCAGCATTCTGCAATATGTAAC  | 2220 |
| Qy | 2221 | CAACATGTCACAAACAAGCAGCATGTAACAGACTGGCACATGTGCCAGCTGAATTTAAAA      | 2280 |
| Db | 2221 | <br>CAACATGTCACAAACAAGCAGCATGTAACAGACTGGCACATGTGCCAGCTGAATTTAAAA  | 2280 |
| Qy | 2281 | TATAATACTTTTAAAAAGAAAATTATTACATCCTTTACATTCAAGTAAAGATCAAACCTCA     | 2340 |
| Db | 2281 | <br>TATAATACTTTTAAAAAGAAAATTATTACATCCTTTACATTCAAGTAAAGATCAAACCTCA | 2340 |
| Qy | 2341 | CAAAGAGAAATAGAATGTTTGAAAGGCTATCCCAAAGACTTTTTTGAATCTGTCATTCA       | 2400 |
| Db | 2341 | <br>CAAAGAGAAATAGAATGTTTGAAAGGCTATCCCAAAGACTTTTTTGAATCTGTCATTCA   | 2400 |
| Qy | 2401 | CATACCCTGTGAAGACAATACTATCTACAATTTTTTCAGGATTATTAAAATCTTCTTTTT      | 2460 |
| Db | 2401 | <br>CATACCCTGTGAAGACAATACTATCTACAATTTTTTCAGGATTATTAAAATCTTCTTTTT  | 2460 |
| Qy | 2461 | TCACTATCGTAGCTTAAACTCTGTTTGGTTTTGTCATCTGTAAATACTTACCTACATACA      | 2520 |
| Db | 2461 | <br>TCACTATCGTAGCTTAAACTCTGTTTGGTTTTGTCATCTGTAAATACTTACCTACATACA  | 2520 |
| Qy | 2521 | CTGCATGTAGATGATTAAATGAGGGCAGGCCCTGTGCTCATAGCTTTACGATGGAGAGAT      | 2580 |
| Db | 2521 | <br>CTGCATGTAGATGATTAAATGAGGGCAGGCCCTGTGCTCATAGCTTTACGATGGAGAGAT  | 2580 |
| Qy | 2581 | GCCAGTGACCTCATAATAAAGACTGTGAAGTGCCTGGTGCAGTGTCCACATGACAAAGGG      | 2640 |
| Db | 2581 | <br>GCCAGTGACCTCATAATAAAGACTGTGAAGTGCCTGGTGCAGTGTCCACATGACAAAGGG  | 2640 |
| Qy | 2641 | GCAGGTAGCACCTCTCTCACCCATGCTGTGGTTAAAATGGTTTCTAGCATATGTATAAT       | 2700 |
| Db | 2641 | <br>GCAGGTAGCACCTCTCTCACCCATGCTGTGGTTAAAATGGTTTCTAGCATATGTATAAT   | 2700 |
| Qy | 2701 | GCTATAGTTAAAATACTATTTTTCAAATCATACAGATTAGTACATTTAACAGCTACCTG       | 2760 |
| Db | 2701 | <br>GCTATAGTTAAAATACTATTTTTCAAATCATACAGATTAGTACATTTAACAGCTACCTG   | 2760 |
| Qy | 2761 | TAAAGCTTATTACTAATTTTTGTATTATTTTTGTAAATAGCCAATAGAAAAGTTTGCTTG      | 2820 |
| Db | 2761 | <br>TAAAGCTTATTACTAATTTTTGTATTATTTTTGTAAATAGCCAATAGAAAAGTTTGCTTG  | 2820 |
| Qy | 2821 | ACATGGTGCTTTTCTTTCATCTAGAGGCAAAACTGCTTTTTGAGACCGTAAGAACCTCTT      | 2880 |
|    |      |   |      |

Db 2821 ACATGGTGCTTTTCTTTCATCTAGAGGCAAACTGCTTTTTGAGACCGTAAGAACCTCTT 2880  
 Qy 2881 AGCTTTGTGCGTTCCTGCCTAATTTTTATATCTTCTAAGCAAAGTGCCTTAGGATAGCTT 2940  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 2881 AGCTTTGTGCGTTCCTGCCTAATTTTTATATCTTCTAAGCAAAGTGCCTTAGGATAGCTT 2940  
 Qy 2941 GGGATGAGATGTGTGTGAAAGTATGTACAAGAGAAAACGGAAGAGAGAGGAAATGAGGTG 3000  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 2941 GGGATGAGATGTGTGTGAAAGTATGTACAAGAGAAAACGGAAGAGAGAGGAAATGAGGTG 3000  
 Qy 3001 GGGTTGGAGGAAACCCATGGGGACAGATTCCCATTCCTTAGCCTAACGTTTCGTCATTGCCT 3060  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 3001 GGGTTGGAGGAAACCCATGGGGACAGATTCCCATTCCTTAGCCTAACGTTTCGTCATTGCCT 3060  
 Qy 3061 CGTCACATCAATGCAAAAGGTCTGATTTTGTTCAGCAAAACACAGTGCAATGTTCTCA 3120  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 3061 CGTCACATCAATGCAAAAGGTCTGATTTTGTTCAGCAAAACACAGTGCAATGTTCTCA 3120  
 Qy 3121 GAGTGACTTTCGAAATAAATTGGGCCCCAAGAGCTTTAACTCGGTCTTAAAATATGCCCAA 3180  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 3121 GAGTGACTTTCGAAATAAATTGGGCCCCAAGAGCTTTAACTCGGTCTTAAAATATGCCCAA 3180  
 Qy 3181 ATTTTTACTTTGTTTTTCTTTTAATAGGCTGGGCCACATGTTGGAATAAGCTAGTAATG 3240  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 3181 ATTTTTACTTTGTTTTTCTTTTAATAGGCTGGGCCACATGTTGGAATAAGCTAGTAATG 3240  
 Qy 3241 TTGTTTTCTGTCAATATTGAATGTGATGGTACAGTAAACCAAACCAACAATGTGGCCA 3300  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 3241 TTGTTTTCTGTCAATATTGAATGTGATGGTACAGTAAACCAAACCAACAATGTGGCCA 3300  
 Qy 3301 GAAAGAAAGAGCAATAATAATTAATTCACACACCATATGGATTCTATTTATAAATCACCC 3360  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 3301 GAAAGAAAGAGCAATAATAATTAATTCACACACCATATGGATTCTATTTATAAATCACCC 3360  
 Qy 3361 ACAAACTTGTTCTTTAATTTTCATCCCAATCACTTTTTTCAGAGGCCTGTTATCATAGAAGT 3420  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 3361 ACAAACTTGTTCTTTAATTTTCATCCCAATCACTTTTTTCAGAGGCCTGTTATCATAGAAGT 3420  
 Qy 3421 CATTTTAGACTCTCAATTTTAAATTAATTTTGAATCACTAATATTTTCACAGTTTATTAA 3480  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 3421 CATTTTAGACTCTCAATTTTAAATTAATTTTGAATCACTAATATTTTCACAGTTTATTAA 3480  
 Qy 3481 TATATTTAATTTCTATTTAAATTTTAGATTATTTTATTACCATGTACTGAATTTTACA 3540  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 3481 TATATTTAATTTCTATTTAAATTTTAGATTATTTTATTACCATGTACTGAATTTTACA 3540  
 Qy 3541 TCCTGATACCCTTTCCTTCTCCATGTCAGTATCATGTTCTCTAATTATCTTGCCAAATTT 3600  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 3541 TCCTGATACCCTTTCCTTCTCCATGTCAGTATCATGTTCTCTAATTATCTTGCCAAATTT 3600  
 Qy 3601 TGAAACTACACACAAAAAGCATACTTGCATTATTTATAATAAAAATTGCATTCACTGGCTT 3660  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 3601 TGAAACTACACACAAAAAGCATACTTGCATTATTTATAATAAAAATTGCATTCACTGGCTT 3660  
 Qy 3661 TTTAAAAAAATGTTTGATTCAAACTTTAACATACTGATAAGTAAGAAACAATTATAAT 3720  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 3661 TTTAAAAAAATGTTTGATTCAAACTTTAACATACTGATAAGTAAGAAACAATTATAAT 3720

|    |      |  |      |
|----|------|--|------|
| Qy | 3721 | TTCTTTACATACTCAAACCAAGATAGAAAAAGGTGCTATCGTTCAACTTCAAACATGT   | 3780 |
|    |      |  |      |
| Db | 3721 | TTCTTTACATACTCAAACCAAGATAGAAAAAGGTGCTATCGTTCAACTTCAAACATGT   | 3780 |
| Qy | 3781 | TTCCTAGTATTAAGGACTTTAATATAGCAACAGACAAAATTATTGTTAACATGGATGTTA | 3840 |
|    |      |  |      |
| Db | 3781 | TTCCTAGTATTAAGGACTTTAATATAGCAACAGACAAAATTATTGTTAACATGGATGTTA | 3840 |
| Qy | 3841 | CAGCTCAAAGATTTATAAAAGATTTTAACCTATTTTCTCCCTTATTATCCACTGCTAAT  | 3900 |
|    |      |  |      |
| Db | 3841 | CAGCTCAAAGATTTATAAAAGATTTTAACCTATTTTCTCCCTTATTATCCACTGCTAAT  | 3900 |
| Qy | 3901 | GTGGATGTATGTTCAAACACCTTTTAGTATTGATAGCTTACATATGGCCAAAGGAATACA | 3960 |
|    |      |  |      |
| Db | 3901 | GTGGATGTATGTTCAAACACCTTTTAGTATTGATAGCTTACATATGGCCAAAGGAATACA | 3960 |
| Qy | 3961 | GTTTATAGCAAACATGGGTATGCTGTAGCTAACTTTATAAAAGTGAATATAACAATGT   | 4020 |
|    |      |  |      |
| Db | 3961 | GTTTATAGCAAACATGGGTATGCTGTAGCTAACTTTATAAAAGTGAATATAACAATGT   | 4020 |
| Qy | 4021 | AAAAAATTATATATCTGGGAGGATTTTTTGGTTGCCTAAAGTGGCTATAGTTACTGATTT | 4080 |
|    |      |  |      |
| Db | 4021 | AAAAAATTATATATCTGGGAGGATTTTTTGGTTGCCTAAAGTGGCTATAGTTACTGATTT | 4080 |
| Qy | 4081 | TTTATTATGTAAGCAAACCAATAAAAAATTTAAGTTTTTTTAACAACTACCTTATTTTTC | 4140 |
|    |      |  |      |
| Db | 4081 | TTTATTATGTAAGCAAACCAATAAAAAATTTAAGTTTTTTTAACAACTACCTTATTTTTC | 4140 |
| Qy | 4141 | ACTGTACAGACACTAATTCATTAATACTAATTGATTGTTTAAAAGAAATATAAATGTGA  | 4200 |
|    |      |  |      |
| Db | 4141 | ACTGTACAGACACTAATTCATTAATACTAATTGATTGTTTAAAAGAAATATAAATGTGA  | 4200 |
| Qy | 4201 | CAAGTGGACATTATTTATGTTAAATATACAATTATCAAGCAAGTATGAAGTTATTCAATT | 4260 |
|    |      |  |      |
| Db | 4201 | CAAGTGGACATTATTTATGTTAAATATACAATTATCAAGCAAGTATGAAGTTATTCAATT | 4260 |
| Qy | 4261 | AAAATGCCACATTTCTGGTCTCTGGG                                   | 4286 |
|    |      |  |      |
| Db | 4261 | AAAATGCCACATTTCTGGTCTCTGGG                                   | 4286 |

RESULT 4

US-10-007-926A-177

; Sequence 177, Application US/10007926A

; Publication No. US20030143539A1

; GENERAL INFORMATION:

; APPLICANT: BERTUCCI, FRANCOIS

; APPLICANT: HOULGATTE, REMI

; APPLICANT: BIRNBAUM, DANIEL

; APPLICANT: NGUYEN, CATHERINE

; APPLICANT: VIENS, PATRICE

; APPLICANT: FERT, VINCENT

; TITLE OF INVENTION: GENE EXPRESSION PROFILING OF PRIMARY BREAST CARCINOMAS

; TITLE OF INVENTION: USING ARRAYS OF CANDIDATE GENES

; FILE REFERENCE: 1546-R-00

; CURRENT APPLICATION NUMBER: US/10/007,926A



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; CURRENT FILING DATE: 2001-12-07
; PRIOR APPLICATION NUMBER: 60/254,090
; PRIOR FILING DATE: 2000-12-08
; NUMBER OF SEQ ID NOS: 468
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 177
; LENGTH: 4286
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: endothelin receptor type b (EDNRB) gene.
US-10-007-926A-177
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Query Match          99.6%; Score 4284.4; DB 15; Length 4286;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4285; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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Qy      1 GAGACATTCCGGTGGGGGACTCTGGCCAGCCCAGCAACGTGGATCCTGAGAGCACTCCC 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 GAGACATTCCGGTGGGGGACTCTGGCCAGCCCAGCAACGTGGATCCTGAGAGCACTCCC 60

Qy     61 AGGTAGGCATTTGCCCCGGTGGGACGCCTTGCCAGAGCAGTGTGTGGCAGGCCCCCGTGG 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 AGGTAGGCATTTGCCCCGGTGGGACGCCTTGCCAGAGCAGTGTGTGGCAGGCCCCCGTGG 120

Qy    121 AGGATCAACACAGTGGCTGAACACTGGGAAGGAACTGGTACTTGGAGTCTGGACATCTGA 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 AGGATCAACACAGTGGCTGAACACTGGGAAGGAACTGGTACTTGGAGTCTGGACATCTGA 180

Qy    181 AACTTGGCTCTGAAACTGCGGAGCGGCCACCGGACGCCTTCTGGAGCAGGTAGCAGCATG 240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 AACTTGGCTCTGAAACTGCGCAGCGGCCACCGGACGCCTTCTGGAGCAGGTAGCAGCATG 240

Qy    241 CAGCCGCCTCCAAGTCTGTGCGGACGCGCCCTGGTTGCGCTGGTTCTTGCCTGCGGCCTG 300
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 CAGCCGCCTCCAAGTCTGTGCGGACGCGCCCTGGTTGCGCTGGTTCTTGCCTGCGGCCTG 300

Qy    301 TCGCGGATCTGGGGAGAGGAGAGAGGCTTCCCGCCTGACAGGGCCACTCCGCTTTTGCAA 360
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 TCGCGGATCTGGGGAGAGGAGAGAGGCTTCCCGCCTGACAGGGCCACTCCGCTTTTGCAA 360

Qy    361 ACCGCAGAGATAATGACGCCACCCACTAAGACCTTATGGCCCAAGGGTTCCAACGCCAGT 420
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 ACCGCAGAGATAATGACGCCACCCACTAAGACCTTATGGCCCAAGGGTTCCAACGCCAGT 420

Qy    421 CTGGCGCGGTTCGTTGGCACCTGCGGAGGTGCCTAAAGGAGACAGGACGGCAGGATCTCCG 480
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 CTGGCGCGGTTCGTTGGCACCTGCGGAGGTGCCTAAAGGAGACAGGACGGCAGGATCTCCG 480

Qy    481 CCACGCACCATCTCCCCTCCCCCGTGCCAAGGACCCATCGAGATCAAGGAGACTTTCAAA 540
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 CCACGCACCATCTCCCCTCCCCCGTGCCAAGGACCCATCGAGATCAAGGAGACTTTCAAA 540

Qy    541 TACATCAACACGGTTGTGTCTTGCCTTGTGTTTCGTGCTGGGGATCATCGGGAACCTCACA 600
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 TACATCAACACGGTTGTGTCTTGCCTTGTGTTTCGTGCTGGGGATCATCGGGAACCTCACA 600
```

|    |      |  |      |
|----|------|--|------|
| Qy | 601  | CTTCTGAGAATTATCTACAAGAACAAGTGCATGCGAAACGGTCCCAATATCTTGATCGCC | 660  |
|    |      |  |      |
| Db | 601  | CTTCTGAGAATTATCTACAAGAACAAGTGCATGCGAAACGGTCCCAATATCTTGATCGCC | 660  |
| Qy | 661  | AGCTTGGCTCTGGGAGACCTGCTGCACATCGTCATTGACATCCCTATCAATGTCTACAAG | 720  |
|    |      |  |      |
| Db | 661  | AGCTTGGCTCTGGGAGACCTGCTGCACATCGTCATTGACATCCCTATCAATGTCTACAAG | 720  |
| Qy | 721  | CTGCTGGCAGAGGACTGGCCATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTCATACAG | 780  |
|    |      |  |      |
| Db | 721  | CTGCTGGCAGAGGACTGGCCATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTCATACAG | 780  |
| Qy | 781  | AAAGCCTCCGTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATATCGA | 840  |
|    |      |  |      |
| Db | 781  | AAAGCCTCCGTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATATCGA | 840  |
| Qy | 841  | GCTGTTGCTTCTTGGAGTAGAATTAAAGGAATTGGGGTTCCAAAATGGACAGCAGTAGAA | 900  |
|    |      |  |      |
| Db | 841  | GCTGTTGCTTCTTGGAGTAGAATTAAAGGAATTGGGGTTCCAAAATGGACAGCAGTAGAA | 900  |
| Qy | 901  | ATTGTTTTGATTTGGGTGGTCTCTGTGGTTCTGGCTGTCCCTGAAGCCATAGGTTTTGAT | 960  |
|    |      |  |      |
| Db | 901  | ATTGTTTTGATTTGGGTGGTCTCTGTGGTTCTGGCTGTCCCTGAAGCCATAGGTTTTGAT | 960  |
| Qy | 961  | ATAATTACGATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTTCAG | 1020 |
|    |      |  |      |
| Db | 961  | ATAATTACGATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTTCAG | 1020 |
| Qy | 1021 | AAGACAGCTTTCATGCAGTTTTACAAGACAGCAAAAGATTGGTGGCTGTTCACTTTCTAT | 1080 |
|    |      |  |      |
| Db | 1021 | AAGACAGCTTTCATGCAGTTTTACAAGACAGCAAAAGATTGGTGGCTGTTCACTTTCTAT | 1080 |
| Qy | 1081 | TTCTGCTTGCCATTGGCCATCACTGCATTTTTTTATACACTAATGACCTGTGAAATGTTG | 1140 |
|    |      |  |      |
| Db | 1081 | TTCTGCTTGCCATTGGCCATCACTGCATTTTTTTATACACTAATGACCTGTGAAATGTTG | 1140 |
| Qy | 1141 | AGAAAGAAAAGTGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAAGTG | 1200 |
|    |      |  |      |
| Db | 1141 | AGAAAGAAAAGTGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAAGTG | 1200 |
| Qy | 1201 | GCCAAAACCGTCTTTTGCCTGGTCCTTGTCTTTGCCCTCTGCTGGCTTCCCCTTCACCTC | 1260 |
|    |      |  |      |
| Db | 1201 | GCCAAAACCGTCTTTTGCCTGGTCCTTGTCTTTGCCCTCTGCTGGCTTCCCCTTCACCTC | 1260 |
| Qy | 1261 | AGCAGGATTCTGAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGAACTTTTG | 1320 |
|    |      |  |      |
| Db | 1261 | AGCAGGATTCTGAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGAACTTTTG | 1320 |
| Qy | 1321 | AGCTTTCTGTTGGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCCTGCATT | 1380 |
|    |      |  |      |
| Db | 1321 | AGCTTTCTGTTGGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCCTGCATT | 1380 |
| Qy | 1381 | AACCCAATTGCTCTGTATTTGGTGAGCAAAAGATTCAAAAAGTCTTTAAGTCATGCTTA  | 1440 |
|    |      |  |      |
| Db | 1381 | AACCCAATTGCTCTGTATTTGGTGAGCAAAAGATTCAAAAAGTCTTTAAGTCATGCTTA  | 1440 |
| Qy | 1441 | TGCTGCTGGTGCCAGTCATTTGAAGAAAAACAGTCCTTGGAGGAAAAGCAGTCGTGCTTA | 1500 |

|    |      |  |      |
|----|------|--|------|
| Db | 1441 | <br>TGCTGCTGGTGCCAGTCATTTGAAGAAAACAGTCCTTGGAGGAAAAGCAGTCGTGCTTA    | 1500 |
| Qy | 1501 | AAGTTCAAAGCTAATGATCACGGATATGACAACTTCCGTTCCAGTAATAAATACAGCTCA       | 1560 |
| Db | 1501 | <br>AAGTTCAAAGCTAATGATCACGGATATGACAACTTCCGTTCCAGTAATAAATACAGCTCA   | 1560 |
| Qy | 1561 | TCTTGAAAGAAGAACTATTCACTGTATTTTCTTTTATATTGGACCGAAGTCATTAA           | 1620 |
| Db | 1561 | <br>TCTTGAAAGAAGAACTATTCACTGTATTTTCTTTTATATTGGACCGAAGTCATTAA       | 1620 |
| Qy | 1621 | AACAAAATGAAACATTTGCCAAAACAAAACAAAACACTATGTATTTGCACAGCACACTAT       | 1680 |
| Db | 1621 | <br>AACAAAATGAAACATTTGCCAAAACAAAACAAAACACTATGTATTTGCACAGCACACTAT   | 1680 |
| Qy | 1681 | TAAAAATATTAAGTGTAAATTATTTTAACACTCACAGCTACATATGACATTTTATGAGCTGT     | 1740 |
| Db | 1681 | <br>TAAAAATATTAAGTGTAAATTATTTTAACACTCACAGCTACATATGACATTTTATGAGCTGT | 1740 |
| Qy | 1741 | TTACGGCATGGAAAGAAAATCAGTGGGAATTAAGAAAGCCTCGTCGTGAAAGCACTTAAT       | 1800 |
| Db | 1741 | <br>TTACGGCATGGAAAGAAAATCAGTGGGAATTAAGAAAGCCTCGTCGTGAAAGCACTTAAT   | 1800 |
| Qy | 1801 | TTTTTACAGTTAGCACTTCAACATAGCTCTTAACAACCTCCAGGATATTCACACAACACT       | 1860 |
| Db | 1801 | <br>TTTTTACAGTTAGCACTTCAACATAGCTCTTAACAACCTCCAGGATATTCACACAACACT   | 1860 |
| Qy | 1861 | TAGGCTTAAAAATGAGCTCACTCAGAATTTCTATTCTTTCTAAAAAGAGATTTATTTTAA       | 1920 |
| Db | 1861 | <br>TAGGCTTAAAAATGAGCTCACTCAGAATTTCTATTCTTTCTAAAAAGAGATTTATTTTAA   | 1920 |
| Qy | 1921 | AATCAATGGGACTCTGATATAAAGGAAGAATAAGTCACTGTAAAACAGAACTTTTAAATG       | 1980 |
| Db | 1921 | <br>AATCAATGGGACTCTGATATAAAGGAAGAATAAGTCACTGTAAAACAGAACTTTTAAATG   | 1980 |
| Qy | 1981 | AAGCTTAAATTACTCAATTTAAATTTTAAATCCTTTAAACAACCTTTTCAATTAATAT         | 2040 |
| Db | 1981 | <br>AAGCTTAAATTACTCAATTTAAATTTTAAATCCTTTAAACAACCTTTTCAATTAATAT     | 2040 |
| Qy | 2041 | TATCACACTATTATCAGATTGTAATTAGATGCAAATGAGAGAGCAGTTTAGTTGTTGCAT       | 2100 |
| Db | 2041 | <br>TATCACACTATTATCAGATTGTAATTAGATGCAAATGAGAGAGCAGTTTAGTTGTTGCAT   | 2100 |
| Qy | 2101 | TTTTCGGACACTGGAAACATTTAAATGATCAGGAGGGAGTAACAGAAAGAGCAAGGCTGT       | 2160 |
| Db | 2101 | <br>TTTTCGGACACTGGAAACATTTAAATGATCAGGAGGGAGTAACAGAAAGAGCAAGGCTGT   | 2160 |
| Qy | 2161 | TTTTGAAAATCATTACACTTTCACTAGAAGCCCAAACCTCAGCATTCTGCAATATGTAAC       | 2220 |
| Db | 2161 | <br>TTTTGAAAATCATTACACTTTCACTAGAAGCCCAAACCTCAGCATTCTGCAATATGTAAC   | 2220 |
| Qy | 2221 | CAACATGTCACAAACAAGCAGCATGTAACAGACTGGCACATGTGCCAGCTGAATTTAAAA       | 2280 |
| Db | 2221 | <br>CAACATGTCACAAACAAGCAGCATGTAACAGACTGGCACATGTGCCAGCTGAATTTAAAA   | 2280 |
| Qy | 2281 | TATAATACTTTTAAAAAGAAAATTATTACATCCTTTACATTTCAGTTAAGATCAAACCTCA      | 2340 |
|    |      |  |      |

Db 2281 TATAATACTTTTAAAAAGAAAATTATTACATCCTTTACATTTCAGTTAAGATCAAACCTCA 2340

Qy 2341 CAAAGAGAAATAGAATGTTTGAAAGGCTATCCCAAAGACTTTTTGAATCTGTCATTCA 2400  
 |||

Db 2341 CAAAGAGAAATAGAATGTTTGAAAGGCTATCCCAAAGACTTTTTGAATCTGTCATTCA 2400

Qy 2401 CATACCCTGTGAAGACAATACTATCTACAATTTTTTCAGGATTATTAATCTTCTTTT 2460  
 |||

Db 2401 CATACCCTGTGAAGACAATACTATCTACAATTTTTTCAGGATTATTAATCTTCTTTT 2460

Qy 2461 TCACTATCGTAGCTTAAACTCTGTTTGGTTTTGTCATCTGTAAATACTTACCTACATACA 2520  
 |||

Db 2461 TCACTATCGTAGCTTAAACTCTGTTTGGTTTTGTCATCTGTAAATACTTACCTACATACA 2520

Qy 2521 CTGCATGTAGATGATTAAATGAGGGCAGGCCCTGTGCTCATAGCTTTACGATGGAGAGAT 2580  
 |||

Db 2521 CTGCATGTAGATGATTAAATGAGGGCAGGCCCTGTGCTCATAGCTTTACGATGGAGAGAT 2580

Qy 2581 GCCAGTGACCTCATAATAAAGACTGTGAACTGCCTGGTGCAGTGTCCACATGACAAAGGG 2640  
 |||

Db 2581 GCCAGTGACCTCATAATAAAGACTGTGAACTGCCTGGTGCAGTGTCCACATGACAAAGGG 2640

Qy 2641 GCAGGTAGCACCTCTCTCACCCATGCTGTGGTTAAATGGTTTCTAGCATATGTATAAT 2700  
 |||

Db 2641 GCAGGTAGCACCTCTCTCACCCATGCTGTGGTTAAATGGTTTCTAGCATATGTATAAT 2700

Qy 2701 GCTATAGTTAAAATACTATTTTTCAAATCATACAGATTAGTACATTTAACAGCTACCTG 2760  
 |||

Db 2701 GCTATAGTTAAAATACTATTTTTCAAATCATACAGATTAGTACATTTAACAGCTACCTG 2760

Qy 2761 TAAAGCTTATTACTAATTTTTGTATTATTTTTGTAAATAGCCAATAGAAAAGTTTGCTTG 2820  
 |||

Db 2761 TAAAGCTTATTACTAATTTTTGTATTATTTTTGTAAATAGCCAATAGAAAAGTTTGCTTG 2820

Qy 2821 ACATGGTGCTTTTCTTTCATCTAGAGGCAAACTGCTTTTTGAGACCGTAAGAACCTCTT 2880  
 |||

Db 2821 ACATGGTGCTTTTCTTTCATCTAGAGGCAAACTGCTTTTTGAGACCGTAAGAACCTCTT 2880

Qy 2881 AGCTTTGTGCGTTCCTGCCTAATTTTTTATATCTTCTAAGCAAAGTGCCTTAGGATAGCTT 2940  
 |||

Db 2881 AGCTTTGTGCGTTCCTGCCTAATTTTTTATATCTTCTAAGCAAAGTGCCTTAGGATAGCTT 2940

Qy 2941 GGGATGAGATGTGTGTGAAAGTATGTACAAGAGAAAACGGAAGAGAGAGGAAATGAGGTG 3000  
 |||

Db 2941 GGGATGAGATGTGTGTGAAAGTATGTACAAGAGAAAACGGAAGAGAGAGGAAATGAGGTG 3000

Qy 3001 GGGTTGGAGGAAACCCATGGGGACAGATTCCCATTCTTAGCCTAACGTTTCGTCATTGCCT 3060  
 |||

Db 3001 GGGTTGGAGGAAACCCATGGGGACAGATTCCCATTCTTAGCCTAACGTTTCGTCATTGCCT 3060

Qy 3061 CGTCACATCAATGCAAAAGGTCTGATTTTGTTCAGCAAAACACAGTGCAATGTTCTCA 3120  
 |||

Db 3061 CGTCACATCAATGCAAAAGGTCTGATTTTGTTCAGCAAAACACAGTGCAATGTTCTCA 3120

Qy 3121 GAGTGACTTTCGAAATAAATTGGGCCCAAGAGCTTTAACTCGGTCTTAAATATGCCCAA 3180  
 |||

Db 3121 GAGTGACTTTCGAAATAAATTGGGCCCAAGAGCTTTAACTCGGTCTTAAATATGCCCAA 3180

Qy 3181 ATTTTACTTTGTTTTCTTTAATAGGCTGGGCCACATGTTGGAAATAAGCTAGTAATG 3240  
 |||  
 Db 3181 ATTTTACTTTGTTTTCTTTAATAGGCTGGGCCACATGTTGGAAATAAGCTAGTAATG 3240

Qy 3241 TTGTTTTCTGTCAATATTGAATGTGATGGTACAGTAAACCAAACCAACAATGTGGCCA 3300  
 |||  
 Db 3241 TTGTTTTCTGTCAATATTGAATGTGATGGTACAGTAAACCAAACCAACAATGTGGCCA 3300

Qy 3301 GAAAGAAAGAGCAATAATAATTAATTCACACACCATATGGATTCTATTTATAAATCACCC 3360  
 |||  
 Db 3301 GAAAGAAAGAGCAATAATAATTAATTCACACACCATATGGATTCTATTTATAAATCACCC 3360

Qy 3361 ACAAACTTGTCTTTAATTTTCATCCCAATCACTTTTTTCAGAGGCCTGTTATCATAGAAGT 3420  
 |||  
 Db 3361 ACAAACTTGTCTTTAATTTTCATCCCAATCACTTTTTTCAGAGGCCTGTTATCATAGAAGT 3420

Qy 3421 CATTTTAGACTCTCAATTTTAAATTAATTTTGAATCACTAATATTTTCACAGTTTATTAA 3480  
 |||  
 Db 3421 CATTTTAGACTCTCAATTTTAAATTAATTTTGAATCACTAATATTTTCACAGTTTATTAA 3480

Qy 3481 TATATTTAATTTCTATTTAAATTTTAGATTATTTTATTACCATGTACTGAATTTTTTACA 3540  
 |||  
 Db 3481 TATATTTAATTTCTATTTAAATTTTAGATTATTTTATTACCATGTACTGAATTTTTTACA 3540

Qy 3541 TCCTGATACCCTTTCCTTCTCCATGTCAGTATCATGTTCTCTAATTATCTTGCCAAATTT 3600  
 |||  
 Db 3541 TCCTGATACCCTTTCCTTCTCCATGTCAGTATCATGTTCTCTAATTATCTTGCCAAATTT 3600

Qy 3601 TGAACTACACACAAAAGCATACTTGCATTATTTATAATAAAATTGCATTCACTGGCTT 3660  
 |||  
 Db 3601 TGAACTACACACAAAAGCATACTTGCATTATTTATAATAAAATTGCATTCACTGGCTT 3660

Qy 3661 TTTAAAAAAATGTTTGATTCAAACCTTTAACATACTGATAAGTAAGAAACAATTATAAT 3720  
 |||  
 Db 3661 TTTAAAAAAATGTTTGATTCAAACCTTTAACATACTGATAAGTAAGAAACAATTATAAT 3720

Qy 3721 TTCTTTACATACTCAAACCAAGATAGAAAAAGGTGCTATCGTTCACTTCAAACATGT 3780  
 |||  
 Db 3721 TTCTTTACATACTCAAACCAAGATAGAAAAAGGTGCTATCGTTCACTTCAAACATGT 3780

Qy 3781 TTCCTAGTATTAAGGACTTTAATATAGCAACAGACAAAATTATTGTTAACATGGATGTTA 3840  
 |||  
 Db 3781 TTCCTAGTATTAAGGACTTTAATATAGCAACAGACAAAATTATTGTTAACATGGATGTTA 3840

Qy 3841 CAGCTCAAAAGATTTATAAAAGATTTTAACCTATTTTCTCCCTTATTATCCACTGCTAAT 3900  
 |||  
 Db 3841 CAGCTCAAAAGATTTATAAAAGATTTTAACCTATTTTCTCCCTTATTATCCACTGCTAAT 3900

Qy 3901 GTGGATGTATGTTCAAACACCTTTTAGTATTGATAGCTTACATATGGCCAAAGGAATACA 3960  
 |||  
 Db 3901 GTGGATGTATGTTCAAACACCTTTTAGTATTGATAGCTTACATATGGCCAAAGGAATACA 3960

Qy 3961 GTTTATAGCAAAACATGGGTATGCTGTAGCTAACTTTATAAAAGTGTAATATAACAATGT 4020  
 |||  
 Db 3961 GTTTATAGCAAAACATGGGTATGCTGTAGCTAACTTTATAAAAGTGTAATATAACAATGT 4020

Qy 4021 AAAAAATTATATATCTGGGAGGATTTTTTGGTTGCCTAAAGTGGCTATAGTTACTGATTT 4080  
 ||||||||||||||||||  
 Db 4021 AAAAAATTATATATCTGGGAGGATTTTTTGGTTGCCTAAAGTGGCTATAGTTACTGATTT 4080  
 Qy 4081 TTTATTATGTAAGCAAACCAATAAAAAATTTAAGTTTTTTTAACTACCTTATTTTTC 4140  
 ||||||||||||||||||  
 Db 4081 TTTATTATGTAAGCAAACCAATAAAAAATTTAAGTTTTTTTAACTACCTTATTTTTC 4140  
 Qy 4141 ACTGTACAGACACTAATTCATTAAATACTAATTGATTGTTTAAAGAAATATAAATGTGA 4200  
 ||||||||||||||||||  
 Db 4141 ACTGTACAGACACTAATTCATTAAATACTAATTGATTGTTTAAAGAAATATAAATGTGA 4200  
 Qy 4201 CAAGTGGACATTATTTATGTTAAATATACAATTATCAAGCAAGTATGAAGTTATTCAATT 4260  
 ||||||||||||||||||  
 Db 4201 CAAGTGGACATTATTTATGTTAAATATACAATTATCAAGCAAGTATGAAGTTATTCAATT 4260  
 Qy 4261 AAAATGCCACATTTCTGGTCTCTGGG 4286  
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 Db 4261 AAAATGCCACATTTCTGGTCTCTGGG 4286

RESULT 5

US-10-120-15

; Sequence 15, Application US/10210120  
 ; Publication No. US20030175736A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Chinnaiyan, Arul M.  
 ; APPLICANT: Rubin, Mark A.  
 ; APPLICANT: Sreekumar, Arun  
 ; TITLE OF INVENTION: Expression Profile of Prostate Cancer  
 ; FILE REFERENCE: UM-07221  
 ; CURRENT APPLICATION NUMBER: US/10/210,120  
 ; CURRENT FILING DATE: 2002-08-01  
 ; PRIOR APPLICATION NUMBER: US 60/309,581  
 ; PRIOR FILING DATE: 2001-08-02  
 ; PRIOR APPLICATION NUMBER: US 60/334,468  
 ; PRIOR FILING DATE: 2001-11-15  
 ; NUMBER OF SEQ ID NOS: 123  
 ; SOFTWARE: PatentIn version 3.2  
 ; SEQ ID NO 15  
 ; LENGTH: 4286  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 US-10-210-120-15

Query Match 99.6%; Score 4284.4; DB 15; Length 4286;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 4285; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GAGACATTCCGGTGGGGGACTCTGGCCAGCCCGAGCAACGTGGATCCTGAGAGCACTCCC 60  
 ||||||||||||||||||  
 Db 1 GAGACATTCCGGTGGGGGACTCTGGCCAGCCCGAGCAACGTGGATCCTGAGAGCACTCCC 60  
 Qy 61 AGGTAGGCATTTGCCCCGGTGGGACGCCTTGCCAGAGCAGTGTGTGGCAGGCCCCCGTGG 120  
 ||||||||||||||||||  
 Db 61 AGGTAGGCATTTGCCCCGGTGGGACGCCTTGCCAGAGCAGTGTGTGGCAGGCCCCCGTGG 120

Qy 121 AGGATCAACACAGTGGCTGAACACTGGGAAGGAAGTGGTACTTGGAGTCTGGACATCTGA 180  
 |||  
 Db 121 AGGATCAACACAGTGGCTGAACACTGGGAAGGAAGTGGTACTTGGAGTCTGGACATCTGA 180

Qy 181 AACTTGGCTCTGAAACTGCGGAGCGGCCACCGACGCCTTCTGGAGCAGGTAGCAGCATG 240  
 |||  
 Db 181 AACTTGGCTCTGAAACTGCGCAGCGGCCACCGACGCCTTCTGGAGCAGGTAGCAGCATG 240

Qy 241 CAGCCGCCTCCAAGTCTGTGCGGACGCGCCCTGGTTGCGCTGGTTCTTGCCTGCGGCCTG 300  
 |||  
 Db 241 CAGCCGCCTCCAAGTCTGTGCGGACGCGCCCTGGTTGCGCTGGTTCTTGCCTGCGGCCTG 300

Qy 301 TCGCGGATCTGGGGAGAGGAGAGAGGCTTCCCGCCTGACAGGGCCACTCCGCTTTTGCAA 360  
 |||  
 Db 301 TCGCGGATCTGGGGAGAGGAGAGAGGCTTCCCGCCTGACAGGGCCACTCCGCTTTTGCAA 360

Qy 361 ACCGCAGAGATAATGACGCCACCCACTAAGACCTTATGGCCCAAGGGTTCCAACGCCAGT 420  
 |||  
 Db 361 ACCGCAGAGATAATGACGCCACCCACTAAGACCTTATGGCCCAAGGGTTCCAACGCCAGT 420

Qy 421 CTGGCGCGGTCGTTGGCACCTGCGGAGGTGCCTAAAGGAGACAGGACGGCAGGATCTCCG 480  
 |||  
 Db 421 CTGGCGCGGTCGTTGGCACCTGCGGAGGTGCCTAAAGGAGACAGGACGGCAGGATCTCCG 480

Qy 481 CCACGCACCATCTCCCCTCCCCGTGCCAAGGACCCATCGAGATCAAGGAGACTTTCAA 540  
 |||  
 Db 481 CCACGCACCATCTCCCCTCCCCGTGCCAAGGACCCATCGAGATCAAGGAGACTTTCAA 540

Qy 541 TACATCAACACGGTTGTGTCCTGCCTTGTGTTGCTGGGGATCATCGGGAAGTCCACA 600  
 |||  
 Db 541 TACATCAACACGGTTGTGTCCTGCCTTGTGTTGCTGGGGATCATCGGGAAGTCCACA 600

Qy 601 CTTCTGAGAATTATCTACAAGAACAAGTGCATGCGAAACGGTCCCAATATCTTGATCGCC 660  
 |||  
 Db 601 CTTCTGAGAATTATCTACAAGAACAAGTGCATGCGAAACGGTCCCAATATCTTGATCGCC 660

Qy 661 AGCTTGGCTCTGGGAGACCTGCTGCACATCGTCATTGACATCCCTATCAATGTCTACAAG 720  
 |||  
 Db 661 AGCTTGGCTCTGGGAGACCTGCTGCACATCGTCATTGACATCCCTATCAATGTCTACAAG 720

Qy 721 CTGCTGGCAGAGGACTGGCCATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTCATACAG 780  
 |||  
 Db 721 CTGCTGGCAGAGGACTGGCCATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTCATACAG 780

Qy 781 AAAGCCTCCGTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATATCGA 840  
 |||  
 Db 781 AAAGCCTCCGTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATATCGA 840

Qy 841 GCTGTTGCTTCTTGAGTAGAATTAAAGGAATTGGGGTTCCAAAATGGACAGCAGTAGAA 900  
 |||  
 Db 841 GCTGTTGCTTCTTGAGTAGAATTAAAGGAATTGGGGTTCCAAAATGGACAGCAGTAGAA 900

Qy 901 ATTGTTTTGATTTGGGTGGTCTCTGTGGTTCTGGCTGTCCCTGAAGCCATAGGTTTTGAT 960  
 |||  
 Db 901 ATTGTTTTGATTTGGGTGGTCTCTGTGGTTCTGGCTGTCCCTGAAGCCATAGGTTTTGAT 960

Qy 961 ATAATTACGATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTTCAG 1020

|    |      |  |      |
|----|------|--|------|
| Db | 961  | ATAATTACGATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTTTCAG  | 1020 |
| Qy | 1021 | AAGACAGCTTTTCATGCAGTTTTACAAGACAGCAAAAGATTGGTGGCTGTTTCAGTTTCTAT | 1080 |
| Db | 1021 | AAGACAGCTTTTCATGCAGTTTTACAAGACAGCAAAAGATTGGTGGCTGTTTCAGTTTCTAT | 1080 |
| Qy | 1081 | TTCTGCTTGCCATTGGCCATCACTGCATTTTTTTATACACTAATGACCTGTGAAATGTTG   | 1140 |
| Db | 1081 | TTCTGCTTGCCATTGGCCATCACTGCATTTTTTTATACACTAATGACCTGTGAAATGTTG   | 1140 |
| Qy | 1141 | AGAAAGAAAAGTGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAAGTG   | 1200 |
| Db | 1141 | AGAAAGAAAAGTGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAAGTG   | 1200 |
| Qy | 1201 | GCCAAAACCGTCTTTTGCCTGGTCCTTGTCTTTGCCCTCTGCTGGCTTCCCCTTCACCTC   | 1260 |
| Db | 1201 | GCCAAAACCGTCTTTTGCCTGGTCCTTGTCTTTGCCCTCTGCTGGCTTCCCCTTCACCTC   | 1260 |
| Qy | 1261 | AGCAGGATTCTGAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGAACTTTTG   | 1320 |
| Db | 1261 | AGCAGGATTCTGAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGAACTTTTG   | 1320 |
| Qy | 1321 | AGCTTTCTGTTGGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCCTGCATT   | 1380 |
| Db | 1321 | AGCTTTCTGTTGGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCCTGCATT   | 1380 |
| Qy | 1381 | AACCCAATTGCTCTGTATTTGGTGAGCAAAAGATTCAAAAAGTCTTTAAGTCATGCTTA    | 1440 |
| Db | 1381 | AACCCAATTGCTCTGTATTTGGTGAGCAAAAGATTCAAAAAGTCTTTAAGTCATGCTTA    | 1440 |
| Qy | 1441 | TGCTGCTGGTGCCAGTCATTTGAAGAAAACAGTCCTTGGAGGAAAAGCAGTCGTGCTTA    | 1500 |
| Db | 1441 | TGCTGCTGGTGCCAGTCATTTGAAGAAAACAGTCCTTGGAGGAAAAGCAGTCGTGCTTA    | 1500 |
| Qy | 1501 | AAGTTCAAAGCTAATGATCACGGATATGACAACTCCGTTCCAGTAATAAATACAGCTCA    | 1560 |
| Db | 1501 | AAGTTCAAAGCTAATGATCACGGATATGACAACTCCGTTCCAGTAATAAATACAGCTCA    | 1560 |
| Qy | 1561 | TCTTGAAAGAAGAACTATTCACTGTATTTTCACTTTCTTTATATTGGACCGAAGTCATTAA  | 1620 |
| Db | 1561 | TCTTGAAAGAAGAACTATTCACTGTATTTTCACTTTCTTTATATTGGACCGAAGTCATTAA  | 1620 |
| Qy | 1621 | AACAAAATGAAACATTTGCCAAAACAAAACAAAAAACTATGTATTTGCACAGCACACTAT   | 1680 |
| Db | 1621 | AACAAAATGAAACATTTGCCAAAACAAAACAAAAAACTATGTATTTGCACAGCACACTAT   | 1680 |
| Qy | 1681 | TAAAATATTAAGTGTAATTATTTTAACACTCACAGCTACATATGACATTTTATGAGCTGT   | 1740 |
| Db | 1681 | TAAAATATTAAGTGTAATTATTTTAACACTCACAGCTACATATGACATTTTATGAGCTGT   | 1740 |
| Qy | 1741 | TTACGGCATGGAAAGAAAATCAGTGGGAATTAAGAAAGCCTCGTCGTGAAAGCACTTAAT   | 1800 |
| Db | 1741 | TTACGGCATGGAAAGAAAATCAGTGGGAATTAAGAAAGCCTCGTCGTGAAAGCACTTAAT   | 1800 |
| Qy | 1801 | TTTTTACAGTTAGCACTTCAACATAGCTCTTAACAACCTCCAGGATATTCACACAACACT   | 1860 |



Db 1801 TTTTACAGTTAGCACTTCAACATAGCTCTTAACAACCTCCAGGATATTCACACAACACT 1860  
 Qy 1861 TAGGCTTAAAAATGAGCTCACTCAGAATTTCTATTCTTTCTAAAAAGAGATTTATTTT 1920  
 Db 1861 TAGGCTTAAAAATGAGCTCACTCAGAATTTCTATTCTTTCTAAAAAGAGATTTATTTT 1920  
 Qy 1921 AATCAATGGGACTCTGATATAAAGGAAGAATAAGTCACTGTAAAACAGAACTTTTAAATG 1980  
 Db 1921 AATCAATGGGACTCTGATATAAAGGAAGAATAAGTCACTGTAAAACAGAACTTTTAAATG 1980  
 Qy 1981 AAGCTTAAATTACTCAATTTAAAATTTTAAAATCCTTTAAAACAACCTTTTCAATTAATAT 2040  
 Db 1981 AAGCTTAAATTACTCAATTTAAAATTTTAAAATCCTTTAAAACAACCTTTTCAATTAATAT 2040  
 Qy 2041 TATCACACTATTATCAGATTGTAATTAGATGCAAATGAGAGAGCAGTTTAGTTGTTGCAT 2100  
 Db 2041 TATCACACTATTATCAGATTGTAATTAGATGCAAATGAGAGAGCAGTTTAGTTGTTGCAT 2100  
 Qy 2101 TTTTCGGGACACTGGAAACATTTAAATGATCAGGAGGGAGTAACAGAAAGAGCAAGGCTGT 2160  
 Db 2101 TTTTCGGGACACTGGAAACATTTAAATGATCAGGAGGGAGTAACAGAAAGAGCAAGGCTGT 2160  
 Qy 2161 TTTTGAAAATCATTACACTTTTCTAGTAAGCCCAAACCTCAGCATTCTGCAATATGTAAC 2220  
 Db 2161 TTTTGAAAATCATTACACTTTTCTAGTAAGCCCAAACCTCAGCATTCTGCAATATGTAAC 2220  
 Qy 2221 CAACATGTCACAAACAAGCAGCATGTAACAGACTGGCACATGTGCCAGCTGAATTTAAAA 2280  
 Db 2221 CAACATGTCACAAACAAGCAGCATGTAACAGACTGGCACATGTGCCAGCTGAATTTAAAA 2280  
 Qy 2281 TATAATACTTTTAAAAAGAAAATTATTACATCCTTTACATTAGTTAAGATCAAACCTCA 2340  
 Db 2281 TATAATACTTTTAAAAAGAAAATTATTACATCCTTTACATTAGTTAAGATCAAACCTCA 2340  
 Qy 2341 CAAAGAGAAATAGAATGTTTGAAAGGCTATCCCAAAGACTTTTTTGAATCTGTCATTCA 2400  
 Db 2341 CAAAGAGAAATAGAATGTTTGAAAGGCTATCCCAAAGACTTTTTTGAATCTGTCATTCA 2400  
 Qy 2401 CATACCCTGTGAAGACAATACTATCTACAATTTTTTCAGGATTATTAATCTTCTTTT 2460  
 Db 2401 CATACCCTGTGAAGACAATACTATCTACAATTTTTTCAGGATTATTAATCTTCTTTT 2460  
 Qy 2461 TCACTATCGTAGCTTAAACTCTGTTTGGTTTTGTCATCTGTAAATACTTACCTACATACA 2520  
 Db 2461 TCACTATCGTAGCTTAAACTCTGTTTGGTTTTGTCATCTGTAAATACTTACCTACATACA 2520  
 Qy 2521 CTGCATGTAGATGATTAAATGAGGGCAGGCCCTGTGCTCATAGCTTTACGATGGAGAGAT 2580  
 Db 2521 CTGCATGTAGATGATTAAATGAGGGCAGGCCCTGTGCTCATAGCTTTACGATGGAGAGAT 2580  
 Qy 2581 GCCAGTGACCTCATAATAAGACTGTGAAGCTGCCTGGTGCAGTGTCCACATGACAAAGGG 2640  
 Db 2581 GCCAGTGACCTCATAATAAGACTGTGAAGCTGCCTGGTGCAGTGTCCACATGACAAAGGG 2640  
 Qy 2641 GCAGGTAGCACCTCTCTCACCCATGCTGTGGTTAAAATGGTTTCTAGCATATGTATAAT 2700  
 Db 2641 GCAGGTAGCACCTCTCTCACCCATGCTGTGGTTAAAATGGTTTCTAGCATATGTATAAT 2700

|    |      |  |      |
|----|------|--|------|
| Qy | 2701 | GCTATAGTTAAAATACTATTTTTTCAAATCATACAGATTAGTACATTTAACAGCTACCTG   | 2760 |
|    |      |  |      |
| Db | 2701 | GCTATAGTTAAAATACTATTTTTTCAAATCATACAGATTAGTACATTTAACAGCTACCTG   | 2760 |
| Qy | 2761 | TAAAGCTTATTACTAATTTTTGTATTATTTTGTAAATAGCCAATAGAAAAGTTTGCTTG    | 2820 |
|    |      |  |      |
| Db | 2761 | TAAAGCTTATTACTAATTTTTGTATTATTTTGTAAATAGCCAATAGAAAAGTTTGCTTG    | 2820 |
| Qy | 2821 | ACATGGTGCTTTTCTTTTCATCTAGAGGCAAACTGCTTTTGTAGACCGTAAGAACCTCTT   | 2880 |
|    |      |  |      |
| Db | 2821 | ACATGGTGCTTTTCTTTTCATCTAGAGGCAAACTGCTTTTGTAGACCGTAAGAACCTCTT   | 2880 |
| Qy | 2881 | AGCTTTGTGCGTTCCTGCCTAATTTTTATATCTTCTAAGCAAAGTGCCTTAGGATAGCTT   | 2940 |
|    |      |  |      |
| Db | 2881 | AGCTTTGTGCGTTCCTGCCTAATTTTTATATCTTCTAAGCAAAGTGCCTTAGGATAGCTT   | 2940 |
| Qy | 2941 | GGGATGAGATGTGTGTGAAAGTATGTACAAGAGAAAACGGAAGAGAGAGGAAATGAGGTG   | 3000 |
|    |      |  |      |
| Db | 2941 | GGGATGAGATGTGTGTGAAAGTATGTACAAGAGAAAACGGAAGAGAGAGGAAATGAGGTG   | 3000 |
| Qy | 3001 | GGGTTGGAGGAAACCCATGGGGACAGATTCCCATTTCTTAGCCTAACGTTTCGTCATTGCCT | 3060 |
|    |      |  |      |
| Db | 3001 | GGGTTGGAGGAAACCCATGGGGACAGATTCCCATTTCTTAGCCTAACGTTTCGTCATTGCCT | 3060 |
| Qy | 3061 | CGTCACATCAATGCAAAAGGTCCTGATTTTGTTCAGCAAAACACAGTGCAATGTTCTCA    | 3120 |
|    |      |  |      |
| Db | 3061 | CGTCACATCAATGCAAAAGGTCCTGATTTTGTTCAGCAAAACACAGTGCAATGTTCTCA    | 3120 |
| Qy | 3121 | GAGTGACTTTCGAAATAAATTGGGCCCAAGAGCTTTAACTCGGTCTTAAAATATGCCCAA   | 3180 |
|    |      |  |      |
| Db | 3121 | GAGTGACTTTCGAAATAAATTGGGCCCAAGAGCTTTAACTCGGTCTTAAAATATGCCCAA   | 3180 |
| Qy | 3181 | ATTTTTACTTTGTTTTTCTTTTAATAGGCTGGGCCACATGTTGGAAATAAGCTAGTAATG   | 3240 |
|    |      |  |      |
| Db | 3181 | ATTTTTACTTTGTTTTTCTTTTAATAGGCTGGGCCACATGTTGGAAATAAGCTAGTAATG   | 3240 |
| Qy | 3241 | TTGTTTTCTGTCAATATTGAATGTGATGGTACAGTAAACCAAACCCAACAATGTGGCCA    | 3300 |
|    |      |  |      |
| Db | 3241 | TTGTTTTCTGTCAATATTGAATGTGATGGTACAGTAAACCAAACCCAACAATGTGGCCA    | 3300 |
| Qy | 3301 | GAAAGAAAGAGCAATAATAATTAATTCACACACCATATGGATTCTATTTATAAATCACCC   | 3360 |
|    |      |  |      |
| Db | 3301 | GAAAGAAAGAGCAATAATAATTAATTCACACACCATATGGATTCTATTTATAAATCACCC   | 3360 |
| Qy | 3361 | ACAAACTTGTTCTTTAATTTTCATCCCAATCACTTTTTTCAGAGGCCTGTTATCATAGAAGT | 3420 |
|    |      |  |      |
| Db | 3361 | ACAAACTTGTTCTTTAATTTTCATCCCAATCACTTTTTTCAGAGGCCTGTTATCATAGAAGT | 3420 |
| Qy | 3421 | CATTTTAGACTCTCAATTTTAAATTAATTTTGAATCACTAATATTTTCACAGTTTATTAA   | 3480 |
|    |      |  |      |
| Db | 3421 | CATTTTAGACTCTCAATTTTAAATTAATTTTGAATCACTAATATTTTCACAGTTTATTAA   | 3480 |
| Qy | 3481 | TATATTTAATTTCTATTTAAATTTTAGATTATTTTATTACCATGTACTGAATTTTACA     | 3540 |
|    |      |  |      |
| Db | 3481 | TATATTTAATTTCTATTTAAATTTTAGATTATTTTATTACCATGTACTGAATTTTACA     | 3540 |

|    |      |  |      |
|----|------|--|------|
| Qy | 3541 | TCCTGATACCCCTTTCCTTCTCCATGTCAGTATCATGTTCTCTAATTATCTTGCCAAATTT  | 3600 |
|    |      |  |      |
| Db | 3541 | TCCTGATACCCCTTTCCTTCTCCATGTCAGTATCATGTTCTCTAATTATCTTGCCAAATTT  | 3600 |
| Qy | 3601 | TGAAACTACACACAAAAAGCATACTTGCAATTATTTATAATAAAATTGCATTTCAGTGGCTT | 3660 |
|    |      |  |      |
| Db | 3601 | TGAAACTACACACAAAAAGCATACTTGCAATTATTTATAATAAAATTGCATTTCAGTGGCTT | 3660 |
| Qy | 3661 | TTTAAAAAAATGTTTGATTCAAAACTTTAACATACTGATAAGTAAGAAACAATTATAAT    | 3720 |
|    |      |  |      |
| Db | 3661 | TTTAAAAAAATGTTTGATTCAAAACTTTAACATACTGATAAGTAAGAAACAATTATAAT    | 3720 |
| Qy | 3721 | TTCTTTACATACTCAAAACCAAGATAGAAAAAGGTGCTATCGTTCAACTTCAAAACATGT   | 3780 |
|    |      |  |      |
| Db | 3721 | TTCTTTACATACTCAAAACCAAGATAGAAAAAGGTGCTATCGTTCAACTTCAAAACATGT   | 3780 |
| Qy | 3781 | TTCCTAGTATTAAGGACTTTAATATAGCAACAGACAAAAATTATTGTTAACATGGATGTTA  | 3840 |
|    |      |  |      |
| Db | 3781 | TTCCTAGTATTAAGGACTTTAATATAGCAACAGACAAAAATTATTGTTAACATGGATGTTA  | 3840 |
| Qy | 3841 | CAGCTCAAAAGATTTATAAAAGATTTTAACTATTTTCTCCCTTATTATCCACTGCTAAT    | 3900 |
|    |      |  |      |
| Db | 3841 | CAGCTCAAAAGATTTATAAAAGATTTTAACTATTTTCTCCCTTATTATCCACTGCTAAT    | 3900 |
| Qy | 3901 | GTGGATGTATGTTCAAACACCTTTTAGTATTGATAGCTTACATATGGCCAAAGGAATACA   | 3960 |
|    |      |  |      |
| Db | 3901 | GTGGATGTATGTTCAAACACCTTTTAGTATTGATAGCTTACATATGGCCAAAGGAATACA   | 3960 |
| Qy | 3961 | GTTTATAGCAAAACATGGGTATGCTGTAGCTAACTTTATAAAAGTGTAATATAACAATGT   | 4020 |
|    |      |  |      |
| Db | 3961 | GTTTATAGCAAAACATGGGTATGCTGTAGCTAACTTTATAAAAGTGTAATATAACAATGT   | 4020 |
| Qy | 4021 | AAAAAATTATATATCTGGGAGGATTTTTTGGTTGCCTAAAGTGGCTATAGTTACTGATTT   | 4080 |
|    |      |  |      |
| Db | 4021 | AAAAAATTATATATCTGGGAGGATTTTTTGGTTGCCTAAAGTGGCTATAGTTACTGATTT   | 4080 |
| Qy | 4081 | TTTATTATGTAAGCAAAACCAATAAAATTTAAGTTTTTTTAACTACCTTATTTTTTC      | 4140 |
|    |      |  |      |
| Db | 4081 | TTTATTATGTAAGCAAAACCAATAAAATTTAAGTTTTTTTAACTACCTTATTTTTTC      | 4140 |
| Qy | 4141 | ACTGTACAGACACTAATTCATTAAATACTAATTGATTGTTTAAAAGAAATATAAATGTGA   | 4200 |
|    |      |  |      |
| Db | 4141 | ACTGTACAGACACTAATTCATTAAATACTAATTGATTGTTTAAAAGAAATATAAATGTGA   | 4200 |
| Qy | 4201 | CAAGTGGACATTATTTATGTTAAATATACAATTATCAAGCAAGTATGAAGTTATTCAATT   | 4260 |
|    |      |  |      |
| Db | 4201 | CAAGTGGACATTATTTATGTTAAATATACAATTATCAAGCAAGTATGAAGTTATTCAATT   | 4260 |
| Qy | 4261 | AAAATGCCACATTTCTGGTCTCTGGG                                     | 4286 |
|    |      |  |      |
| Db | 4261 | AAAATGCCACATTTCTGGTCTCTGGG                                     | 4286 |

RESULT 6

US-10-372-683-48

; Sequence 48, Application US/10372683

; Publication No. US20040009171A1

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; GENERAL INFORMATION:
; APPLICANT: GERRITSEN, MARY E.
; APPLICANT: PEALE JR., FRANKLIN V.
; APPLICANT: WU, THOMAS D.
; TITLE OF INVENTION: METHODS FOR THE TREATMENT OF CARCINOMA
; FILE REFERENCE: P1928R1P1
; CURRENT APPLICATION NUMBER: US/10/372,683
; CURRENT FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: US 10/271,690
; PRIOR FILING DATE: 2002-10-16
; PRIOR APPLICATION NUMBER: US 60/344,534
; PRIOR FILING DATE: 2001-10-18
; NUMBER OF SEQ ID NOS: 49
; SEQ ID NO 48
; LENGTH: 4286
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-372-683-48
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Query Match          99.6%; Score 4284.4; DB 16; Length 4286;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4285; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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QY      1 GAGACATTCCGGTGGGGGACTCTGGCCAGCCCGAGCAACGTGGATCCTGAGAGCACTCCC 60
      |||||||
Db      1 GAGACATTCCGGTGGGGGACTCTGGCCAGCCCGAGCAACGTGGATCCTGAGAGCACTCCC 60

QY     61 AGGTAGGCATTTGCCCCGGTGGGACGCCTTGCCAGAGCAGTGTGTGGCAGGCCCCCGTGG 120
      |||||||
Db     61 AGGTAGGCATTTGCCCCGGTGGGACGCCTTGCCAGAGCAGTGTGTGGCAGGCCCCCGTGG 120

QY    121 AGGATCAACACAGTGGCTGAACACTGGGAAGGAACTGGTACTTGGAGTCTGGACATCTGA 180
      |||||||
Db    121 AGGATCAACACAGTGGCTGAACACTGGGAAGGAACTGGTACTTGGAGTCTGGACATCTGA 180

QY    181 AACTTGGCTCTGAAACTGCGGAGCGGCCACCGGACGCCTTCTGGAGCAGGTAGCAGCATG 240
      |||||||
Db    181 AACTTGGCTCTGAAACTGCGGAGCGGCCACCGGACGCCTTCTGGAGCAGGTAGCAGCATG 240

QY    241 CAGCCGCCTCCAAGTCTGTGCGGACGCGCCCTGGTTGCGCTGGTTCTTGCCTGCGGCCTG 300
      |||||||
Db    241 CAGCCGCCTCCAAGTCTGTGCGGACGCGCCCTGGTTGCGCTGGTTCTTGCCTGCGGCCTG 300

QY    301 TCGCGGATCTGGGGAGAGGAGAGAGAGGCTTCCCGCCTGACAGGGCCACTCCGCTTTTGCAA 360
      |||||||
Db    301 TCGCGGATCTGGGGAGAGGAGAGAGAGGCTTCCCGCCTGACAGGGCCACTCCGCTTTTGCAA 360

QY    361 ACCGCAGAGATAATGACGCCACCCACTAAGACCTTATGGCCCAAGGGTTCCAACGCCAGT 420
      |||||||
Db    361 ACCGCAGAGATAATGACGCCACCCACTAAGACCTTATGGCCCAAGGGTTCCAACGCCAGT 420

QY    421 CTGGCGCGGTCGTTGGCACCTGCGGAGGTGCCTAAAGGAGACAGGACGGCAGGATCTCCG 480
      |||||||
Db    421 CTGGCGCGGTCGTTGGCACCTGCGGAGGTGCCTAAAGGAGACAGGACGGCAGGATCTCCG 480

QY    481 CCACGCACCATCTCCCTCCCCCGTGCCAAGGACCCATCGAGATCAAGGAGACTTTCAA 540
      |||||||
```

Db 481 CCACGCACCATCTCCCCTCCCCCGTGCCAAGGACCCATCGAGATCAAGGAGACTTTCAA 540  
 Qy 541 TACATCAACACGGTTGTGTCTGCCTTGTGTTTCGTGCTGGGGATCATCGGGAACCTCCACA 600  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 541 TACATCAACACGGTTGTGTCTGCCTTGTGTTTCGTGCTGGGGATCATCGGGAACCTCCACA 600  
 Qy 601 CTTCTGAGAATTATCTACAAGAACAAGTGCATGCGAAACGGTCCCAATATCTTGATCGCC 660  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 601 CTTCTGAGAATTATCTACAAGAACAAGTGCATGCGAAACGGTCCCAATATCTTGATCGCC 660  
 Qy 661 AGCTTGGCTCTGGGAGACCTGCTGCACATCGTCATTGACATCCCTATCAATGTCTACAAG 720  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 661 AGCTTGGCTCTGGGAGACCTGCTGCACATCGTCATTGACATCCCTATCAATGTCTACAAG 720  
 Qy 721 CTGCTGGCAGAGGACTGGCCATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTCATACAG 780  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 721 CTGCTGGCAGAGGACTGGCCATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTCATACAG 780  
 Qy 781 AAAGCCTCCGTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATATCGA 840  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 781 AAAGCCTCCGTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATATCGA 840  
 Qy 841 GCTGTTGCTTCTTGGAGTAGAATTAAAGGAATTGGGGTTCCAAAATGGACAGCAGTAGAA 900  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 841 GCTGTTGCTTCTTGGAGTAGAATTAAAGGAATTGGGGTTCCAAAATGGACAGCAGTAGAA 900  
 Qy 901 ATTGTTTTGATTTGGGTGGTCTCTGTGGTCTGGCTGTCCCTGAAGCCATAGGTTTTGAT 960  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 901 ATTGTTTTGATTTGGGTGGTCTCTGTGGTCTGGCTGTCCCTGAAGCCATAGGTTTTGAT 960  
 Qy 961 ATAATTACGATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCCTTCAG 1020  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 961 ATAATTACGATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCCTTCAG 1020  
 Qy 1021 AAGACAGCTTTCATGCAGTTTTTACAAGACAGCAAAAGATTGGTGGCTGTTTCAGTTTCTAT 1080  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 1021 AAGACAGCTTTCATGCAGTTTTTACAAGACAGCAAAAGATTGGTGGCTGTTTCAGTTTCTAT 1080  
 Qy 1081 TTCTGCTTGCCATTGGCCATCACTGCATTTTTTTTATACACTAATGACCTGTGAAATGTTG 1140  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 1081 TTCTGCTTGCCATTGGCCATCACTGCATTTTTTTTATACACTAATGACCTGTGAAATGTTG 1140  
 Qy 1141 AGAAAGAAAAGTGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAAGTG 1200  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 1141 AGAAAGAAAAGTGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAAGTG 1200  
 Qy 1201 GCCAAAACCGTCTTTTGCCTGGTCCTTGCTTTGCCCTCTGCTGGCTTCCCCTTCACCTC 1260  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 1201 GCCAAAACCGTCTTTTGCCTGGTCCTTGCTTTGCCCTCTGCTGGCTTCCCCTTCACCTC 1260  
 Qy 1261 AGCAGGATTCTGAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGAACTTTTG 1320  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 1261 AGCAGGATTCTGAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGAACTTTTG 1320  
 Qy 1321 AGCTTTCTGTTGGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCCTGCATT 1380  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 1321 AGCTTTCTGTTGGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCCTGCATT 1380

|    |      |  |      |
|----|------|--|------|
| Qy | 1381 | AACCCAATTGCTCTGTATTTGGTGAGCAAAAGATTCAAAAAGCTGCTTTAAGTCATGCTTA  | 1440 |
|    |      |  |      |
| Db | 1381 | AACCCAATTGCTCTGTATTTGGTGAGCAAAAGATTCAAAAAGCTGCTTTAAGTCATGCTTA  | 1440 |
| Qy | 1441 | TGCTGCTGGTGCCAGTCATTTGAAGAAAACAGTCCTTGGAGGAAAAGCAGTCGTGCTTA    | 1500 |
|    |      |  |      |
| Db | 1441 | TGCTGCTGGTGCCAGTCATTTGAAGAAAACAGTCCTTGGAGGAAAAGCAGTCGTGCTTA    | 1500 |
| Qy | 1501 | AAGTTCAAAGCTAATGATCACGGATATGACAACTTCCGTTCCAGTAATAAATACAGCTCA   | 1560 |
|    |      |  |      |
| Db | 1501 | AAGTTCAAAGCTAATGATCACGGATATGACAACTTCCGTTCCAGTAATAAATACAGCTCA   | 1560 |
| Qy | 1561 | TCTTGAAAGAAGAACTATTCAGTGTATTTCAATTTCTTTATATTGGACCGAAGTCATTAA   | 1620 |
|    |      |  |      |
| Db | 1561 | TCTTGAAAGAAGAACTATTCAGTGTATTTCAATTTCTTTATATTGGACCGAAGTCATTAA   | 1620 |
| Qy | 1621 | AACAAAATGAAACATTTGCCAAAACAAAACAAAAAACTATGTATTTGCACAGCACACTAT   | 1680 |
|    |      |  |      |
| Db | 1621 | AACAAAATGAAACATTTGCCAAAACAAAACAAAAAACTATGTATTTGCACAGCACACTAT   | 1680 |
| Qy | 1681 | TAAAATATTAAGTGTAAATTATTTAACACTCACAGCTACATATGACATTTTATGAGCTGT   | 1740 |
|    |      |  |      |
| Db | 1681 | TAAAATATTAAGTGTAAATTATTTAACACTCACAGCTACATATGACATTTTATGAGCTGT   | 1740 |
| Qy | 1741 | TTACGGCATGGAAAGAAAATCAGTGGGAATTAAGAAAGCCTCGTCGTGAAAGCACTTAAT   | 1800 |
|    |      |  |      |
| Db | 1741 | TTACGGCATGGAAAGAAAATCAGTGGGAATTAAGAAAGCCTCGTCGTGAAAGCACTTAAT   | 1800 |
| Qy | 1801 | TTTTTACAGTTAGCACTTCAACATAGCTCTTAACAACCTCCAGGATATTCACACAACACT   | 1860 |
|    |      |  |      |
| Db | 1801 | TTTTTACAGTTAGCACTTCAACATAGCTCTTAACAACCTCCAGGATATTCACACAACACT   | 1860 |
| Qy | 1861 | TAGGCTTAAAATGAGCTCACTCAGAATTTCTATTCTTTCTAAAAAGAGATTTATTTTTTA   | 1920 |
|    |      |  |      |
| Db | 1861 | TAGGCTTAAAATGAGCTCACTCAGAATTTCTATTCTTTCTAAAAAGAGATTTATTTTTTA   | 1920 |
| Qy | 1921 | AATCAATGGGACTCTGATATAAAGGAAGAATAAGTCACTGTAAAACAGAACTTTTAAATG   | 1980 |
|    |      |  |      |
| Db | 1921 | AATCAATGGGACTCTGATATAAAGGAAGAATAAGTCACTGTAAAACAGAACTTTTAAATG   | 1980 |
| Qy | 1981 | AAGCTTAAATTACTCAATTTAAATTTTAAATCCTTTAAACAACCTTTTCAATTAATAT     | 2040 |
|    |      |  |      |
| Db | 1981 | AAGCTTAAATTACTCAATTTAAATTTTAAATCCTTTAAACAACCTTTTCAATTAATAT     | 2040 |
| Qy | 2041 | TATCACACTATTATCAGATTGTAATTAGATGCAAATGAGAGAGCAGTTTAGTTGTTGCAT   | 2100 |
|    |      |  |      |
| Db | 2041 | TATCACACTATTATCAGATTGTAATTAGATGCAAATGAGAGAGCAGTTTAGTTGTTGCAT   | 2100 |
| Qy | 2101 | TTTTCGGACACTGGAAACATTTAAATGATCAGGAGGGAGTAACAGAAAGAGCAAGGCTGT   | 2160 |
|    |      |  |      |
| Db | 2101 | TTTTCGGACACTGGAAACATTTAAATGATCAGGAGGGAGTAACAGAAAGAGCAAGGCTGT   | 2160 |
| Qy | 2161 | TTTTGAAAATCATTACACTTTTCACTAGAAAGCCCAAACCTCAGCATTCTGCAATATGTAAC | 2220 |
|    |      |  |      |
| Db | 2161 | TTTTGAAAATCATTACACTTTTCACTAGAAAGCCCAAACCTCAGCATTCTGCAATATGTAAC | 2220 |

Qy 2221 CAACATGTCACAAACAAGCAGCATGTAACAGACTGGCACATGTGCCAGCTGAATTTAAAA 2280  
 |||  
 Db 2221 CAACATGTCACAAACAAGCAGCATGTAACAGACTGGCACATGTGCCAGCTGAATTTAAAA 2280

Qy 2281 TATAATACTTTTAAAAAGAAAATTATTACATCCTTTACATTAGTTAAGATCAAACCTCA 2340  
 |||  
 Db 2281 TATAATACTTTTAAAAAGAAAATTATTACATCCTTTACATTAGTTAAGATCAAACCTCA 2340

Qy 2341 CAAAGAGAAATAGAATGTTTGAAAGGCTATCCCAAAGACTTTTTTGAATCTGTCATTCA 2400  
 |||  
 Db 2341 CAAAGAGAAATAGAATGTTTGAAAGGCTATCCCAAAGACTTTTTTGAATCTGTCATTCA 2400

Qy 2401 CATACCCTGTGAAGACAATACTATCTACAATTTTTTCAGGATTATTAATCTTCTTTTT 2460  
 |||  
 Db 2401 CATACCCTGTGAAGACAATACTATCTACAATTTTTTCAGGATTATTAATCTTCTTTTT 2460

Qy 2461 TCACTATCGTAGCTTAAACTCTGTTTGGTTTTGTCATCTGTAAATACTTACCTACATACA 2520  
 |||  
 Db 2461 TCACTATCGTAGCTTAAACTCTGTTTGGTTTTGTCATCTGTAAATACTTACCTACATACA 2520

Qy 2521 CTGCATGTAGATGATTAAATGAGGGCAGGCCCTGTGCTCATAGCTTTACGATGGAGAGAT 2580  
 |||  
 Db 2521 CTGCATGTAGATGATTAAATGAGGGCAGGCCCTGTGCTCATAGCTTTACGATGGAGAGAT 2580

Qy 2581 GCCAGTGACCTCATAATAAAGACTGTGAAGTGCCTGGTGCAGTGTCCACATGACAAAGGG 2640  
 |||  
 Db 2581 GCCAGTGACCTCATAATAAAGACTGTGAAGTGCCTGGTGCAGTGTCCACATGACAAAGGG 2640

Qy 2641 GCAGGTAGCACCCTCTCTCACCATGCTGTGGTTAAATGGTTTCTAGCATATGTATAAT 2700  
 |||  
 Db 2641 GCAGGTAGCACCCTCTCTCACCATGCTGTGGTTAAATGGTTTCTAGCATATGTATAAT 2700

Qy 2701 GCTATAGTTAAAATACTATTTTTCAAATCATAACAGATTAGTACATTTAACAGCTACCTG 2760  
 |||  
 Db 2701 GCTATAGTTAAAATACTATTTTTCAAATCATAACAGATTAGTACATTTAACAGCTACCTG 2760

Qy 2761 TAAAGCTTATTACTAATTTTTGTATTATTTTTGTAAATAGCCAATAGAAAAGTTTGCTTG 2820  
 |||  
 Db 2761 TAAAGCTTATTACTAATTTTTGTATTATTTTTGTAAATAGCCAATAGAAAAGTTTGCTTG 2820

Qy 2821 ACATGGTGCTTTTCTTTCATCTAGAGGCAAAACTGCTTTTTGAGACCGTAAGAACCTCTT 2880  
 |||  
 Db 2821 ACATGGTGCTTTTCTTTCATCTAGAGGCAAAACTGCTTTTTGAGACCGTAAGAACCTCTT 2880

Qy 2881 AGCTTTGTGCGTTCCTGCCTAATTTTTATATCTTCTAAGCAAAGTGCCTTAGGATAGCTT 2940  
 |||  
 Db 2881 AGCTTTGTGCGTTCCTGCCTAATTTTTATATCTTCTAAGCAAAGTGCCTTAGGATAGCTT 2940

Qy 2941 GGGATGAGATGTGTGTGAAAGTATGTACAAGAGAAAACGGAAGAGAGAGGAAATGAGGTG 3000  
 |||  
 Db 2941 GGGATGAGATGTGTGTGAAAGTATGTACAAGAGAAAACGGAAGAGAGAGGAAATGAGGTG 3000

Qy 3001 GGGTTGGAGGAAACCCATGGGGACAGATTCCCATTCTTAGCCTAACGTCGTCATTGCCT 3060  
 |||  
 Db 3001 GGGTTGGAGGAAACCCATGGGGACAGATTCCCATTCTTAGCCTAACGTCGTCATTGCCT 3060

Qy 3061 CGTCACATCAATGCAAAGGTCCTGATTTTGTTCAGCAAACACAGTGCAATGTTCTCA 3120

|    |      |  |  |      |
|----|------|--|--|------|
| Db | 3061 |  | CGTCACATCAATGCAAAAGGTCCTGATTTTGTTCAGCAAAACACAGTGCAATGTTCTCA  | 3120 |
| Qy | 3121 |  | GAGTGACTTTCGAAATAAATTGGGCCCCAAGAGCTTTAACTCGGTCTTAAATATGCCCAA | 3180 |
| Db | 3121 |  | GAGTGACTTTCGAAATAAATTGGGCCCCAAGAGCTTTAACTCGGTCTTAAATATGCCCAA | 3180 |
| Qy | 3181 |  | ATTTTACTTTGTTTTCTTTAATAGGCTGGGCCACATGTTGGAAATAAGCTAGTAATG    | 3240 |
| Db | 3181 |  | ATTTTACTTTGTTTTCTTTAATAGGCTGGGCCACATGTTGGAAATAAGCTAGTAATG    | 3240 |
| Qy | 3241 |  | TTGTTTTCTGTCAATATTGAATGTGATGGTACAGTAAACCAAAACCAACAATGTGGCCA  | 3300 |
| Db | 3241 |  | TTGTTTTCTGTCAATATTGAATGTGATGGTACAGTAAACCAAAACCAACAATGTGGCCA  | 3300 |
| Qy | 3301 |  | GAAAGAAAGAGCAATAATAATTAATTCACACACCATATGGATTCTATTTATAAATCACCC | 3360 |
| Db | 3301 |  | GAAAGAAAGAGCAATAATAATTAATTCACACACCATATGGATTCTATTTATAAATCACCC | 3360 |
| Qy | 3361 |  | ACAACTTGTTCTTTAATTTTCATCCCAATCACTTTTTCAGAGGCCTGTTATCATAGAAGT | 3420 |
| Db | 3361 |  | ACAACTTGTTCTTTAATTTTCATCCCAATCACTTTTTCAGAGGCCTGTTATCATAGAAGT | 3420 |
| Qy | 3421 |  | CATTTTAGACTCTCAATTTTAAATTAATTTTGAATCACTAATATTTTCACAGTTTATTAA | 3480 |
| Db | 3421 |  | CATTTTAGACTCTCAATTTTAAATTAATTTTGAATCACTAATATTTTCACAGTTTATTAA | 3480 |
| Qy | 3481 |  | TATATTTAATTTCTATTTAAATTTTAGATTATTTTTATTACCATGTACTGAATTTTACA  | 3540 |
| Db | 3481 |  | TATATTTAATTTCTATTTAAATTTTAGATTATTTTTATTACCATGTACTGAATTTTACA  | 3540 |
| Qy | 3541 |  | TCCTGATACCCTTTCCTTCTCCATGTCAGTATCATGTTCTCTAATTATCTTGCCAAATTT | 3600 |
| Db | 3541 |  | TCCTGATACCCTTTCCTTCTCCATGTCAGTATCATGTTCTCTAATTATCTTGCCAAATTT | 3600 |
| Qy | 3601 |  | TGAACTACACACAAAAAGCATACTTGCATTATTTATAATAAAATTGCATTCACTGGCTT  | 3660 |
| Db | 3601 |  | TGAACTACACACAAAAAGCATACTTGCATTATTTATAATAAAATTGCATTCACTGGCTT  | 3660 |
| Qy | 3661 |  | TTTAAAAAAATGTTTGATTCAAACTTTAACATACTGATAAGTAAGAAACAATTATAAT   | 3720 |
| Db | 3661 |  | TTTAAAAAAATGTTTGATTCAAACTTTAACATACTGATAAGTAAGAAACAATTATAAT   | 3720 |
| Qy | 3721 |  | TTCTTTACATACTCAAAACCAAGATAGAAAAAGGTGCTATCGTTCAACTTCAAAACATGT | 3780 |
| Db | 3721 |  | TTCTTTACATACTCAAAACCAAGATAGAAAAAGGTGCTATCGTTCAACTTCAAAACATGT | 3780 |
| Qy | 3781 |  | TTCTTAGTATTAAGGACTTTAATATAGCAACAGACAAAATTATTGTTAACATGGATGTTA | 3840 |
| Db | 3781 |  | TTCTTAGTATTAAGGACTTTAATATAGCAACAGACAAAATTATTGTTAACATGGATGTTA | 3840 |
| Qy | 3841 |  | CAGCTCAAAAGATTTATAAAAGATTTTAACCTATTTTCTCCCTTATTATCCACTGCTAAT | 3900 |
| Db | 3841 |  | CAGCTCAAAAGATTTATAAAAGATTTTAACCTATTTTCTCCCTTATTATCCACTGCTAAT | 3900 |
| Qy | 3901 |  | GTGGATGTATGTTCAAACACCTTTTAGTATTGATAGCTTACATATGGCCAAAGGAATACA | 3960 |



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Db      3901 GTGGATGTATGTTCAAACACCTTTTAGTATTGATAGCTTACATATGGCCAAAGGAATACA 3960
Qy      3961 GTTTATAGCAAAACATGGGTATGCTGTAGCTAACTTTATAAAAAGTGAATATAACAATGT 4020
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      3961 GTTTATAGCAAAACATGGGTATGCTGTAGCTAACTTTATAAAAAGTGAATATAACAATGT 4020
Qy      4021 AAAAAATTATATATCTGGGAGGATTTTTTGGTTGCCTAAAGTGGCTATAGTTACTGATTT 4080
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4021 AAAAAATTATATATCTGGGAGGATTTTTTGGTTGCCTAAAGTGGCTATAGTTACTGATTT 4080
Qy      4081 TTTATTATGTAAGCAAAACCAATAAAAAATTTAAGTTTTTTTAACTACCTTATTTTTC 4140
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4081 TTTATTATGTAAGCAAAACCAATAAAAAATTTAAGTTTTTTTAACTACCTTATTTTTC 4140
Qy      4141 ACTGTACAGACACTAATTCATTAAATACTAATTGATTGTTTAAAGAAATATAAATGTGA 4200
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4141 ACTGTACAGACACTAATTCATTAAATACTAATTGATTGTTTAAAGAAATATAAATGTGA 4200
Qy      4201 CAAGTGGACATTATTTATGTTAAATATACAATTATCAAGCAAGTATGAAGTTATTCAATT 4260
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      4201 CAAGTGGACATTATTTATGTTAAATATACAATTATCAAGCAAGTATGAAGTTATTCAATT 4260
Qy      4261 AAAATGCCACATTTCTGGTCTCTGGG 4286
        ||||||||||||||||||||||
Db      4261 AAAATGCCACATTTCTGGTCTCTGGG 4286

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RESULT 7

US-10-116-802-116

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; Sequence 116, Application US/10116802
; Publication No. US20030065157A1
; GENERAL INFORMATION:
; APPLICANT: Amy Lasek
; TITLE OF INVENTION: GENES EXPRESSED IN LUNG CANCER
; FILE REFERENCE: PA-0045 US
; CURRENT APPLICATION NUMBER: US/10/116,802
; CURRENT FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: 60/281,593
; PRIOR FILING DATE: 2001-04-04
; NUMBER OF SEQ ID NOS: 519
; SOFTWARE: PERL Program
; SEQ ID NO 116
; LENGTH: 4305
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No: 1094000.4
; NAME/KEY: unsure
; LOCATION: 4301-4302
; OTHER INFORMATION: a, t, c, g, or other
US-10-116-802-116

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Query Match          97.7%; Score 4202.4; DB 13; Length 4305;
Best Local Similarity 99.4%; Pred. No. 0;
Matches 4280; Conservative 0; Mismatches 18; Indels 8; Gaps 6;

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Qy 1 GAGACATTCCGGTGGGGGACTCTGGCCAGCCCGAGCAACGTGGATCCTGAGAGCACTCCC 60  
 |||  
 Db 1 GAGACATTCCGGTGGGGGACTCTGGCCAGCCCGAGCAACGTGGATCCTGAGAGCACTCCC 60

Qy 61 AGGTAGGCATTTGCCCCGGTGGGACGCCTTGCCAGAGCAGTGTGTGGCAGGCCCCCGTGG 120  
 |||  
 Db 61 AGGTAGGCATTTGCCCCGGTGGGACGCCTTGCCAGAGCAGTGTGTGGCAGGCCCCCGTGG 120

Qy 121 AGGATCAACACAGTGGCTGAACACTGGGAAGGAACTGGTACTTGGAGTCTGGACATCTGA 180  
 |||  
 Db 121 AGGATCAACACAGTGGCTGAACACTGGGAAGGAACTGGTACTTGGAGTCTGGACATCTGA 180

Qy 181 AACTTGGCTCTGAAACTGCGGAGCGGCCACCGACGCCTTCTGGAGCAGGTAGCAGCATG 240  
 |||  
 Db 181 AACTTGGCTCTGAAACTGCGGAGCGGCCACCGACGCCTTCTGGAGCAGGTAGCAGCATG 240

Qy 241 CAGCCGCCTCCAAGTCTGTGCGGACGCGCCCTGGTTGCGCTGGTTCTTGCTGCGGCCTG 300  
 |||  
 Db 241 CAGCCGCCTCCAAGTCTGTGCGGACGCGCCCTGGTTGCGCTGGTTCTTGCTGCGGCCTG 300

Qy 301 TCGCGGATCTGGGGAGAGGAGAGAGGCTTCCCGCCTGACAGGGCCACTCCGCTTTTGCAA 360  
 |||  
 Db 301 TCGCGGATCTGGGGAGAGGAGAGAGGCTTCCCGCCTGACAGGGCCACTCCGCTTTTGCAA 360

Qy 361 ACCGCAGAGATAATGACGCCACCCACTAAGACCTTATGGCCCAAGGGTTCCAACGCCAGT 420  
 |||  
 Db 361 ACCGCAGAGATAATGACGCCACCCACTAAGACCTTATGGCCCAAGGGTTCCAACGCCAGT 420

Qy 421 CTGGCGCGGTTCGTTGGCACCTGCGGAGGTGCCTAAAGGAGACAGGACGGCAGGATCTCCG 480  
 |||  
 Db 421 CTGGCGCGGTTCGTTGGCACCTGCGGAGGTGCCTAAAGGAGACAGGACGGCAGGATCTCCG 480

Qy 481 CCACGCACCATCTCCCCTCCCCCGTGCCAAGGACCCATCGAGATCAAGGAGACTTTCAA 540  
 |||  
 Db 481 CCACGCACCATCTCCCCTCCCCCGTGCCAAGGACCCATCGAGATCAAGGAGACTTTCAA 540

Qy 541 TACATCAACACGGTTGTGTCCTGCCTTGTGTTTCGTGCTGGGGATCATCGGGAACCTCACA 600  
 |||  
 Db 541 TACATCAACACGGTTGTGTCCTGCCTTGTGTTTCGTGCTGGGGATCATCGGGAACCTCACA 600

Qy 601 CTTCTGAGAATTATCTACAAGAACAAGTGCATGCGAAACGGTCCCAATATCTTGATCGCC 660  
 |||  
 Db 601 CTTCTGAGAATTATCTACAAGAACAAGTGCATGCGAAACGGTCCCAATATCTTGATCGCC 660

Qy 661 AGCTTGGCTCTGGGAGACCTGCTGCACATCGTCATTGACATCCCTATCAATGTCTACAAG 720  
 |||  
 Db 661 AGCTTGGCTCTGGGAGACCTGCTGCACATCGTCATTGACATCCCTATCAATGTCTACAAG 720

Qy 721 CTGCTGGCAGAGGACTGGCCATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTTCATACAG 780  
 |||  
 Db 721 CTGCTGGCAGAGGACTGGCCATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTTCATACAG 780

Qy 781 AAAGCCTCCGTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATATCGA 840  
 |||  
 Db 781 AAAGCCTCCGTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATATCGA 840

Qy 841 GCTGTTGCTTCTTGGAGTAGAATTAAAGGAATTGGGGTTCCAAAATGGACAGCAGTAGAA 900

|    |      |  |      |
|----|------|--|------|
| Db | 841  | <br>GCTGTTGCTTCTTGGAGTAGAATTAAAGGAATTGGGGTCCAAAATGGACAGCAGTAGAA    | 900  |
| Qy | 901  | ATTGTTTTGATTTGGGTGGTCTCTGTGGTTCTGGCTGTCCCTGAAGCCATAGGTTTTGAT       | 960  |
| Db | 901  | <br>ATTGTTTTGATTTGGGTGGTCTCTGTGGTTCTGGCTGTCCCTGAAGCCATAGGTTTTGAT   | 960  |
| Qy | 961  | ATAATTACGATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTTCAG       | 1020 |
| Db | 961  | <br>ATAATTACGATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTTCAG   | 1020 |
| Qy | 1021 | AAGACAGCTTTTCATGCAGTTTTACAAGACAGCAAAAGATTGGTGGCTGTTTCAGTTTCTAT     | 1080 |
| Db | 1021 | <br>AAGACAGCTTTTCATGCAGTTTTACAAGACAGCAAAAGATTGGTGGCTGTTTCAGTTTCTAT | 1080 |
| Qy | 1081 | TTCTGCTTGCCATTGGCCATCACTGCATTTTTTTATACACTAATGACCTGTGAAATGTTG       | 1140 |
| Db | 1081 | <br>TTCTGCTTGCCATTGGCCATCACTGCATTTTTTTATACACTAATGACCTGTGAAATGTTG   | 1140 |
| Qy | 1141 | AGAAAGAAAAGTGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAAGTG       | 1200 |
| Db | 1141 | <br>AGAAAGAAAAGTGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAAGTG   | 1200 |
| Qy | 1201 | GCCAAAACCGTCTTTTGCCTGGTCTTGTCTTTGCCCTCTGCTGGCTTCCCCTTCACCTC        | 1260 |
| Db | 1201 | <br>GCCAAAACCGTCTTTTGCCTGGTCTTGTCTTTGCCCTCTGCTGGCTTCCCCTTCACCTC    | 1260 |
| Qy | 1261 | AGCAGGATTCTGAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGAACTTTTG       | 1320 |
| Db | 1261 | <br>AGCAGGATTCTGAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGAACTTTTG   | 1320 |
| Qy | 1321 | AGCTTTCTGTTGGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCCTGCATT       | 1380 |
| Db | 1321 | <br>AGCTTTCTGTTGGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCCTGCATT   | 1380 |
| Qy | 1381 | AACCCAATTGCTCTGTATTTGGTGAGCAAAAGATTCAAAAAGTCTTTAAGTCATGCTTA        | 1440 |
| Db | 1381 | <br>AACCCAATTGCTCTGTATTTGGTGAGCAAAAGATTCAAAAAGTCTTTAAGTCATGCTTA    | 1440 |
| Qy | 1441 | TGCTGCTGGTGCCAGTCATTTGAAGAAAAACAGTCCTTGGAGGAAAAGCAGTCGTGCTTA       | 1500 |
| Db | 1441 | <br>TGCTGCTGGTGCCAGTCATTTGAAGAAAAACAGTCCTTGGAGGAAAAGCAGTCGTGCTTA   | 1500 |
| Qy | 1501 | AAGTTCAAAGCTAATGATCACGGATATGACAACTCCGTTCCAGTAATAAATACAGCTCA        | 1560 |
| Db | 1501 | <br>AAGTTCAAAGCTAATGATCACGGATATGACAACTCCGTTCCAGTAATAAATACAGCTCA    | 1560 |
| Qy | 1561 | TCTTGAAAGAAGAACTATTCAGTATTTTCTTTATATTGGACCGAAGTCATTAA              | 1620 |
| Db | 1561 | <br>TCTTGAAAGAAGAACTATTCAGTATTTTCTTTATATTGGACCGAAGTCATTAA          | 1620 |
| Qy | 1621 | AACAAAATGAAACATTTGCCAAAACAAAACAAAAAACTATGTATTTGCACAGCACACTAT       | 1680 |
| Db | 1621 | <br>AACAAAATGAAACATTTGCCAAAACAAAACAAAAAACTATGTATTTGCACAGCACACTAT   | 1680 |
| Qy | 1681 | TAAAATATTAAGTGTAATTATTTTAACACTCACAGCTACATATGACATTTTATGAGCTGT       | 1740 |
|    |      |  |      |

|    |      |   |      |
|----|------|---|------|
| Db | 1681 | TAAAATATTAAGTGTAATTATTTTAACTCACAGCTACATATGACATTTTATGAGCTGT    | 1740 |
| Qy | 1741 | TTACGGCATGGAAAGAAAATCAGTGGGAATTAAGAAAGCCTCGTCGTGAAAGCACTTAAT  | 1800 |
|    |      |   |      |
| Db | 1741 | TTACGGCATGGAAAGAAAATCAGTGGGAATTAAGAAAGCCTCGTCGTGAAAGCACTTAAT  | 1800 |
| Qy | 1801 | TTTTTACAGTTAGCACTTCAACATAGCTCTTAACAACCTCCAGGATATTCACACAACACT  | 1860 |
|    |      |   |      |
| Db | 1801 | TTTTTACAGTTAGCACTTCAACATAGCTCTTAACAACCTCCAGGATATTCACACAACACT  | 1860 |
| Qy | 1861 | TAGGCTTAAAAATGAGCTCACTCAGAAATTTCTATTCTTTCTAAAAAGAGATTTATTTT   | 1920 |
|    |      |   |      |
| Db | 1861 | TAGGCTTAAAAATGAGCTCACTCAGAAATTTCTATTCTTTCTAAAAAGAGATTTATTTT   | 1920 |
| Qy | 1921 | AATCAATGGGACTCTGATATAAGGAAGAATAAGTCACTGTAAACAGAACTTTTAAATG    | 1980 |
|    |      |   |      |
| Db | 1921 | AATCAATGGGACTCTGATATAAGGAAGAATAAGTCACTGTAAACAGAACTTTTAAATG    | 1980 |
| Qy | 1981 | AAGCTTAAATTACTCAATTTAAATTTTAAATCCTTTAAACAACTTTTCAATTAATAT     | 2040 |
|    |      |   |      |
| Db | 1981 | AAGCTTAAATTACTCAATTTAAATTTTAAATCCTTTAAACAACTTTTCAATTAATAT     | 2040 |
| Qy | 2041 | TATCACACTATTATCAGATTGTAATTAGATGCAAATGAGAGAGCAGTTTAGTTGTTGCAT  | 2100 |
|    |      |   |      |
| Db | 2041 | TATCACACTATTATCAGATTGTAATTAGATGCAAATGAGAGAGCAGTTTAGTTGTTGCAT  | 2100 |
| Qy | 2101 | TTTTTCGGACACTGGAAACATTTAAATGATCAGGAGGGAGTAACAGAAAGAGCAAGGCTGT | 2160 |
|    |      |   |      |
| Db | 2101 | TTTTTCGGACACTGGAAACATTTAAATGATCAGGAGGGAGTAACAGAAAGAGCAAGGCTGT | 2160 |
| Qy | 2161 | TTTTGAAAATCATTACACTTTCAC--TAGAAGCCCAAACCTCAGCATT-CTGCAATATGT  | 2217 |
|    |      |   |      |
| Db | 2161 | TTTTGAAAATCATTACACTTTCACCTAGAAGCCCAAACCTCAGCATTCCTGCAATATGT   | 2220 |
| Qy | 2218 | AA-CCAACATGTCACAAACAAGCAG--CATGTAACAGACTGGCACATGTG-CCAGCTGAA  | 2273 |
|    |      |   |      |
| Db | 2221 | AACCCAACATGTCACAAACAAGCCAGCCATGTAACAGACTGGCACATGTGCCAGCTGAA   | 2280 |
| Qy | 2274 | TTTAAATATAATACTTTTAAAAAGAAAATTATTACATCCTTTACATTAGTTAAGATCA    | 2333 |
|    |      |   |      |
| Db | 2281 | TTTAAATATAATACTTTTAAAAAGAAAATTATTACATCCTTTACATTAGTTAAGATCA    | 2340 |
| Qy | 2334 | AACCTCACAAAGAGAAATAGAATGTTTGAAAGGCTATCCCAAAGACTTTTTTGAATCTG   | 2393 |
|    |      |   |      |
| Db | 2341 | AACCTCACAAAGAGAAATAGAATGTTTGAAAGGCTATCCCAAAGACTTTTTTGAATCTG   | 2400 |
| Qy | 2394 | TCATTACATACCCTGTGAAGACAATACTATCTACAATTTTTTTCAGGATTATTAAATCT   | 2453 |
|    |      |   |      |
| Db | 2401 | TCATTACATACCCTGTGAAGACAATACTATCTACAATTTTTTTCAGGATTATTAAATCT   | 2460 |
| Qy | 2454 | TCTTTTTTCACTATCGTAGCTTAAACTCTGTTTGGTTTTGTCATCTGTAAATACTTACCT  | 2513 |
|    |      |   |      |
| Db | 2461 | TCTTCTTTCATCTATCGTAGCTTAAACTCTGTTTGGTTTTGTCATCTGTAAATACTTACCT | 2520 |
| Qy | 2514 | ACATACACTGCATGTAGATGATTAAATGAGGGCAGGCCCTGTGCTCATAGCTTTACGATG  | 2573 |
|    |      |   |      |
| Db | 2521 | ACATACACTGCATGTAGATGATTAAATGAGGGCAGGCCCTGTGCTCATAGCTTTACGATG  | 2580 |

|    |      |   |      |
|----|------|---|------|
| Qy | 2574 | GAGAGATGCCAGTGACCTCATAATAAAGACTGTGAACTGCCTGGTGCAGTGTCCACATGA  | 2633 |
|    |      |   |      |
| Db | 2581 | GAGAGATGCCAGTGACCTCATAATAAAGACTGTGAACTGCCTGGTGCAGTGTCCACATGA  | 2640 |
| Qy | 2634 | CAAAGGGGCAGGTAGCACCCCTCTCTCACCCATGCTGTGGTTAAAATGGTTTCTAGCATAT | 2693 |
|    |      |   |      |
| Db | 2641 | CAAAGGGGCAGGTAGCACCCCTCTCTCACCCATGCTGTGGTTAAAATGGTTTCTAGCATAT | 2700 |
| Qy | 2694 | GTATAATGCTATAGTTAAAATACTATTTTTCAAATCATACAGATTAGTACATTTAACAG   | 2753 |
|    |      |   |      |
| Db | 2701 | GTATAATGCTATAGTTAAAATACTATTTTTCAAATCATACAGATTAGTACATTTAACAG   | 2760 |
| Qy | 2754 | CTACCTGTAAAGCTTATTACTAATTTTTGTATTATTTTTGTAAATAGCCAATAGAAAAGT  | 2813 |
|    |      |   |      |
| Db | 2761 | CTACCTGTAAAGCTTATTACTAATTTTTGTATTATTTTTGTAAATAGCCAATAGAAAAGT  | 2820 |
| Qy | 2814 | TTGCTTGACATGGTGCTTTTCTTTCATCTAGAGGCAAAACGCTTTTGTAGACCGTAAGA   | 2873 |
|    |      |   |      |
| Db | 2821 | TTGCTTGACATGGTGCTTTTCTTTCATCTAGAGGCAAAACGCTTTTGTAGACCGTAAGA   | 2880 |
| Qy | 2874 | ACCTCTTAGCTTTGTGCGTTCCTGCCTAATTTTTATATCTTCTAAGCAAAGTGCCTTAGG  | 2933 |
|    |      |   |      |
| Db | 2881 | ACCTCTTAGCTTTGTGCGTTCCTGCCTAATTTTTATATCTTCTAAGCAAAGTGCCTTAGG  | 2940 |
| Qy | 2934 | ATAGCTTGGGATGAGATGTGTGTGAAAGTATGTACAAGAGAAAACGGAAGAGAGAGGAAA  | 2993 |
|    |      |   |      |
| Db | 2941 | ATAGCTTGGGATGAGATGTGTGTGAAAGTATGTACAAGAGAAAACGGAAGAGAGAGGAAA  | 3000 |
| Qy | 2994 | TGAGGTGGGGTTGGAGGAAACCCATGGGGACAGATCCCATTCTTAGCCTAACGTTTCGTC  | 3053 |
|    |      |   |      |
| Db | 3001 | TGAGGTGGGGTTGGAGGAAACCCATGGGGACAGATCCCATTCTTAGCCTAACGTTTCGTC  | 3060 |
| Qy | 3054 | ATTGCCTCGTCACATCAATGCAAAGGTCTGATTTTGTTCAGCAAACACAGTGCAAT      | 3113 |
|    |      |   |      |
| Db | 3061 | ATTGCCTCGTCACATCAATGCAAAGGTCTGATTTTGTTCAGCAAACACAGTGCAAT      | 3120 |
| Qy | 3114 | GTTCTCAGAGTGACTTTTCAAATAAATTGGGCCCAAGAGCTTTAACTCGGTCTTAAATA   | 3173 |
|    |      |   |      |
| Db | 3121 | GTTCTCAGAGTGACTTTTCAAATAAATTGGGCCCAAGAGCTTTAACTCGGTCTTAAATA   | 3180 |
| Qy | 3174 | TGCCCAAATTTTTACTTTGTTTTCTTTTAATAGGCTGGGCCACATGTTGGAAATAAGCT   | 3233 |
|    |      |   |      |
| Db | 3181 | TGCCCAAATTTTTACTTTGTTTTCTTTTAATAGGCTGGGCCACATGTTGGAAATAAGCT   | 3240 |
| Qy | 3234 | AGTAATGTTGTTTTCTGTCAATATTGAATGTGATGGTACAGTAAACCAAACCAACAAT    | 3293 |
|    |      |   |      |
| Db | 3241 | AGTAATGTTGTTTTCTGTCAATATTGAATGTGATGGTACAGTAAACCAAACCAACAAT    | 3300 |
| Qy | 3294 | GTGGCCAGAAAGAAAGAGCAATAATAATTAATTCACACACCATATGGATTCTATTTATAA  | 3353 |
|    |      |   |      |
| Db | 3301 | GTGGCCAGAAAGAAAGAGCAATAATAATTAATTCACACACCATATGGATTCTATTTATAA  | 3360 |
| Qy | 3354 | ATCACCCACAAACTTGTCTTTAATTTTCATCCCAATCACTTTTTTCAGAGGCCTGTTATCA | 3413 |
|    |      |   |      |
| Db | 3361 | ATCACCCACAAACTTGTCTTTAATTTTCATCCCAATCACTTTTTTCAGAGGCCTGTTATCA | 3420 |

|    |      |  |      |
|----|------|--|------|
| Qy | 3414 | TAGAAGTCATTTTAGACTCTCAATTTTAAATTAATTTTGAATCACTAATATTTTCACAGT | 3473 |
|    |      |  |      |
| Db | 3421 | TAGAAGTCATTTTAGACTCTCAATTTTAAATTAATTTTGAATCACTAATATTTTCACAGT | 3480 |
| Qy | 3474 | TTATTAATATATTTAATTTCTATTTAAATTTTAGATTATTTTATTACCATGTACTGAAT  | 3533 |
|    |      |  |      |
| Db | 3481 | TTATTAATATATTTAATTTCTATTTAAATTTTAGATTATTTTATTACCATGTACTGAAT  | 3540 |
| Qy | 3534 | TTTACATCCTGATACCCCTTTCCTTCTCCATGTCAGTATCATGTTCTCTAATTATCTTGC | 3593 |
|    |      |  |      |
| Db | 3541 | TTTACATCCTGATACCCCTTTCCTTCTCCATGTCAGTATCATGTTCTCTAATTATCTTGC | 3600 |
| Qy | 3594 | CAAATTTTGAAACTACACACAAAAAGCATACTTGCATTATTTATAATAAAATTGCATTCA | 3653 |
|    |      |  |      |
| Db | 3601 | CAAATTTTGAAACTACACACAAAAAGCATACTTGCATTATTTATAATAAAATTGCATTCA | 3660 |
| Qy | 3654 | GTGGCTTTTAAAAAAATGTTTGATTCAAACTTTAACATACTGATAAGTAAGAAACAA    | 3713 |
|    |      |  |      |
| Db | 3661 | GTGGCTTTT-AAAAAAATGTTTGATTCAAACTTTAACATACTGATAAGTAAGAAACAA   | 3719 |
| Qy | 3714 | TTATAATTTCTTTACATACTCAAACCAAGATAGAAAAAGGTGCTATCGTTCAACTTCAA  | 3773 |
|    |      |  |      |
| Db | 3720 | TTATAATTTCTTTACATACTCAAACCAAGATAGAAAAAGGTGCTATCGTTCAACTTCAA  | 3779 |
| Qy | 3774 | AACATGTTTCCTAGTATTAAGGACTTTAATATAGCAACAGACAAAATTATTGTTAACATG | 3833 |
|    |      |  |      |
| Db | 3780 | AACATGTTTCCTAGTATTAAGGACTTTAATATAGCAACAGACAAAATTATTGTTAACATG | 3839 |
| Qy | 3834 | GATGTTACAGCTCAAAGATTTATAAAAGATTTTAACCTATTTTCTCCCTTATTATCCAC  | 3893 |
|    |      |  |      |
| Db | 3840 | GATGTTACAGCTCAAAGATTTATAAAAGATTTTAACCTATTTTCTCCCTTATTATCCAC  | 3899 |
| Qy | 3894 | TGCTAATGTGGATGTATGTTCAAACACCTTTTAGTATTGATAGCTTACATATGGCCAAAG | 3953 |
|    |      |  |      |
| Db | 3900 | TGCTAATGTGGATGTATGTTCAAACACCTTTTAGTATTGATAGCTTACATATGGCCAAAG | 3959 |
| Qy | 3954 | GAATACAGTTTATAGCAAAACATGGGTATGCTGTAGCTAACTTTATAAAAGTGTAATATA | 4013 |
|    |      |  |      |
| Db | 3960 | GAATACAGTTTATAGCAAAACATGGGTATGCTGTAGCTAACTTTATAAAAGTGTAATATA | 4019 |
| Qy | 4014 | ACAATGTAAAAAATTATATATCTGGGAGGATTTTTTGGTTGCCTAAAGTGGCTATAGTTA | 4073 |
|    |      |  |      |
| Db | 4020 | ACAATGTAAAAAATTATATATCTGGGAGGATTTTTTGGTTGCCTAAAGTGGCTATAGTTA | 4079 |
| Qy | 4074 | CTGATTTTTTATTATGTAAGCAAAACCAATAAAAATTTAAGTTTTTTTAACTACCTT    | 4133 |
|    |      |  |      |
| Db | 4080 | CTGATTTTTTATTATGTAAGCAAAACCAATAAAAATTTAAGTTTTTTTAACTACCTT    | 4139 |
| Qy | 4134 | ATTTTTCACTGTACAGACACTAATTCATTAAATACTAATTGATTGTTTAAAGAAATATA  | 4193 |
|    |      |  |      |
| Db | 4140 | ATTTTTCACTGTACAGACACTAATTCATTAAATACTAATTGATTGTTTAAAGAAATATA  | 4199 |
| Qy | 4194 | AATGTGACAAGTGGACATTATTTATGTTAAATATACAATTATCAAGCAAGTATGAAGTTA | 4253 |
|    |      |  |      |
| Db | 4200 | AATGTGACAAGTGGACATTATTTATGTTAAATATACAATTATCAAGCAAGTATGAAGTTA | 4259 |
| Qy | 4254 | TTCAATTAAAATGCCACATTTCTGGTCTCTGGGAAAAAAAAAAAAA               | 4299 |

Db 4260 TTCAATTAAATGCCACATTTCTGGTCAAAAAAAAAAAGNNAGA 4305

RESULT 8

US-10-020-141-5/c

; Sequence 5, Application US/10020141

; Publication No. US20030092013A1

; GENERAL INFORMATION:

; APPLICANT: McCarthy, Jeanette

; APPLICANT: Ableson, Allen

; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF VASCULAR DISEASE

; FILE REFERENCE: MMI-002

; CURRENT APPLICATION NUMBER: US/10/020,141

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; SOFTWARE: FastSEQ for Windows Version 4.0

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; LENGTH: 183337

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-020-141-5

Query Match 66.1%; Score 2841.8; DB 15; Length 183337;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 2854; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

|    |       |  |       |
|----|-------|--|-------|
| Qy | 1430  | AGTCATGCTTATGCTGCTGGTGCCAGTCATTTGAAGAAAACAGTCCTTGGAGGAAAAGC  | 1489  |
|    |       |  |       |
| Db | 72830 | AGTCATGCTTATGCTGCTGGTGCCAGTCATTTGAAGAAAACAGTCCTTGGAGGAAAAGC  | 72771 |
| Qy | 1490  | AGTCGTGCTTAAAGTTCAAAGCTAATGATCACGGATATGACAACTTCCGTTCCAGTAATA | 1549  |
|    |       |  |       |
| Db | 72770 | AGTCGTGCTTAAAGTTCAAAGCTAATGATCACGGATATGACAACTTCCGTTCCAGTAATA | 72711 |
| Qy | 1550  | AATACAGCTCATCTTGAAAGAAGAACTATTCAGTGTATTTTCTTTTATATTGGACC     | 1609  |
|    |       |  |       |
| Db | 72710 | AATACAGCTCATCTTGAAAGAAGAACTATTCAGTGTATTTTCTTTTATATTGGACC     | 72651 |
| Qy | 1610  | GAAGTCATTAAACAAAATGAAACATTTGCCAAAACAAAACAAAACAACTATGTATTTGCA | 1669  |
|    |       |  |       |
| Db | 72650 | GAAGTCATTAAACAAAATGAAACATTTGCCAAAACAAAACAAAACAACTATGTATTTGCA | 72591 |
| Qy | 1670  | CAGCACACTATTAAATATTAAGTGTAATTATTTTAACACTCACAGCTACATATGACATT  | 1729  |
|    |       |  |       |
| Db | 72590 | CAGCACACTATTAAATATTAAGTGTAATTATTTTAACACTCACAGCTACATATGACATT  | 72531 |
| Qy | 1730  | TTATGAGCTGTTTACGGCATGGAAAGAAAATCAGTGGGAATTAAGAAAGCCTCGTCGTGA | 1789  |
|    |       |  |       |
| Db | 72530 | TTATGAGCTGTTTACGGCATGGAAAGAAAATCAGTGGGAATTAAGAAAGCCTCGTCGTGA | 72471 |
| Qy | 1790  | AAGCACTTAATTTTTTACAGTTAGCACTTCAACATAGCTCTTAACAACCTCCAGGATATT | 1849  |
|    |       |  |       |

Db 72470 AAGCACTTAATTTTTTACAGTTAGCACTTCAACATAGCTCTTAACAACCTCCAGGATATT 72411

Qy 1850 CACACAACACTTAGGCTTAAAAATGAGCTCACTCAGAATTTCTATTCTTTCTAAAAAGAG 1909  
 |||

Db 72410 CACACAACACTTAGGCTTAAAAATGAGCTCACTCAGAATTTCTATTCTTTCTAAAAAGAG 72351

Qy 1910 ATTTATTTTTTAAATCAATGGGACTCTGATATAAAGGAAGAATAAGTCACTGTAAAAACAGA 1969  
 |||

Db 72350 ATTTATTTTTTAAATCAATGGGACTCTGATATAAAGGAAGAATAAGTCACTGTAAAAACAGA 72291

Qy 1970 ACTTTTAAATGAAGCTTAAATTACTCAATTTAAAAATTTTAAAAATCCTTTAAAAACAACCTT 2029  
 |||

Db 72290 ACTTTTAAATGAAGCTTAAATTACTCAATTTAAAAATTTTAAAAATCCTTTAAAAACAACCTT 72231

Qy 2030 TCAATTAATATTATCACACTATTATCAGATTGTAATTAGATGCAAATGAGAGAGCAGTTT 2089  
 |||

Db 72230 TCAATTAATATTATCACACTATTATCAGATTGTAATTAGATGCAAATGAGAGAGCAGTTT 72171

Qy 2090 AGTTGTTGCATTTTTTCGGACACTGGAAACATTTAAATGATCAGGAGGGAGTAACAGAAAAG 2149  
 |||

Db 72170 AGTTGTTGCATTTTTTCGGACACTGGAAACATTTAAATGATCAGGAGGGAGTAACAGAAAAG 72111

Qy 2150 AGCAAGGCTGTTTTTGAAATCATTACACTTTTACTAGAAAGCCCAAACCTCAGCATTCTG 2209  
 |||

Db 72110 AGCAAGGCTGTTTTTGAAATCATTACACTTTTACTAGAAAGCCCAAACCTCAGCATTCTG 72051

Qy 2210 CAATATGTAACCAACATGTCACAAACAAGCAGCATGTAACAGACTGGCACATGTGCCAGC 2269  
 |||

Db 72050 CAATATGTAACCAACATGTCACAAACAAGCAGCATGTAACAGACTGGCACATGTGCCAGC 71991

Qy 2270 TGAATTTAAATATAATACTTTTTAAAAAGAAAATTATTACATCCTTTACATTTCAGTTAAG 2329  
 |||

Db 71990 TGAATTTAAATATAATACTTTTTAAAAAGAAAATTATTACATCCTTTACATTTCAGTTAAG 71931

Qy 2330 ATCAAACCTCACAAAGAGAAATAGAATGTTTGAAAGGCTATCCCAAAGACTTTTTTGAA 2389  
 |||

Db 71930 ATCAAACCTCACAAAGAGAAATAGAATGTTTGAAAGGCTATCCCAAAGACTTTTTTGAA 71871

Qy 2390 TCTGTCATTACATACCCTGTGAAGACAATACTATCTACAATTTTTTTCAGGATTATTAAA 2449  
 |||

Db 71870 TCTGTCATTACATACCCTGTGAAGACAATACTATCTACAATTTTTTTCAGGATTATTAAA 71811

Qy 2450 ATCTTCTTTTTTCACTATCGTAGCTTAAACTCTGTTTGGTTTTGTCATCTGTAAATACTT 2509  
 |||

Db 71810 ATCTTCTTCTTTCACTATCGTAGCTTAAACTCTGTTTGGTTTTGTCATCTGTAAATACTT 71751

Qy 2510 ACCTACATACACTGCATGTAGATGATTAAATGAGGGCAGGCCCTGTGCTCATAGCTTTAC 2569  
 |||

Db 71750 ACCTACATACACTGCATGTAGATGATTAAATGAGGGCAGGCCCTGTGCTCATAGCTTTAC 71691

Qy 2570 GATGGAGAGATGCCAGTGACCTCATAATAAAGACTGTGAACTGCCTGGTGCAGTGTCCAC 2629  
 |||

Db 71690 GATGGAGAGATGCCAGTGACCTCATAATAAAGACTGTGAACTGCCTGGTGCAGTGTCCAC 71631

Qy 2630 ATGACAAAGGGGCAGGTAGCACCCCTCTCTACCCATGCTGTGGTTAAAATGGTTTCTAGC 2689  
 |||

Db 71630 ATGACAAAGGGGCAGGTAGCACCCCTCTCTACCCATGCTGTGGTTAAAATGGTTTCTAGC 71571



|    |       |  |       |
|----|-------|--|-------|
| Qy | 2690  | ATATGTATAATGCTATAGTTAAAAATACTATTTTTTCAAAATCATACAGATTAGTACATTTA | 2749  |
|    |       |  |       |
| Db | 71570 | ATATGTATAATGCTATAGTTAAAAATACTATTTTTTCAAAATCATACAGATTAGTACATTTA | 71511 |
| Qy | 2750  | ACAGCTACCTGTAAAGCTTATTACTAATTTTTGTATTATTTTTGTAAATAGCCAATAGAA   | 2809  |
|    |       |  |       |
| Db | 71510 | ACAGCTACCTGTAAAGCTTATTACTAATTTTTGTATTATTTTTGTAAATAGCCAATAGAA   | 71451 |
| Qy | 2810  | AAGTTTGCTTGACATGGTGCTTTTCTTTCATCTAGAGGCAAACTGCTTTTTGAGACCGT    | 2869  |
|    |       |  |       |
| Db | 71450 | AAGTTTGCTTGACATGGTGCTTTTCTTTCATCTAGAGGCAAACTGCTTTTTGAGACCGT    | 71391 |
| Qy | 2870  | AAGAACCTCTTAGCTTTGTGCGTTCCTGCCTAATTTTTATATCTTCTAAGCAAAGTGCCT   | 2929  |
|    |       |  |       |
| Db | 71390 | AAGAACCTCTTAGCTTTGTGCGTTCCTGCCTAATTTTTATATCTTCTAAGCAAAGTGCCT   | 71331 |
| Qy | 2930  | TAGGATAGCTTGGGATGAGATGTGTGTGAAAGTATGTACAAGAGAAAAACGGAAGAGAGAG  | 2989  |
|    |       |  |       |
| Db | 71330 | TAGGATAGCTTGGGATGAGATGTGTGTGAAAGTATGTACAAGAGAAAAACGGAAGAGAGAG  | 71271 |
| Qy | 2990  | GAAATGAGGTGGGGTTGGAGGAAACCCATGGGGACAGATTCCCATTCTTAGCCTAACGTT   | 3049  |
|    |       |  |       |
| Db | 71270 | GAAATGAGGTGGGGTTGGAGGAAACCCATGGGGACAGATTCCCATTCTTAGCCTAACGTT   | 71211 |
| Qy | 3050  | CGTCATTGCCTCGTCACATCAATGCAAAAGGTCCTGATTTTGTTCAGCAAACACAGTG     | 3109  |
|    |       |  |       |
| Db | 71210 | CGTCATTGCCTCGTCACATCAATGCAAAAGGTCCTGATTTTGTTCAGCAAACACAGTG     | 71151 |
| Qy | 3110  | CAATGTTCTCAGAGTGACTTTTCGAAATAAATTGGGCCCAAGAGCTTTAACTCGGTCTTAA  | 3169  |
|    |       |  |       |
| Db | 71150 | CAATGTTCTCAGAGTGACTTTTCGAAATAAATTGGGCCCAAGAGCTTTAACTCGGTCTTAA  | 71091 |
| Qy | 3170  | AATATGCCCAAATTTTTACTTTGTTTTTCTTTTAATAGGCTGGGCCACATGTTGGAAATA   | 3229  |
|    |       |  |       |
| Db | 71090 | AATATGCCCAAATTTTTACTTTGTTTTTCTTTTAATAGGCTGGGCCACATGTTGGAAATA   | 71031 |
| Qy | 3230  | AGCTAGTAATGTTGTTTTCTGTCAATATTGAATGTGATGGTACAGTAAACCAAACCCAA    | 3289  |
|    |       |  |       |
| Db | 71030 | AGCTAGTAATGTTGTTTTCTGTCAATATTGAATGTGATGGTACAGTAAACCAAACCCAA    | 70971 |
| Qy | 3290  | CAATGTGGCCAGAAAGAAAGAGCAATAATAATTAATTCACACACCATATGGATTCTATTT   | 3349  |
|    |       |  |       |
| Db | 70970 | CAATGTGGCCAGAAAGAAAGAGCAATAATAATTAATTCACACACCATATGGATTCTATTT   | 70911 |
| Qy | 3350  | ATAAATCACCCACAACTTGTTCCTTAATTTTCATCCCAATCACTTTTTTCAGAGGCCTGTT  | 3409  |
|    |       |  |       |
| Db | 70910 | ATAAATCACCCACAACTTGTTCCTTAATTTTCATCCCAATCACTTTTTTCAGAGGCCTGTT  | 70851 |
| Qy | 3410  | ATCATAGAAGTCATTTTAGACTCTCAATTTTAAATTAATTTTGAATCACTAATATTTTCA   | 3469  |
|    |       |  |       |
| Db | 70850 | ATCATAGAAGTCATTTTAGACTCTCAATTTTAAATTAATTTTGAATCACTAATATTTTCA   | 70791 |
| Qy | 3470  | CAGTTTATTAATATATTTAATTTCTATTTAAATTTTAGATTATTTTTATTACCATGTACT   | 3529  |
|    |       |  |       |
| Db | 70790 | CAGTTTATTAATATATTTAATTTCTATTTAAATTTTAGATTATTTTTATTACCATGTACT   | 70731 |

|    |       |  |       |
|----|-------|--|-------|
| Qy | 3530  | GAATTTTACATCCTGATACCTTTTCCTTCTCCATGTCAGTATCATGTTCTCTAATTATC  | 3589  |
|    |       |  |       |
| Db | 70730 | GAATTTTACATCCTGATACCTTTTCCTTCTCCATGTCAGTATCATGTTCTCTAATTATC  | 70671 |
| Qy | 3590  | TTGCCAAATTTTGAAACTACACACAAAAAGCATACTTGCATTATTTATAATAAAATTGCA | 3649  |
|    |       |  |       |
| Db | 70670 | TTGCCAAATTTTGAAACTACACACAAAAAGCATACTTGCATTATTTATAATAAAATTGCA | 70611 |
| Qy | 3650  | TTCAGTGGCTTTTAAAAAAATGTTTGATTCAAACTTTAACATACTGATAAGTAAGAA    | 3709  |
|    |       |  |       |
| Db | 70610 | TTCAGTGGCTTTT-AAAAAAATGTTTGATTCAAACTTTAACATACTGATAAGTAAGAA   | 70552 |
| Qy | 3710  | ACAATTATAATTTCTTTACATACTCAAACCAAGATAGAAAAAGGTGCTATCGTTCAACT  | 3769  |
|    |       |  |       |
| Db | 70551 | ACAATTATAATTTCTTTACATACTCAAACCAAGATAGAAAAAGGTGCTATCGTTCAACT  | 70492 |
| Qy | 3770  | TCAAAACATGTTTCCTAGTATTAAGGACTTTAATATAGCAACAGACAAAATTATTGTAA  | 3829  |
|    |       |  |       |
| Db | 70491 | TCAAAACATGTTTCCTAGTATTAAGGACTTTAATATAGCAACAGACAAAATTATTGTAA  | 70432 |
| Qy | 3830  | CATGGATGTTACAGCTCAAAGATTTATAAAAGATTTTAACCTATTTTCTCCCTTATTAT  | 3889  |
|    |       |  |       |
| Db | 70431 | CATGGATGTTACAGCTCAAAGATTTATAAAAGATTTTAACCTATTTTCTCCCTTATTAT  | 70372 |
| Qy | 3890  | CCACTGCTAATGTGGATGTATGTTCAAACACCTTTTAGTATTGATAGCTTACATATGGCC | 3949  |
|    |       |  |       |
| Db | 70371 | CCACTGCTAATGTGGATGTATGTTCAAACACCTTTTAGTATTGATAGCTTACATATGGCC | 70312 |
| Qy | 3950  | AAAGGAATACAGTTTATAGCAAACATGGGTATGCTGTAGCTAACTTTATAAAAGTGTA   | 4009  |
|    |       |  |       |
| Db | 70311 | AAAGGAATACAGTTTATAGCAAACATGGGTATGCTGTAGCTAACTTTATAAAAGTGTA   | 70252 |
| Qy | 4010  | TATAACAATGTAAAAAATTATATATCTGGGAGGATTTTTTGGTTGCCTAAAGTGGCTATA | 4069  |
|    |       |  |       |
| Db | 70251 | TATAACAATGTAAAAAATTATATATCTGGGAGGATTTTTTGGTTGCCTAAAGTGGCTATA | 70192 |
| Qy | 4070  | GTTACTGATTTTTTATTATGTAAGCAAACCAATAAAAATTTAAGTTTTTTTAACTA     | 4129  |
|    |       |  |       |
| Db | 70191 | GTTACTGATTTTTTATTATGTAAGCAAACCAATAAAAATTTAAGTTTTTTTAACTA     | 70132 |
| Qy | 4130  | CCTTATTTTTCCTGTACAGACCTAATTCATTAAATACTAATTGATTGTTTAAAGAAA    | 4189  |
|    |       |  |       |
| Db | 70131 | CCTTATTTTTCCTGTACAGACCTAATTCATTAAATACTAATTGATTGTTTAAAGAAA    | 70072 |
| Qy | 4190  | TATAAATGTGACAAGTGGACATTATTTATGTTAAATATACAATTATCAAGCAAGTATGAA | 4249  |
|    |       |  |       |
| Db | 70071 | TATAAATGTGACAAGTGGACATTATTTATGTTAAATATACAATTATCAAGCAAGTATGAA | 70012 |
| Qy | 4250  | GTTATTCAATTAAAATGCCACATTTCTGGTCTCTGGG                        | 4286  |
|    |       |  |       |
| Db | 70011 | GTTATTCAATTAAAATGCCACATTTCTGGTCTCTGGG                        | 69975 |

RESULT 9

US-10-116-802-117

; Sequence 117, Application US/10116802

; Publication No. US20030065157A1

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; GENERAL INFORMATION:
; APPLICANT: Amy Lasek
; TITLE OF INVENTION: GENES EXPRESSED IN LUNG CANCER
; FILE REFERENCE: PA-0045 US
; CURRENT APPLICATION NUMBER: US/10/116,802
; CURRENT FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: 60/281,593
; PRIOR FILING DATE: 2001-04-04
; NUMBER OF SEQ ID NOS: 519
; SOFTWARE: PERL Program
; SEQ ID NO 117
; LENGTH: 1892
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No: 1094000.5
US-10-116-802-117
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Query Match          39.2%; Score 1684.6; DB 13; Length 1892;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 1698; Conservative 0; Mismatches 4; Indels 1; Gaps 1;
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Qy      178 TGAAACTTGGCTCTGAAACTGCGGAGCGGCCACCGACGCCTTCTGGAGCAGGTAGCAGC 237
      ||  || |||||||||||||||||||||||||||||||||||||||||||||||
Db      190 TGTCTCTAGGCTCTGAAACTGCGGAGCGGCCACCGACGCCTTCTGGAGCAGGTAGCAGC 249

Qy      238 ATGCAGCCGCCTCCAAGTCTGTGCGGACGCGCCCTGGTTGCGCTGGTTCTTGCCTGCGGC 297
      |||||||||||||||||||||||||||||||||||||||||||||||
Db      250 ATGCAGCCGCCTCCAAGTCTGTGCGGACGCGCCCTGGTTGCGCTGGTTCTTGCCTGCGGC 309

Qy      298 CTGTCGCGGATCTGGGGAGAGGAGAGAGGCTTCCCGCCTGACAGGGCCACTCCGCTTTTG 357
      |||||||||||||||||||||||||||||||||||||||||||||||
Db      310 CTGTCGCGGATCTGGGGAGAGGAGAGAGGCTTCCCGCCTGACAGGGCCACTCCGCTTTTG 369

Qy      358 CAAACCGCAGAGATAATGACGCCACCCACTAAGACCTTATGGCCCAAGGGTTCCAACGCC 417
      |||||||||||||||||||||||||||||||||||||||||||||||
Db      370 CAAACCGCAGAGATAATGACGCCACCCACTAAGACCTTATGGCCCAAGGGTTCCAACGCC 429

Qy      418 AGTCTGGCGCGGTCGTTGGCACCTGCGGAGGTGCCTAAAGGAGACAGGACGGCAGGATCT 477
      |||||||||||||||||||||||||||||||||||||||||||||||
Db      430 AGTCTGGCGCGGTCGTTGGCACCTGCGGAGGTGCCTAAAGGAGACAGGACGGCAGGATCT 489

Qy      478 CCGCCACGCACCATCTCCCCTCCCCCGTGCCAAGGACCCATCGAGATCAAGGAGACTTTC 537
      |||||||||||||||||||||||||||||||||||||||||||||||
Db      490 CCGCCACGCACCATCTCCCCTCCCCCGTGCCAAGGACCCATCGAGATCAAGGAGACTTTC 549

Qy      538 AAATACATCAACACGGTTGTGTCTGCCTTGTGTTTCGTGCTGGGGATCATCGGGAACCTCC 597
      |||||||||||||||||||||||||||||||||||||||||||||||
Db      550 AAATACATCAACACGGTTGTGTCTGCCTTGTGTTTCGTGCTGGGGATCATCGGGAACCTCC 609

Qy      598 ACACTTCTGAGAATTATCTACAAGAACAAGTGCATGCGAAACGGTCCCAATATCTTGATC 657
      |||||||||||||||||||||||||||||||||||||||||||||||
Db      610 ACACTTCTGAGAATTATCTACAAGAACAAGTGCATGCGAAACGGTCCCAATATCTTGATC 669

Qy      658 GCCAGCTTGGCTCTGGGAGACCTGCTGCACATCGTCATTGACATCCCTATCAATGTCTAC 717
      |||||||||||||||||||||||||||||||||||||||||||||||
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Db 670 GCCAGCTTGGCTCTGGGAGACCTGCTGCACATCGTCATTGACATCCCTATCAATGTCTAC 729  
 Qy 718 AAGCTGCTGGCAGAGGACTGGCCATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTCATA 777  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 730 AAGCTGCTGGCAGAGGACTGGCCATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTCATA 789  
 Qy 778 CAGAAAGCCTCCGTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATAT 837  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 790 CAGAAAGCCTCCGTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATAT 849  
 Qy 838 CGAGCTGTTGCTTCTTGGAGTAGAATTAAAGGAATTGGGGTTCCAAAATGGACAGCAGTA 897  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 850 CGAGCTGTTGCTTCTTGGAGTAGAATTAAAGGAATTGGGGTTCCAAAATGGACAGCAGTA 909  
 Qy 898 GAAATTGTTTTGATTTGGGTGGTCTCTGTGGTTCT-GGCTGTCCCTGAAGCCATAGGTTT 956  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 910 GAAATTGTTTTGATTTGGGTGGTCTCTGTGGTTCTGGGCTGTCCCTGAAGCCATAGGTTT 969  
 Qy 957 TGATATAATTACGATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGT 1016  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 970 TGATATAATTACGATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGT 1029  
 Qy 1017 TCAGAAGACAGCTTTCATGCAGTTTTTACAAGACAGCAAAGATTGGTGGCTGTTTCAGTTT 1076  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 1030 TCAGAAGACAGCTTTCATGCAGTTTTTACAAGACAGCAAAGATTGGTGGCTGTTTCAGTTT 1089  
 Qy 1077 CTATTTCTGCTTGCCATTGGCCATCACTGCATTTTTTTATACACTAATGACCTGTGAAAT 1136  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 1090 CTATTTCTGCTTGCCATTGGCCATCACTGCATTTTTTTATACACTAATGACCTGTGAAAT 1149  
 Qy 1137 GTTGAGAAAGAAAAGTGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGA 1196  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 1150 GTTGAGAAAGAAAAGTGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGA 1209  
 Qy 1197 AGTGGCCAAAACCGTCTTTTGCCTGGTCTTGTCTTTGCCCTCTGCTGGCTTCCCCTTCA 1256  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 1210 AGTGGCCAAAACCGTCTTTTGCCTGGTCTTGTCTTTGCCCTCTGCTGGCTTCCCCTTCA 1269  
 Qy 1257 CCTCAGCAGGATTCTGAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGAACT 1316  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 1270 CCTCAGCAGGATTCTGAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGAACT 1329  
 Qy 1317 TTTGAGCTTTCTGTTGGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCCTG 1376  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 1330 TTTGAGCTTTCTGTTGGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCCTG 1389  
 Qy 1377 CATTAACCCAATTGCTCTGTATTTGGTGAGCAAAAGATTCAAAAAGTCTTTAAGTCATG 1436  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 1390 CATTAACCCAATTGCTCTGTATTTGGTGAGCAAAAGATTCAAAAAGTCTTTAAGTCATG 1449  
 Qy 1437 CTTATGCTGCTGGTGCCAGTCATTTGAAGAAAAACAGTCCTTGGAGGAAAAGCAGTCGTG 1496  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 1450 CTTATGCTGCTGGTGCCAGTCATTTGAAGAAAAACAGTCCTTGGAGGAAAAGCAGTCGTG 1509  
 Qy 1497 CTTAAAGTTCAAAGCTAATGATCACGGATATGACAACTTCCGTTCCAGTAATAAATACAG 1556  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 1510 CTTAAAGTTCAAAGCTAATGATCACGGATATGACAACTTCCGTTCCAGTAATAAATACAG 1569

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Qy      1557 CTCATCTTGAAAGAAGAACTATTCACTGTATTTTCATTTTCTTTATATTGGACCGAAGTCA 1616
          |||
Db      1570 CTCATCTTGAAAGAAGAACTATTCACTGTATTTTCATTTTCTTTATATTGGACCGAAGTCA 1629

Qy      1617 TTAAACAAAATGAAACATTTGCCAAAACAAAACAAAAAACTATGTATTTGCACAGCACA 1676
          |||
Db      1630 TTAAACAAAATGAAACATTTGCCAAAACAAAACAAAAAACTATGTATTTGCACAGCACA 1689

Qy      1677 CTATTAAAATATTAAGTGTAATTATTTTAACACTCACAGCTACATATGACATTTTATGAG 1736
          |||
Db      1690 CTATTAAAATATTAAGTGTAATTATTTTAACACTCACAGCTACATATGACATTTTATGAG 1749

Qy      1737 CTGTTTACGGCATGGAAAGAAAATCAGTGGGAATTAAGAAAGCCTCGTCGTGAAAGCACT 1796
          |||
Db      1750 CTGTTTACGGCATGGAAAGAAAATCAGTGGGAATTAAGAAAGCCTCGTCGTGAAAGCACT 1809

Qy      1797 TAATTTTTTACAGTTAGCACTTCAACATAGCTCTTAACAACCTCCAGGATATTCACACAA 1856
          |||
Db      1810 TAATTTTTTACAGTTAGCACTTCAACATAGCTCTTAACAACCTCCAGGATATTCACACAA 1869

Qy      1857 CACTTAGGCTTAAAAATGAGCTC 1879
          |||
Db      1870 CACTTAGGCTTAAAAATGAGCTC 1892

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RESULT 10

US-10-116-802-118

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; Sequence 118, Application US/10116802
; Publication No. US20030065157A1
; GENERAL INFORMATION:
; APPLICANT: Amy Lasek
; TITLE OF INVENTION: GENES EXPRESSED IN LUNG CANCER
; FILE REFERENCE: PA-0045 US
; CURRENT APPLICATION NUMBER: US/10/116,802
; CURRENT FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: 60/281,593
; PRIOR FILING DATE: 2001-04-04
; NUMBER OF SEQ ID NOS: 519
; SOFTWARE: PERL Program
; SEQ ID NO 118
; LENGTH: 1877
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No: 1222734CB1
US-10-116-802-118

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Query Match          39.0%; Score 1676.6; DB 13; Length 1877;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1679; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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```

Qy      178 TGAAACTTGGCTCTGAAACTGCGGAGCGGCCACCGGACGCCTTCTGGAGCAGGTAGCAGC 237
          ||
Db      190 TGTCTCTAGGCTCTGAAACTGCGGAGCGGCCACCGGACGCCTTCTGGAGCAGGTAGCAGC 249

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|    |      |   |      |
|----|------|---|------|
| Qy | 238  | ATGCAGCCGCCTCCAAGTCTGTGCGGACGCGCCCTGGTTGCGCTGGTTCTTGCCTGCGGC  | 297  |
|    |      |   |      |
| Db | 250  | ATGCAGCCGCCTCCAAGTCTGTGCGGACGCGCCCTGGTTGCGCTGGTTCTTGCCTGCGGC  | 309  |
| Qy | 298  | CTGTCGCGGATCTGGGGAGAGGAGAGAGGCTTCCCGCCTGACAGGGCCACTCCGCTTTTG  | 357  |
|    |      |   |      |
| Db | 310  | CTGTCGCGGATCTGGGGAGAGGAGAGAGGCTTCCCGCCTGACAGGGCCACTCCGCTTTTG  | 369  |
| Qy | 358  | CAAACCGCAGAGATAATGACGCCACCCACTAAGACCTTATGGCCCAAGGGTTCCAACGCC  | 417  |
|    |      |   |      |
| Db | 370  | CAAACCGCAGAGATAATGACGCCACCCACTAAGACCTTATGGCCCAAGGGTTCCAACGCC  | 429  |
| Qy | 418  | AGTCTGGCGCGGTTCGTTGGCACCTGCGGAGGTGCCTAAAGGAGACAGGACGGCAGGATCT | 477  |
|    |      |   |      |
| Db | 430  | AGTCTGGCGCGGTTCGTTGGCACCTGCGGAGGTGCCTAAAGGAGACAGGACGGCAGGATCT | 489  |
| Qy | 478  | CCGCCACGCACCATCTCCCTCCCCGTGCCAAGGACCCATCGAGATCAAGGAGACTTTC    | 537  |
|    |      |   |      |
| Db | 490  | CCGCCACGCACCATCTCCCTCCCCGTGCCAAGGACCCATCGAGATCAAGGAGACTTTC    | 549  |
| Qy | 538  | AAATACATCAACACGGTTGTGTCTGCCTTGTGTTCTGTGCTGGGGATCATCGGGAACCTCC | 597  |
|    |      |   |      |
| Db | 550  | AAATACATCAACACGGTTGTGTCTGCCTTGTGTTCTGTGCTGGGGATCATCGGGAACCTCC | 609  |
| Qy | 598  | ACACTTCTGAGAATTATCTACAAGAACAAGTGCATGCGAAACGGTCCCAATATCTTGATC  | 657  |
|    |      |   |      |
| Db | 610  | ACACTTCTGAGAATTATCTACAAGAACAAGTGCATGCGAAACGGTCCCAATATCTTGATC  | 669  |
| Qy | 658  | GCCAGCTTGGCTCTGGGAGACCTGCTGCACATCGTCATTGACATCCCTATCAATGTCTAC  | 717  |
|    |      |   |      |
| Db | 670  | GCCAGCTTGGCTCTGGGAGACCTGCTGCACATCGTCATTGACATCCCTATCAATGTCTAC  | 729  |
| Qy | 718  | AAGCTGCTGGCAGAGGACTGGCCATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTCATA  | 777  |
|    |      |   |      |
| Db | 730  | AAGCTGCTGGCAGAGGACTGGCCATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTCATA  | 789  |
| Qy | 778  | CAGAAAGCCTCCGTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATAT  | 837  |
|    |      |   |      |
| Db | 790  | CAGAAAGCCTCCGTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATAT  | 849  |
| Qy | 838  | CGAGCTGTTGCTTCTTGGAGTAGAATTAAGGAATTGGGGTTCCAAAATGGACAGCAGTA   | 897  |
|    |      |   |      |
| Db | 850  | CGAGCTGTTGCTTCTTGGAGTAGAATTAAGGAATTGGGGTTCCAAAATGGACAGCAGTA   | 909  |
| Qy | 898  | GAAATTGTTTTGATTTGGGTGGTCTCTGTGGTTCTGGCTGTCCCTGAAGCCATAGGTTTT  | 957  |
|    |      |   |      |
| Db | 910  | GAAATTGTTTTGATTTGGGTGGTCTCTGTGGTTCTGGCTGTCCCTGAAGCCATAGGTTTT  | 969  |
| Qy | 958  | GATATAATTACGATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTT  | 1017 |
|    |      |   |      |
| Db | 970  | GATATAATTACGATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTT  | 1029 |
| Qy | 1018 | CAGAAGACAGCTTTCATGCAGTTTTACAAGACAGCAAAAGATTGGTGGCTGTTTCAGTTTC | 1077 |
|    |      |   |      |
| Db | 1030 | CAGAAGACAGCTTTCATGCAGTTTTACAAGACAGCAAAAGATTGGTGGCTGTTTCAGTTTC | 1089 |
| Qy | 1078 | TATTTCTGCTTGCCATTGGCCATCACTGCATTTTTTTTATACATAATGACCTGTGAAATG  | 1137 |

|    |      |   |      |
|----|------|---|------|
| Db | 1090 | <br>TATTTCTGCTTGCCATTGGCCATCACTGCATTTTTTTATACACTAATGACCTGTGAAATG  | 1149 |
| Qy | 1138 | TTGAGAAAGAAAAGTGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAA      | 1197 |
| Db | 1150 | <br>TTGAGAAAGAAAAGTGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAA  | 1209 |
| Qy | 1198 | GTGGCCAAAACCGTCTTTTGCCTGGTCCTTGTCTTTGCCCTCTGCTGGCTTCCCCTTCAC      | 1257 |
| Db | 1210 | <br>GTGGCCAAAACCGTCTTTTGCCTGGTCCTTGTCTTTGCCCTCTGCTGGCTTCCCCTTCAC  | 1269 |
| Qy | 1258 | CTCAGCAGGATTCTGAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGAACTT      | 1317 |
| Db | 1270 | <br>CTCAGCAGGATTCTGAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGAACTT  | 1329 |
| Qy | 1318 | TTGAGCTTTCTGTTGGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCCTGC      | 1377 |
| Db | 1330 | <br>TTGAGCTTTCTGTTGGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCCTGC  | 1389 |
| Qy | 1378 | ATTAACCCAATTGCTCTGTATTTGGTGAGCAAAAGATTCAAAAACCTGCTTTAAGTCATGC     | 1437 |
| Db | 1390 | <br>ATTAACCCAATTGCTCTGTATTTGGTGAGCAAAAGATTCAAAAACCTGCTTTAAGTCATGC | 1449 |
| Qy | 1438 | TTATGCTGCTGGTGCCAGTCATTTGAAGAAAAACAGTCCTTGGAGGAAAAGCAGTCGTGC      | 1497 |
| Db | 1450 | <br>TTATGCTGCTGGTGCCAGTCATTTGAAGAAAAACAGTCCTTGGAGGAAAAGCAGTCGTGC  | 1509 |
| Qy | 1498 | TTAAAGTTCAAAGCTAATGATCACGGATATGACAACCTCCGTTCCAGTAATAAATACAGC      | 1557 |
| Db | 1510 | <br>TTAAAGTTCAAAGCTAATGATCACGGATATGACAACCTCCGTTCCAGTAATAAATACAGC  | 1569 |
| Qy | 1558 | TCATCTTGAAAGAAGAACTATTCACTGTATTTCAATTTCTTTATATTGGACCGAAGTCAT      | 1617 |
| Db | 1570 | <br>TCATCTTGAAAGAAGAACTATTCACTGTATTTCAATTTCTTTATATTGGACCGAAGTCAT  | 1629 |
| Qy | 1618 | TAAAACAAAATGAAACATTTGCCAAAACAAAACAAAAAACTATGTATTTGCACAGCACAC      | 1677 |
| Db | 1630 | <br>TAAAACAAAATGAAACATTTGCCAAAACAAAACAAAAAACTATGTATTTGCACAGCACAC  | 1689 |
| Qy | 1678 | TATTAAATATTAAGTGTAATTATTTTAACACTCACAGCTACATATGACATTTTATGAGC       | 1737 |
| Db | 1690 | <br>TATTAAATATTAAGTGTAATTATTTTAACACTCACAGCTACATATGACATTTTATGAGC   | 1749 |
| Qy | 1738 | TGTTTACGGCATGGAAAGAAAATCAGTGGGAATTAAGAAAGCCTCGTCGTGAAAGCACTT      | 1797 |
| Db | 1750 | <br>TGTTTACGGCATGGAAAGAAAATCAGTGGGAATTAAGAAAGCCTCGTCGTGAAAGCACTT  | 1809 |
| Qy | 1798 | AATTTTTTACAGTTAGCACTTCAACATAGCTCTTAACAACTTCCAGGATATTCACACAAC      | 1857 |
| Db | 1810 | <br>AATTTTTTACAGTTAGCACTTCAACATAGCTCTTAACAACTTCCAGGATATTCACACAAC  | 1869 |
| Qy | 1858 | ACT 1860  |      |
|    |      |   |      |
| Db | 1870 | ACT 1872  |      |

US-10-305-720-1203  
; Sequence 1203, Application US/10305720  
; Publication No. US20040010136A1  
; GENERAL INFORMATION:  
; APPLICANT: Au-Young, Janice K.; Seilhamer, Jeffrey J.  
; TITLE OF INVENTION: Composition for the Detection of Signaling Pathway Gene Expression  
; FILE REFERENCE: PA-0002-1 CON  
; CURRENT APPLICATION NUMBER: US/10/305,720  
; CURRENT FILING DATE: 2002-11-26  
; PRIOR APPLICATION NUMBER: 09/016,434  
; PRIOR FILING DATE: 1998-01-30  
; NUMBER OF SEQ ID NOS: 1490  
; SOFTWARE: PERL Program  
; SEQ ID NO 1203  
; LENGTH: 1470  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc\_feature  
; OTHER INFORMATION: GenBank ID No. US20040010136A1 gl82275  
US-10-305-720-1203

Query Match 34.1%; Score 1466.8; DB 16; Length 1470;  
Best Local Similarity 99.9%; Pred. No. 8.3e-291;  
Matches 1468; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

|    |     |   |     |
|----|-----|---|-----|
| Qy | 192 | GAAACTGCGGAGCGGCCACCGGACGCCTTCTGGAGCAGGTAGCAGCATGCAGCCGCCTCC  | 251 |
|    |     |   |     |
| Db | 1   | GAAACTGCGGACGGGCCACCGGACGCCTTCTGGAGCAGGTAGCAGCATGCAGCCGCCTCC  | 60  |
| Qy | 252 | AAGTCTGTGCGGACGCGCCCTGGTTGCGCTGGTTCTTGCCTGCGGCCTGTCGCGGATCTG  | 311 |
|    |     |   |     |
| Db | 61  | AAGTCTGTGCGGACGCGCCCTGGTTGCGCTGGTTCTTGCCTGCGGCCTGTCGCGGATCTG  | 120 |
| Qy | 312 | GGGAGAGGAGAGAGGCTTCCCGCCTGACAGGGCCACTCCGCTTTTGAAACCGCAGAGAT   | 371 |
|    |     |   |     |
| Db | 121 | GGGAGAGGAGAGAGGCTTCCCGCCTGACAGGGCCACTCCGCTTTTGAAACCGCAGAGAT   | 180 |
| Qy | 372 | AATGACGCCACCCACTAAGACCTTATGGCCCAAGGGTTCCAACGCCAGTCTGGCGCGGTC  | 431 |
|    |     |   |     |
| Db | 181 | AATGACGCCACCCACTAAGACCTTATGGCCCAAGGGTTCCAACGCCAGTCTGGCGCGGTC  | 240 |
| Qy | 432 | GTTGGCACCTGCGGAGGTGCCTAAAGGAGACAGGACGGCAGGATCTCCGCCACGCACCAT  | 491 |
|    |     |   |     |
| Db | 241 | GTTGGCACCTGCGGAGGTGCCTAAAGGAGACAGGACGGCAGGATCTCCGCCACGCACCAT  | 300 |
| Qy | 492 | CTCCCCCTCCCCCGTGCCAAGGACCCATCGAGATCAAGGAGACTTTCAAATACATCAACAC | 551 |
|    |     |   |     |
| Db | 301 | CTCCCCCTCCCCCGTGCCAAGGACCCATCGAGATCAAGGAGACTTTCAAATACATCAACAC | 360 |
| Qy | 552 | GGTTGTGTCTTGCCTTGTGTTTCGTGCTGGGGATCATCGGGAATCCACACTTCTGAGAAT  | 611 |
|    |     |   |     |
| Db | 361 | GGTTGTGTCTTGCCTTGTGTTTCGTGCTGGGGATCATCGGGAATCCACACTTCTGAGAAT  | 420 |
| Qy | 612 | TATCTACAAGAACAAGTGCATGCGAAACGGTCCCAATATCTTGATCGCCAGCTTGGCTCT  | 671 |
|    |     |   |     |



|    |      |   |      |
|----|------|---|------|
| Db | 421  | TATCTACAAGAACAAGTGCATGCGAAACGGTCCCAATATCTTGATCGCCAGCTTGGCTCT  | 480  |
| Qy | 672  | GGGAGACCTGCTGCACATCGTCATTGACATCCCTATCAATGTCTACAAGCTGCTGGCAGA  | 731  |
|    |      |   |      |
| Db | 481  | GGGAGACCTGCTGCACATCGTCATTGACATCCCTATCAATGTCTACAAGCTGCTGGCAGA  | 540  |
| Qy | 732  | GGACTGGCCATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTCATACAGAAAGCCTCCGT  | 791  |
|    |      |   |      |
| Db | 541  | GGACTGGCCATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTCATACAGAAAGCCTCCGT  | 600  |
| Qy | 792  | GGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATATCGAGCTGTTGCTTC  | 851  |
|    |      |   |      |
| Db | 601  | GGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATATCGAGCTGTTGCTTC  | 660  |
| Qy | 852  | TTGGAGTAGAATTAAAGGAATTGGGGTTCAAAATGGACAGCAGTAGAAATTGTTTTGAT   | 911  |
|    |      |   |      |
| Db | 661  | TTGGAGTAGAATTAAAGGAATTGGGGTTCAAAATGGACAGCAGTAGAAATTGTTTTGAT   | 720  |
| Qy | 912  | TTGGGTGGTCTCTGTGGTTCTGGCTGTCCCTGAAGCCATAGGTTTTGATATAATTACGAT  | 971  |
|    |      |   |      |
| Db | 721  | TTGGGTGGTCTCTGTGGTTCTGGCTGTCCCTGAAGCCATAGGTTTTGATATAATTACGAT  | 780  |
| Qy | 972  | GGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTTCAGAAGACAGCTTT  | 1031 |
|    |      |   |      |
| Db | 781  | GGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTTCAGAAGACAGCTTT  | 840  |
| Qy | 1032 | CATGCAGTTTTACAAGACAGCAAAGATTGGTGGCTGTTCAGTTTTCTATTTCTGCTTGCC  | 1091 |
|    |      |   |      |
| Db | 841  | CATGCAGTTTTACAAGACAGCAAAGATTGGTGGCTGTTCAGTTTTCTATTTCTGCTTGCC  | 900  |
| Qy | 1092 | ATTGGCCATCACTGCATTTTTTTATACACTAATGACCTGTGAAATGTTGAGAAAGAAAAG  | 1151 |
|    |      |   |      |
| Db | 901  | ATTGGCCATCACTGCATTTTTTTATACACTAATGACCTGTGAAATGTTGAGAAAGAAAAG  | 960  |
| Qy | 1152 | TGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAAGTGGCCAAAACCGT  | 1211 |
|    |      |   |      |
| Db | 961  | TGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAAGTGGCCAAAACCGT  | 1020 |
| Qy | 1212 | CTTTTGCCCTGGTCCTTGTCTTTGCCCTCTGCTGGCTTCCCCTTCACCTCAGCAGGATTCT | 1271 |
|    |      |   |      |
| Db | 1021 | CTTTTGCCCTGGTCCTTGTCTTTGCCCTCTGCTGGCTTCCCCTTCACCTCAGCAGGATTCT | 1080 |
| Qy | 1272 | GAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGAACCTTTTGAGCTTTCTGTT | 1331 |
|    |      |   |      |
| Db | 1081 | GAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGAACCTTTTGAGCTTTCTGTT | 1140 |
| Qy | 1332 | GGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCCTGCATTAACCCAATTGC  | 1391 |
|    |      |   |      |
| Db | 1141 | GGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCCTGCATTAACCCAATTGC  | 1200 |
| Qy | 1392 | TCTGTATTTGGTGAGCAAAAGATTCAAAAAGTCTTTAAGTCATGCTTATGCTGCTGGTG   | 1451 |
|    |      |   |      |
| Db | 1201 | TCTGTATTTGGTGAGCAAAAGATTCAAAAAGTCTTTAAGTCATGCTTATGCTGCTGGTG   | 1260 |
| Qy | 1452 | CCAGTCATTTGAAGAAAAACAGTCCTTGAGGAAAAGCAGTCGTGCTTAAAGTTCAAAGC   | 1511 |
|    |      |   |      |
| Db | 1261 | CCAGTCATTTGAAGAAAAACAGTCCTTGAGGAAAAGCAGTCGTGCTTAAAGTTCAAAGC   | 1320 |

Qy 1512 TAATGATCACGGATATGACAACTTCCGTTCCAGTAATAAATACAGCTCATCTTGAAAGAA 1571  
 |||  
 Db 1321 TAATGATCACGGATATGACAACTTCCGTTCCAGTAATAAATACAGCTCATCTTGAAAGAA 1380  
 |||  
 Qy 1572 GAACTATTCACTGTATTTTCAATTTTCTTTATATTGGACCGAAGTCATTAAAAACAAAATGAA 1631  
 |||  
 Db 1381 GAACTATTCACTGTATTTTCAATTTTCTTTATATTGGACCGAAGTCATTAAAAACAAAATGAA 1440  
 |||  
 Qy 1632 ACATTTGCCAAAACAAAACAAAAAACTATG 1661  
 |||  
 Db 1441 ACATTTGCCAAAACAAAACAAAAAACTATG 1470

RESULT 12

US-10-311-671-28

; Sequence 28, Application US/10311671

; Publication No. US20040072996A1

; GENERAL INFORMATION:

; APPLICANT: INCYTE GENOMICS, INC.

; APPLICANT: LAL, Preeti G.

; APPLICANT: BAUGHN, Mariah R.

; APPLICANT: HAFALIA, April J. A.

; APPLICANT: NGUYEN, Danniel B.

; APPLICANT: GANDHI, Ameena R.

; APPLICANT: KALLICK, Deborah A.

; APPLICANT: GRIFFIN, Jennifer A.

; APPLICANT: YUE, Henry

; APPLICANT: KHAN, Farrah A.

; APPLICANT: ARVIZU, Chandra S.

; APPLICANT: LU, Dyung Aina M.

; APPLICANT: TRIBOULEY, Catherine M.

; APPLICANT: LU, Yan

; APPLICANT: CHAWLA, Narinder K.

; APPLICANT: GRAUL, Richard

; APPLICANT: YAO, Monique G.

; APPLICANT: YANG, Junming

; APPLICANT: RAMKUMAR, Jayalaxmi

; APPLICANT: AU-YOUNG, Janice K.

; APPLICANT: ELLIOTT, Vicki S.

; APPLICANT: HERNANDEZ, Roberto

; APPLICANT: WALSH, Roderick T.

; APPLICANT: BOROWSKY, Mark L.

; APPLICANT: THORNTON, Michael B.

; APPLICANT: HE, Ann

; TITLE OF INVENTION: G-PROTEIN COUPLED RECEPTORS

; FILE REFERENCE: PI-0131 USN

; CURRENT APPLICATION NUMBER: US/10/311,671

; CURRENT FILING DATE: 2002-12-16

; PRIOR APPLICATION NUMBER: PCT/US01/19275

; PRIOR FILING DATE: 2001-06-15

; PRIOR APPLICATION NUMBER: 60/212,483

; PRIOR FILING DATE: 2000-06-16

; PRIOR APPLICATION NUMBER: 60/213,954

; PRIOR FILING DATE: 2000-06-22

; PRIOR APPLICATION NUMBER: 60/215,209

; PRIOR FILING DATE: 2000-06-29

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; PRIOR APPLICATION NUMBER: 60/216,595
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: 60/218,936
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: 60/219,154
; PRIOR FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: 60/220,141
; PRIOR FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PERL Program
; SEQ ID NO 28
; LENGTH: 1632
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No: 6792419CB1
US-10-311-671-28
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Query Match          32.3%; Score 1389; DB 12; Length 1632;
Best Local Similarity 100.0%; Pred. No. 8.6e-275;
Matches 1389; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy      186 GGCTCTGAAACTGCGGAGCGGCCACCGGACGCCTTCTGGAGCAGGTAGCAGCATGCAGCC 245
          |||
Db      236 GGCTCTGAAACTGCGGAGCGGCCACCGGACGCCTTCTGGAGCAGGTAGCAGCATGCAGCC 295

Qy      246 GCCTCCAAGTCTGTGCGGACGCGCCCTGGTTGCGCTGGTTCTTGCCTGCGGCCTGTCGCG 305
          |||
Db      296 GCCTCCAAGTCTGTGCGGACGCGCCCTGGTTGCGCTGGTTCTTGCCTGCGGCCTGTCGCG 355

Qy      306 GATCTGGGGAGAGGAGAGAGGCTTCCCGCCTGACAGGGCCACTCCGCTTTTGCAAACCGC 365
          |||
Db      356 GATCTGGGGAGAGGAGAGAGGCTTCCCGCCTGACAGGGCCACTCCGCTTTTGCAAACCGC 415

Qy      366 AGAGATAATGACGCCACCCACTAAGACCTTATGGCCCAAGGGTTCCAACGCCAGTCTGGC 425
          |||
Db      416 AGAGATAATGACGCCACCCACTAAGACCTTATGGCCCAAGGGTTCCAACGCCAGTCTGGC 475

Qy      426 GCGGTCGTTGGCACCTGCGGAGGTGCCTAAAGGAGACAGGACGGCAGGATCTCCGCCACG 485
          |||
Db      476 GCGGTCGTTGGCACCTGCGGAGGTGCCTAAAGGAGACAGGACGGCAGGATCTCCGCCACG 535

Qy      486 CACCATCTCCCCTCCCCCGTGCCAAGGACCCATCGAGATCAAGGAGACTTTCAAATACAT 545
          |||
Db      536 CACCATCTCCCCTCCCCCGTGCCAAGGACCCATCGAGATCAAGGAGACTTTCAAATACAT 595

Qy      546 CAACACGGTTGTGTCCTGCCTTGTGTTTCGTGCTGGGGATCATCGGGAATCCACACTTCT 605
          |||
Db      596 CAACACGGTTGTGTCCTGCCTTGTGTTTCGTGCTGGGGATCATCGGGAATCCACACTTCT 655

Qy      606 GAGAATTATCTACAAGAACAAGTGCATGCGAAACGGTCCCAATATCTTGATCGCCAGCTT 665
          |||
Db      656 GAGAATTATCTACAAGAACAAGTGCATGCGAAACGGTCCCAATATCTTGATCGCCAGCTT 715

Qy      666 GGCTCTGGGAGACCTGCTGCACATCGTCATTGACATCCCTATCAATGTCTACAAGCTGCT 725
          |||
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|    |      |  |      |
|----|------|--|------|
| Db | 716  | GGCTCTGGGAGACCTGCTGCACATCGTCATTGACATCCCTATCAATGTCTACAAGCTGCT   | 775  |
| Qy | 726  | GGCAGAGGACTGGCCATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTCATACAGAAAGC   | 785  |
|    |      |  |      |
| Db | 776  | GGCAGAGGACTGGCCATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTCATACAGAAAGC   | 835  |
| Qy | 786  | CTCCGTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATATCGAGCTGT   | 845  |
|    |      |  |      |
| Db | 836  | CTCCGTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATATCGAGCTGT   | 895  |
| Qy | 846  | TGCTTCTTGGAGTAGAATTAAAGGAATTGGGGTTCAAAATGGACAGCAGTAGAAATTGT    | 905  |
|    |      |  |      |
| Db | 896  | TGCTTCTTGGAGTAGAATTAAAGGAATTGGGGTTCAAAATGGACAGCAGTAGAAATTGT    | 955  |
| Qy | 906  | TTTGATTTGGGTGGTCTCTGTGGTTCTGGCTGTCCCTGAAGCCATAGGTTTGTATATAAT   | 965  |
|    |      |  |      |
| Db | 956  | TTTGATTTGGGTGGTCTCTGTGGTTCTGGCTGTCCCTGAAGCCATAGGTTTGTATATAAT   | 1015 |
| Qy | 966  | TACGATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTTCAGAAGAC   | 1025 |
|    |      |  |      |
| Db | 1016 | TACGATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTTCAGAAGAC   | 1075 |
| Qy | 1026 | AGCTTTTCATGCAGTTTTTACAAGACAGCAAAGATTGGTGGCTGTTTCAGTTTCTATTTCTG | 1085 |
|    |      |  |      |
| Db | 1076 | AGCTTTTCATGCAGTTTTTACAAGACAGCAAAGATTGGTGGCTGTTTCAGTTTCTATTTCTG | 1135 |
| Qy | 1086 | CTTGCCATTGGCCATCACTGCATTTTTTTTATACACTAATGACCTGTGAAATGTTGAGAAA  | 1145 |
|    |      |  |      |
| Db | 1136 | CTTGCCATTGGCCATCACTGCATTTTTTTTATACACTAATGACCTGTGAAATGTTGAGAAA  | 1195 |
| Qy | 1146 | GAAAAGTGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAAGTGGCCAA   | 1205 |
|    |      |  |      |
| Db | 1196 | GAAAAGTGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAAGTGGCCAA   | 1255 |
| Qy | 1206 | AACCGTCTTTTGCCTGGTCCTTGTCTTTGCCCTCTGCTGGCTTCCCCTTCACCTCAGCAG   | 1265 |
|    |      |  |      |
| Db | 1256 | AACCGTCTTTTGCCTGGTCCTTGTCTTTGCCCTCTGCTGGCTTCCCCTTCACCTCAGCAG   | 1315 |
| Qy | 1266 | GATTCTGAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGAACCTTTTGAGCTT  | 1325 |
|    |      |  |      |
| Db | 1316 | GATTCTGAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGAACCTTTTGAGCTT  | 1375 |
| Qy | 1326 | TCTGTTGGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCCTGCATTAACCC   | 1385 |
|    |      |  |      |
| Db | 1376 | TCTGTTGGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCCTGCATTAACCC   | 1435 |
| Qy | 1386 | AATTGCTCTGTATTTGGTGAGCAAAAGATTCAAAAACCTGCTTTAAGTCATGCTTATGCTG  | 1445 |
|    |      |  |      |
| Db | 1436 | AATTGCTCTGTATTTGGTGAGCAAAAGATTCAAAAACCTGCTTTAAGTCATGCTTATGCTG  | 1495 |
| Qy | 1446 | CTGGTGCCAGTCATTTGAAGAAAAACAGTCCTTGGAGGAAAAGCAGTCGTGCTTAAAGTT   | 1505 |
|    |      |  |      |
| Db | 1496 | CTGGTGCCAGTCATTTGAAGAAAAACAGTCCTTGGAGGAAAAGCAGTCGTGCTTAAAGTT   | 1555 |
| Qy | 1506 | CAAAGCTAATGATCACGGATATGACAACTTCCGTTCCAGTAATAAATACAGCTCATCTTG   | 1565 |
|    |      |  |      |
| Db | 1556 | CAAAGCTAATGATCACGGATATGACAACTTCCGTTCCAGTAATAAATACAGCTCATCTTG   | 1615 |

Qy 1566 AAAGAAGAA 1574  
|||||||  
Db 1616 AAAGAAGAA 1624

RESULT 13

US-09-826-509-496

; Sequence 496, Application US/09826509

; Publication No. US20030204073A1

; GENERAL INFORMATION:

; APPLICANT: Lehmann-Bruinsma, Karin

; APPLICANT: Liaw, Chen W.

; APPLICANT: Lin, I-Lin

; TITLE OF INVENTION: No. US20030204073A1-Endogenous, Constitutively Activated  
Known G

; TITLE OF INVENTION: Protein-Coupled Receptors

; FILE REFERENCE: AREN-207

; CURRENT APPLICATION NUMBER: US/09/826,509

; CURRENT FILING DATE: 2001-04-05

; PRIOR APPLICATION NUMBER: 60/195,747

; PRIOR FILING DATE: 2000-04-07

; PRIOR APPLICATION NUMBER: 09/170,496

; PRIOR FILING DATE: 1998-10-13

; NUMBER OF SEQ ID NOS: 589

; SOFTWARE: PatentIn Version 2.1

; SEQ ID NO 496

; LENGTH: 1329

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-826-509-496

Query Match 30.8%; Score 1322.6; DB 11; Length 1329;

Best Local Similarity 99.7%; Pred. No. 3.3e-261;

Matches 1325; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 238 ATGCAGCCGCCTCCAAGTCTGTGCGGACGCGCCCTGGTTGCGCTGGTTCTTGCCTGCGGC 297  
|||||||

Db 1 ATGCAGCCGCCTCCAAGTCTGTGCGGACGCGCCCTGGTTGCGCTGGTTCTTGCCTGCGGC 60

Qy 298 CTGTCGCGGATCTGGGGAGAGGAGAGAGGCTTCCCGCCTGACAGGGCCACTCCGCTTTTG 357  
|||||||

Db 61 CTGTCGCGGATCTGGGGAGAGGAGAGAGGCTTCCCGCCGACAGGGCCACTCCGCTTTTG 120

Qy 358 CAAACCGCAGAGATAATGACGCCACCCACTAAGACCTTATGGCCCAAGGGTTCCAACGCC 417  
|||||||

Db 121 CAAACCGCAGAGATAATGACGCCACCCACTAAGACCTTATGGCCCAAGGGTTCCAACGCC 180

Qy 418 AGTCTGGCGCGGTCGTTGGCACCTGCGGAGGTGCCTAAAGGAGACAGGACGGCAGGATCT 477  
|||||||

Db 181 AGTCTGGCGCGGTCGTTGGCACCTGCGGAGGTGCCTAAAGGAGACAGGACGGCAGGATCT 240

Qy 478 CCGCCACGCACCATCTCCCTCCCCCGTGCCAAGGACCCATCGAGATCAAGGAGACTTTC 537  
|||||||

Db 241 CCGCCACGCACCATCTCCCTCCCCCGTGCCAAGGACCCATCGAGATCAAGGAGACTTTC 300

Qy 538 AAATACATCAACACGGTTGTGTCTGCCTTGTGTTCTGTGCTGGGGATCATCGGGAACCTCC 597

|    |      |  |      |
|----|------|--|------|
| Db | 301  | <br>AAATACATCAACACGGTTGTGTCTGCCTTGTGTTTCGTGCTGGGGATCATCGGGAACCTCC  | 360  |
| Qy | 598  | ACACTTCTGAGAATTATCTACAAGAACAAGTGCATGCGAAACGGTCCCAATATCTTGATC       | 657  |
| Db | 361  | <br>ACACTTCTGAGAATTATCTACAAGAACAAGTGCATGCGAAACGGTCCCAATATCTTGATC   | 420  |
| Qy | 658  | GCCAGCTTGGCTCTGGGAGACCTGCTGCACATCGTCATTGACATCCCTATCAATGTCTAC       | 717  |
| Db | 421  | <br>GCCAGCTTGGCTCTGGGAGACCTGCTGCACATCGTCATTGACATCCCTATCAATGTCTAC   | 480  |
| Qy | 718  | AAGCTGCTGGCAGAGGACTGGCCATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTCATA       | 777  |
| Db | 481  | <br>AAGCTGCTGGCAGAGGACTGGCCATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTCATA   | 540  |
| Qy | 778  | CAGAAAGCCTCCGTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATAT       | 837  |
| Db | 541  | <br>CAGAAAGCCTCCGTGGGAATCACTGTGCTGAGTCTATGTGCTCTGAGTATTGACAGATAT   | 600  |
| Qy | 838  | CGAGCTGTTGCTTCTTGGAGTAGAATTAAGGAATTGGGGTTCCAAAATGGACAGCAGTA        | 897  |
| Db | 601  | <br>CGAGCTGTTGCTTCTTGGAGTAGAATTAAGGAATTGGGGTTCCAAAATGGACAGCAGTA    | 660  |
| Qy | 898  | GAAATTGTTTTGATTTGGGTGGTCTCTGTGGTTCTGGCTGTCCCTGAAGCCATAGGTTTT       | 957  |
| Db | 661  | <br>GAAATTGTTTTGATTTGGGTGGTCTCTGTGGTTCTGGCTGTCCCTGAAGCCATAGGTTTT   | 720  |
| Qy | 958  | GATATAATTACGATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTT       | 1017 |
| Db | 721  | <br>GATATAATTACGATGGACTACAAAGGAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTT   | 780  |
| Qy | 1018 | CAGAAGACAGCTTTCATGCAGTTTTTACAAGACAGCAAAAGATTGGTGGCTGTTTCAGTTTC     | 1077 |
| Db | 781  | <br>CAGAAGACAGCTTTCATGCAGTTTTTACAAGACAGCAAAAGATTGGTGGCTGTTTCAGTTTC | 840  |
| Qy | 1078 | TATTTCTGCTTGCCATTGGCCATCACTGCATTTTTTTTATACACTAATGACCTGTGAAATG      | 1137 |
| Db | 841  | <br>TATTTCTGCTTGCCATTGGCCATCACTGCATTTTTTTTATACACTAATGACCTGTGAAATG  | 900  |
| Qy | 1138 | TTGAGAAAGAAAAGTGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAA       | 1197 |
| Db | 901  | <br>TTGAGAAAGAAAAGTGGCATGCAGATTGCTTTAAATGATCACCTAAAGCAGAGACGGGAA   | 960  |
| Qy | 1198 | GTGGCCAAAACCGTCTTTTGCCTGGTCCTTGTCTTTGCCCTCTGCTGGCTTCCCCTTCAC       | 1257 |
| Db | 961  | <br>GTGAAGAAAACCGTCTTTTGCCTGGTCCTTGTCTTTGCCCTCTGCTGGCTTCCCCTTCAC   | 1020 |
| Qy | 1258 | CTCAGCAGGATTCTGAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGAACTT       | 1317 |
| Db | 1021 | <br>CTCAGCAGGATTCTGAAGCTCACTCTTTATAATCAGAATGATCCCAATAGATGTGAACTT   | 1080 |
| Qy | 1318 | TTGAGCTTTCTGTTGGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCCTGC       | 1377 |
| Db | 1081 | <br>TTGAGCTTTCTGTTGGTATTGGACTATATTGGTATCAACATGGCTTCACTGAATTCCTGC   | 1140 |
| Qy | 1378 | ATTAACCCAATTGCTCTGTATTTGGTGAGCAAAAGATTCAAAAAGTCTTTAAGTCATGC        | 1437 |
|    |      |  |      |

|    |     |   |     |
|----|-----|---|-----|
| Qy | 203 | GCGGCCACCGGACGCCTTCTGGAGCAGGTAGCAGCATGCAGCCGCCTCCAAGTCTGTGCG  | 262 |
|    |     |   |     |
| Db | 200 | GCGGCCACCGGACG-CTTCTGGAGCAGGTAGCAGCATGCAGCCGCCTCCAAGTCTGTGCG  | 258 |
| Qy | 263 | GACGCGCCCTGGTTGCGCTGGTTCTTGCCTGCGGCCTGTGCGGGATCTGGGGAGAGGAGA  | 322 |
|    |     |   |     |
| Db | 259 | GACGCGCCCTGGTTGCGCTGGTTCTTGCCTGCGGCCTGTGCGGGATCTGGGGAGAGGAGA  | 318 |
| Qy | 323 | GAGGCTTCCCGCCTGACAGGGCCACTCCGCTTTTGCAAACCGCAGAGATAATGACGCCAC  | 382 |
|    |     |   |     |
| Db | 319 | GAGGCTTCCCGCCCAGACAGGGCCACTCCGCTTTTGCAAACCGCAGAGATAATGACGCCAC | 378 |
| Qy | 383 | CCACTAAGACCTTATGGCCCAAGGGTTCCAACGCCAGTCTGGCGCGGTCTGTTGGCACCTG | 442 |
|    |     |   |     |
| Db | 379 | CCACTAAGACCTTATGGCCCAAGGGTTCCAACGCCAGTCTGGCGCGGTCTGTTGGCACCTG | 438 |
| Qy | 443 | CGGAGGTGCCTAAAGGAGACAGGACGGCAGGATCTCCGCCACGCACCATCTCCCCTCCCC  | 502 |
|    |     |   |     |

|    |      |  |      |
|----|------|--|------|
| Db | 439  | CGGAGGTGCCTAAAGGAGACAGGACGGCAGGATCTCCGCCACGCACCATCTCCCCTCCCC   | 498  |
| Qy | 503  | CGTGCCAAGGACCCATCGAGATCAAGGAGACTTTCAAATACATCAACACGGTTGTGTCCT   | 562  |
| Db | 499  | CGTGCCAAGGACCCATCGAGATCAAGGAGACTTTCAAATACATCAACACGGTTGTGTCCT   | 558  |
| Qy | 563  | GCCTTGTGTTTCGTGCTGGGGATCATCGGGAACCTCCACACTTCTGAGAATTATCTACAAGA | 622  |
| Db | 559  | GCCTTGTGTTTCGTGCTGGGGATCATCGGGAACCTCCACACTTCTGAGAATTATCTACAAGA | 618  |
| Qy | 623  | ACAAGTGCATGCGAAACGGTCCCAATATCTTGATCGCCAGCTTGGCTCTGGGAGACCTGC   | 682  |
| Db | 619  | ACAAGTGCATGCGAAACGGTCCCAATATCTTGATCGCCAGCTTGGCTCTGGGAGACCTGC   | 678  |
| Qy | 683  | TGCACATCGTCATTGACATCCCTATCAATGTCTACAAGCTGCTGGCAGAGGACTGGCCAT   | 742  |
| Db | 679  | TGCACATCGTCATTGACATCCCTATCAATGTCTACAAGCTGCTGGCAGAGGACTGGCCAT   | 738  |
| Qy | 743  | TTGGAGCTGAGATGTGTAAGCTGGTGCCTTTCATACAGAAAGCCTCCGTGGGAATCACTG   | 802  |
| Db | 739  | TTGGAGCTGAGATGTGTAAGCTGGTGCCTTTCATACAGAAAGCCTCCGTGGGAATCACTG   | 798  |
| Qy | 803  | TGCTGAGTCTATGTGCTCTGAGTATTGACAGATATCGAGCTGTTGCTTCTTGGAGTAGAA   | 862  |
| Db | 799  | TGCTGAGTCTATGTGCTCTGAGTATTGACAGATATCGAGCTGTTGCTTCTTGGAGTAGAA   | 858  |
| Qy | 863  | TTAAAGGAATTGGGGTTCCAAAATGGACAGCAGTAGAAATTGTTTGGATTGGGTGGTCT    | 922  |
| Db | 859  | TTAAAGGAATTGGGGTTCCAAAATGGACAGCAGTAGAAATTGTTTGGATTGGGTGGTCT    | 918  |
| Qy | 923  | CTGTGGTTCTGGCTGTCCCTGAAGCCATAGGTTTTGATATAATTACGATGGACTACAAAG   | 982  |
| Db | 919  | CTGTGGTTCTGGCTGTCCCTGAAGCCATAGGTTTTGATATAATTACGATGGACTACAAAG   | 978  |
| Qy | 983  | GAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTTCAGAAGACAGCTTTCATGCAGTTTT   | 1042 |
| Db | 979  | GAAGTTATCTGCGAATCTGCTTGCTTCATCCCGTTCAGAAGACAGCTTTCATGCAGTTTT   | 1038 |
| Qy | 1043 | ACAAGACAGCAAAAGATTGGTGGCTGTTTCAGTTTCTATTTCTGCTTGCCATTGGCCATCA  | 1102 |
| Db | 1039 | ACAAGACAGCAAAAGATTGGTGGCTGTTTCAGTTTCTATTTCTGCTTGCCATTGGCCATCA  | 1098 |
| Qy | 1103 | CTGCATTTTTTTTATACACTAATGACCTGTGAAATGTTGAGAAAAGAAAGTGGCATGCAGA  | 1162 |
| Db | 1099 | CTGCATTTTTTTTATACACTAATGACCTGTGAAATGTTGAGAAAAGAAAGTGGCATGCAGA  | 1158 |
| Qy | 1163 | TTGCTTTAAATGATCACCTAAAGCAGAGACGGGAAGTGGCCAAAACCGTCTTTTGCCTGG   | 1222 |
| Db | 1159 | TTGCTTTAAATGATCACCTAAAGCAGAGACGGGAAGTGGCCAAAACCGTCTTTTGCCTGG   | 1218 |
| Qy | 1223 | TCCTTGTCTTTGCCCTCTGCTGGCTTCCCTTCACCTCAGCAGGATTCTGAAGCTCACTC    | 1282 |
| Db | 1219 | TCCTTGTCTTTGCCCTCTGCTGGCTTCCCTTCACCTCAGCAGGATTCTGAAGCTCACTC    | 1278 |
| Qy | 1283 | TTTATAATCAGAATGATCCCAATAGATGTGAACTTTTGAGCTTTCTGTTGGTATTGGACT   | 1342 |
| Db | 1279 | TTTATAATCAGAATGATCCCAATAGATGTGAACTTTTGAGCTTTCTGTTGGTATTGGACT   | 1338 |



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Qy      1343 ATATTGGTATCAACATGGCTTCACTGAATTCCTGCATTAACCCAATTGCTCTGTATTTGG 1402
          |||
Db      1339 ATATTGGTATCAACATGGCTTCACTGAATTCCTGCATTAACCCAATTGCTCTGTATTTGG 1398

Qy      1403 TGAGCAAAGATTCAAAAAGTCTTTAAGTC 1433
          |||
Db      1399 TGAGCAAAGATTCAAAAAGTCTTTAAGGC 1429

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RESULT 15

US-09-778-927A-27

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; Sequence 27, Application US/09778927A
; Patent No. US20020068342A1
; GENERAL INFORMATION:
; APPLICANT: KHOSRAVI, Rami et al.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID AND AMINO ACID SEQUENCES AND NOVEL
; TITLE OF INVENTION: VARIANTS OF ALTERNATIVE SPLICING
; FILE REFERENCE: 2786-0160P
; CURRENT APPLICATION NUMBER: US/09/778,927A
; CURRENT FILING DATE: 2001-02-08
; PRIOR APPLICATION NUMBER: IL 134453
; PRIOR FILING DATE: 2000-02-09
; PRIOR APPLICATION NUMBER: IL135341
; PRIOR FILING DATE: 2000-03-29
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 27
; LENGTH: 800
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(800 )
; OTHER INFORMATION: n = a,c,g,t any unknown or other
US-09-778-927A-27

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Query Match          17.7%; Score 763.2; DB 9; Length 800;
Best Local Similarity 98.3%; Pred. No. 2e-146;
Matches 771; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

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Qy      1 GAGACATTCCGGTGGGGGACTCTGGCCAGCCCAGCAACGTGGATCCTGAGAGCACTCCC 60
          |||
Db      1 GAGACATTCCGGTGGGGGACTCTGGCCAGCCCAGCAACGTGGATCCTGAGAGCACTCCC 60

Qy      61 AGGTAGGCATTTGCCCCGGTGGGACGCCTTGCCAGAGCAGTGTGTGGCAGGCCCCCGTGG 120
          |||
Db      61 AGGTAGGCATTTGCCCCGGTGGGACGCCTTGCCAGAGCAGTGTGTGGCAGGCCCCCGTGG 120

Qy      121 AGGATCAACACAGTGGCTGAACACTGGGAAGGAAGTGGTACTTGGAGTCTGGACATCTGA 180
          |||
Db      121 AGGATCAACACAGTGGCTGAACACTGGGAAGGAAGTGGTACTTGGAGTCTGGACATCTGA 180

Qy      181 AACTTGGCTCTGAAACTGCGGAGCGGCCACCGGACGCCTTCTGGAGCAGGTAGCAGCATG 240
          |||
Db      181 AACTTGGCTCTGAAACTGCGGAGCGGCCACCGGACGCCTTCTGGAGCAGGTAGCAGCATG 240

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|    |     |  |     |
|----|-----|--|-----|
| Qy | 241 | CAGCCGCCTCCAAGTCTGTGCGGACGCGCCCTG                            | 300 |
|    |     |  |     |
| Db | 241 | CAGCCGCCTCCAAGTCTGTGCGGACGCGCCCTG                            | 300 |
| Qy | 301 | TCGCGGATCTGGGGAGAGGAGAGAGGCTTCCCGCCTGACAGGGCCACTCCGCTTTTGCAA | 360 |
|    |     |  |     |
| Db | 301 | TCGCGGATCTGGGGAGAGGAGAGAGGCTTCCCGCCTGACAGGGCCACTCCGCTTTTGCAA | 360 |
| Qy | 361 | ACCGCAGAGATAATGACGCCACCCACTAAGACCTTATGGCCCAAGGGTTCCAACGCCAGT | 420 |
|    |     |  |     |
| Db | 361 | ACCGCAGAGATAATGACGCCACCCACTAAGACCTTATGGCCCAAGGGTTCCAACGCCAGT | 420 |
| Qy | 421 | CTGGCGCGGTCGTTGGCACCTGCGGAGGTGCCTAAAGGAGACAGGACGGCAGGATCTCCG | 480 |
|    |     |  |     |
| Db | 421 | CTGGCGCGGTCGTTGGCACCTGCGGAGGTGCCTAAAGGAGACAGGACGGCAGGATCTCCG | 480 |
| Qy | 481 | CCACGCACCATCTCCCCTCCCCCGTGCCAAGGACCCATCGAGATCAAGGAGACTTTCAA  | 540 |
|    |     |  |     |
| Db | 481 | CCACGCACCATCTCCCCTCCCCCGTGCCAAGGACCCATCGAGATCAAGGAGACTTTCAA  | 540 |
| Qy | 541 | TACATCAACACGGTTGTGTCCTGCCTTGTGTTTCGTGCTGGGGATCATCGGGA        | 600 |
|    |     |  |     |
| Db | 541 | TACATCAACACGGTTGTGTCCTGCCTTGTGTTTCGTGCTGGGGATCATCGGGA        | 600 |
| Qy | 601 | CTTCTGAGAATTATCTACAAGAACAAGTGCATGCGAAACGGTCCCAATATCTTGATCGCC | 660 |
|    |     |  |     |
| Db | 601 | CTTCTGAGAATTATCTACAAGAACAAGTGCATGCGAAACGGTCCCAATATCTTGATCGCC | 660 |
| Qy | 661 | AGCTTGGCTCTGGGAGACCTGCTGCACATCGTCATTGACATCCCTATCAATGTCTACAAG | 720 |
|    |     |  |     |
| Db | 661 | AGCTTGGCTCTGGGAGACCTGCTGCACATCGTCATTGACATCCCTATCAATGTCTACAAG | 720 |
| Qy | 721 | CTGCTGGCAGAGGACTGGCCATTTGGAGCTGAGATGTGTAAGCTGGTGCCTTTCATACAG | 780 |
|    |     |  |     |
| Db | 721 | CTGCTGGCAGAGGACTGGCCATTTGGAGCTGAGATGTGCCAGGTAGGAGCGTTCACCCAC | 780 |
| Qy | 781 | AAAG 784   |     |
|    |     |  |     |
| Db | 781 | CCAG 784   |     |

Search completed: May 15, 2004, 00:12:39  
 Job time : 1645.24 secs